

Db 241 GGAGCGATGATTTCAACAGTCTCTGATCTCAAGCCCTTATGAGACCTGATTAACGGG 300
Qy 301 AACGTGCTGACAGACTTATGGGGAAGTAAGATATATATGTTCAATTTCAAGTGGCG 360
Db 301 AACGTGCTGACAGACTTATGGGGAAGTAAGATATATATGTTCAATTTCAAGTGGCG 360
Qy 361 AAGATGAGGCAATGATCTCTTCAACGACATTTTGTGTCGATGACGTTGAACGTTGG 420
Db 361 AAGATGAGGCAATGATCTCTTCAACGACATTTTGTGTCGATGACGTTGAACGTTGG 420
Qy 421 GAATGACAGGCAATTTCAAAAAAGATAAAAAGGCACTGATTAATTTAAAGCTTAT 480
Db 421 GAATGACAGGCAATTTCAAAAAAGATAAAAAGGCACTGATTAATTTAAAGCTTAT 480
Qy 481 GGAACGAAAAAGGATGATGAGGAGGAGAGTGTGATGACCTCAACTCAACG 540
Db 481 GGAACGAAAAAGGATGATGAGGAGGAGAGTGTGATGACCTCAACTCAACG 540
Qy 541 CTTTGGGCTTCGAACCTCCGACTACAGGATACACTGTCTTCAGATGTTTGAACG 600
Db 541 CTTTGGGCTTCGAACCTCCGACTACAGGATACACTGTCTTCAGATGTTTGAACG 600
Qy 601 TTTTAAAGCAAAATGCGCAATTTTCTCACTGCACTGCAATTTCAATGAGGAGAGA 660
Db 601 TTTTAAAGCAAAATGCGCAATTTTCTCACTGCACTGCAATTTCAATGAGGAGAGA 660
Qy 661 TTAAAGGCGTCTCAATTTATTCAGGCGCTCCCTGTCCTTCCGGCGAGAAAGTTA 720
Db 661 TTAAAGGCGTCTCAATTTATTCAGGCGCTCCCTGTCCTTCCGGCGAGAAAGTTA 720
Qy 721 TGAATGAGCTGAAAAATTTCTCTCAAAATTTTAAAGAAAGCCCTGCAAAAGTTCCG 780
Db 721 TGAATGAGCTGAAAAATTTCTCTCAAAATTTTAAAGAAAGCCCTGCAAAAGTTCCG 780
Qy 781 CATCGATATCTTTCACTAGATAGCGGACGTTCTGGAATATGTTGGCAACCAATT 840
Db 781 CATCGATATCTTTCACTAGATAGCGGACGTTCTGGAATATGTTGGCAACCAATT 840
Qy 841 TGCCACGCTTGAAGCAAGAAATTAATGACGTCCTTGGACAGACACTTAAATTAAGA 900
Db 841 TGCCACGCTTGAAGCAAGAAATTAATGACGTCCTTGGACAGACACTTAAATTAAGA 900
Qy 901 AAGCGCGCGAAAACTTTAGAACTTGGCAAAATTTGGAATTCATATATTTCACTCTTAC 960
Db 901 AAGCGCGCGAAAACTTTAGAACTTGGCAAAATTTGGAATTCATATATTTCACTCTTAC 960
Qy 961 AAGAGAGAGATTAATAATGTTTCCGATGCTGAAAGACCTCGGCTCTCTGAGATGA 1020
Db 961 AAGAGAGAGATTAATAATGTTTCCGATGCTGAAAGACCTCGGCTCTCTGAGATGA 1020
Qy 1021 CCTTCTGCGACATGTCAGCTGGAATCTACGCTTGGCTTCCGATTTGCGTTGCGAGC 1080
Db 1021 CCTTCTGCGACATGTCAGCTGGAATCTACGCTTGGCTTCCGATTTGCGTTGCGAGC 1080
Qy 1081 CTCAACATTTGATTCAGACTCGGCTTTACCAAGATGCTCATTTATCAACGTTCTTG 1140
Db 1081 CTCAACATTTGATTCAGACTCGGCTTTACCAAGATGCTCATTTATCAACGTTCTTG 1140
Qy 1141 ACAGCATATAGAGCTTTCCGACACAGTACAGAGCTGGAATCTTTCACACGCAATTA 1200
Db 1141 ACAGCATATAGAGCTTTCCGACACAGTACAGAGCTGGAATCTTTCACACGCAATTA 1200
Qy 1201 AAGATGAGGATCCGTCGCGAGTGAATGCTTCCAGATATATGAAAGAGATGATGA 1260
Db 1201 AAGATGAGGATCCGTCGCGAGTGAATGCTTCCAGATATATGAAAGAGATGATGA 1260
Qy 1261 TGGTTTATCACACCGTAAATGAATGCTCGATGAGGAGAGGCTCAAGCCGAGACA 1320
Db 1261 TGGTTTATCACACCGTAAATGAATGCTCGATGAGGAGAGGCTCAAGCCGAGACA 1320
Qy 1321 CGCTCAACTATAGCAAGAGCTTGGAGGCGCTGTTTGAATTCGATATGACAGAAAGAA 1380
Db 1321 CGCTCAACTATAGCAAGAGCTTGGAGGCGCTGTTTGAATTCGATATGACAGAAAGAA 1380

Qy 1381 AGTGAATGCGCACTGTTATCTGCCACGTTTGAGAGATCTTGGAGAACGGGAAAGTTA 1440
Db 1381 AGTGAATGCGCACTGTTATCTGCCACGTTTGAGAGATCTTGGAGAACGGGAAAGTTA 1440
Qy 1441 GCTCTGCTCATCCGCCATGCGCACTGCAACCCATTCTGAAGTTGACATCCCTTCTG 1500
Db 1441 GCTCTGCTCATCCGCCATGCGCACTGCAACCCATTCTGAAGTTGACATCCCTTCTG 1500
Qy 1501 ATCAATCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGACTTATATGATCAATCC 1560
Db 1501 ATCAATCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGACTTATATGATCAATCC 1560
Qy 1561 TTGATTAAGAGGTGATACAGGTGCTACAGGAGAGAGGCGCCCTGAGAGAAAGCTT 1620
Db 1561 TTGATTAAGAGGTGATACAGGTGCTACAGGAGAGAGGCGCCCTGAGAGAAAGCTT 1620
Qy 1621 CGTCTATATCATGTTATATGAAAGCAATCTGATTAACGGAAGAAATGCTTGAATC 1680
Db 1621 CGTCTATATCATGTTATATGAAAGCAATCTGATTAACGGAAGAAATGCTTGAATC 1680
Qy 1681 ATATCACTTCATGATGAGGAGCGCATCGAAGATTAATTTGGAGCTTCTAAAGCAG 1740
Db 1681 ATATCACTTCATGATGAGGAGCGCAATCGAAGATTAATTTGGAGCTTCTAAAGCAG 1740
Qy 1741 ACAACAGTGTCCCATCACTTCCAAAGAAACAGCAATTTGACATAGCAGAGTTTGGCATC 1800
Db 1741 ACAACAGTGTCCCATCACTTCCAAAGAAACAGCAATTTGACATAGCAGAGTTTGGCATC 1800
Qy 1801 ACGGTTACAGATACCGAGATGCTACAGCTTTGCCAAGTTGAAACAAAGATTTGGTGA 1860
Db 1801 ACGGTTACAGATACCGAGATGCTACAGCTTTGCCAAGTTGAAACAAAGATTTGGTGA 1860
Qy 1861 TGAGAACGTCATTAACCTGTGCTTGTATACACACTTCAATCTCAATATTAATCTG 1920
Db 1861 TGAGAACGTCATTAACCTGTGCTTGTATACACACTTCAATCTCAATATTAATCTG 1920
Qy 1921 AGGATGCGCTATGAGGTATATAGGCAACAAATTAATATGTTGTGTTAGTAAAGC 1980
Db 1921 AGGATGCGCTATGAGGTATATAGGCAACAAATTAATATGTTGTGTTAGTAAAGC 1980
Qy 1981 TGTATTTATGAAAAAATTTTAAAAAATTTTAAAAA 2013
Db 1981 TGTATTTATGAAAAAATTTTAAAAAATTTTAAAAA 2013

RESULT 2
US-09-360-545-3
Sequence 3, Application US/09360545
Patent No. 6429014
GENERAL INFORMATION:
APPLICANT: Croceau, Rodney B
APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
APPLICANT: Phillips, Michael A
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REFERENCE: wsl13885
CURRENT APPLICATION NUMBER: US/09/360,545
EARLIER FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6)..(1892)
OTHER INFORMATION: Clone Ag3.18 encoding pinene synthase

US-09-360-545-3

Query Match	64.9%	Score 1306.8;	DB 4;	Length 2018;
Best Local Similarity	81.0%;	Pred. No. 0;		
Matches 1595;	Conservative	0;	Mismatches 342;	Indels 33; Gaps 5

QY	68	CAGGTGCGCTCAGTGGTCTTCTCATGAGATTAAGGCTCTCGGTAAACAATCCCAACT	127
Db	53	CAAAATCGTGAATGAGTTTACCCAGACCTTAAAGGCTCTCTCTAAACAATTCACGCTT	112
QY	128	TGGAATCTGCAGGCGCGGGGAAATCCGTGGCGCATTCATTAACATGTGTGTGACAAGGT	187
Db	113	AGGAATAGATAGGCGAAGGGAATATCATCTCTTCATCAGCAATGAGCTCTACACCGT	172
QY	188	CGCATCTAAGTATTTCTGTACAGAGACGCGTGGCAATATCATTTCCAACTGTGGACGA	247
Db	173	TGTAAACCGATATGGTGTACAAAGACGATGGCGCATTTCCATTCAACTCTGGGACGA	232
QY	248	TGATTTCAATACAGTCTCGATCTCAAGCCCTTAATGAGACACCTGATTTACCGGGAAACGTG	307
Db	233	TGATGTCAATACAGTCT---TTACCAACGCGTTATAGAAAATCGTACCTGGACGTGC	289
QY	308	TGACAGACTTATTTGGGGAAGTAAAGATATATGTTCATATTTCAATGCGCGTGAAGATG	367
Db	290	TGABAATCTAATCGGGGAAGTAAAG---AACTGTTCATTTGATGTCAATTAAGAAGATG	346
QY	368	AG-----GCAATGATCTCTCTTCAACGACTTTTGTGTGTGATGACGTTGA	412
Db	347	AGAGTTAATGAGTCCGCTCAATGATCTCATTCACGCTTTGGATTTGTGACACGCTTGA	406
QY	413	ACGTTTGGGAATCGACAGCAATTCCTAAAAAAGATTAATAAAACGGACCTGATATGTTAA	472
Db	407	ACGTTTGGGGAATCCATTAACATTTCTAAAGATGAGATTAATCGCGCTTGATTAATGTTTA	466
QY	473	CAGTTATTTGGAACGAAAAAGGCAATTGATGTGGGAGGAGAGTGTGTGACTGACCTCAA	532
Db	467	CAGTTATTTGGGCGGAAAATGGCATTCGATGCGGAGGGAGAGTGTGTGTTACTGATCTGAA	526
QY	533	CTCAACCGCTTTGGGGCTTTGCAACTCTCCGACTACAGGATACACTGTGTCTTCAGATGT	592
Db	527	CTCAACTGCGTTGGGGCTTGCAAACCTTACGACTACACGGAATCCGAGTCTTTCAGATGT	586
QY	593	TTTTAAACGTTTTTAAAGCAAAAATGGGCAATTTTCTCCACATGCGCAATATTCAGATAGA	652
Db	587	TTTTAAAGCTTTCAAGAGCCAAATATGGGCAATTTTCTCTGCTCTGAAAAATATTCACACAGA	646
QY	653	GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTCGTGGCTTTCCCGGCGA	712
Db	647	TGAAGAGATCAGAGGCGTTCTGAATTTATTCGGGCGCTCCCTCATTTGCTTCCAGGGGA	706
QY	713	GAAAGTTATGATGTAAGCTGAAGCAACTTCTCTACAAATATTTTAAGAGAAGCCCTGCAAAA	772
Db	707	GAAAATTAATGATGAGCTGAATTCCTTCTTACCAAAATATTTTAAAGAAAGCCCTGCAAAA	766
QY	773	GATTCGCGGCAATCCAGTATACCTTTCTCACTAGAGATAGGGACGTTCTGAAATATGTTGGCA	832
Db	767	GATTCGCGTCTCAAGT---CTTCCGAGAGATTCGGGACGTTTGGAAATATGTTGGCA	823
QY	833	CACCAATTTGCGACGCTTGGGAAGCAAGGAATTAATGACGTCCTTGGACACACATPA	892
Db	824	CACATTAATTTGCGCGGATTTGGAAGCAAGGAATTAATCAATCAAGCTTTGGACAGGACATGA	883
QY	893	AAATPAAGAGC-----CGCGGAATCTTTTAAACCTTGCAAAATTTGGAATTTCAA	943
Db	884	GAACACGAGTCATATGTGAAGAGCAAAAACCTTTTAAACCTTCGCAAAATTTGAAGTTCAA	943
QY	944	TATATTTCACTCTTACAAAGAGAGAGATTAACATGTTTTCCGATGGTGAAGACATC	1003
Db	944	CATCTTTCAATCTTTACAAAAGAGGAGATTTGAAGATCTGGTCAATGTTGAAGGAATC	1003
QY	1004	GGGTTCTCTGAGATGACCTTCTGTGCACTGTGTCACTGCGAATATCTACGCTTTGGCTTC	1063
Db	1004	GGGTTTTCTGAGATGACCTTCTGTGCGACATGTGTCACTGGAATATCTACATTTGGCTTC	1063

OY	1064	CTGCATTTGCGCTCAGAGCTCAAACTTTCGGAATTGACAGTGGCTTTTACCAAGATGTCGA	11233
Dp	1064	CTGCATTTGCGCTCAGAGCTCAAACTTTCGGAATTGACAGTGGCTTTTACCAAGATGTCGA	11222
OY	1124	TCCTTATCAGCGTTTCTTGACGACATGTACGACGCTCTTGGGCA CAGTACGACGCTGGAACT	11833
Dp	1124	TCCTTATCAGCGTTTCTTGACGATGTATGTACGACACTTGGGCA CAGTACGACGCTGGAACT	1183
OY	1184	CTTTCACACCGCAATTTAAAGATGGGATCCGTCCGCGATGGAAATGCTTCCAGATATAT	12434
Dp	1184	CTTTCACACCGCAATTTAAAGATGGGATCCGTCCGATGATTTGCCATTCAGATATAT	1243
OY	1244	GAAAGAGGTGTACATGATGGTTTATCAACCGGTAAATGAAATGGCTGAGTGGCAGAGAA	1303
Dp	1244	GAAAGAGGTGTACATGAGGTTTATCGACACCGTAAATGAAATGGCTGAGAGGCAGAGAA	130
OY	1304	GGCTCAAGGCGCGAAGACAGCTCAACTATGTACAAAGCAGGCTTGGAGGCGGTGTTGATTC	1363
Dp	1304	GGCTCAAGGCGCGAATATGCTCAATATGCTCGGGAAGCTTGGAGGCTTATATTTGATTC	136
OY	1364	GTATATGACGAGAACAAAGTGGATGCGCACTGTTATCTGCCACGTTTGAGAGTACTT	1422
Dp	1364	GTATATGACAAAGAACAAAGTGGATGCGCACTGTTACTCTGCCCTCTTTGATGATGACTTA	1422
OY	1424	GGAAAGCGGGAAGTTTAGCTCTGCTCATCCGCCATGGCACAATGGAAACCATTTGACGCTT	1483
Dp	1424	CGAATAATGGGAAGTTTAGCTGTGTGATCGATATCGCATTTGAAACCCATTTGACACAT	1483
OY	1484	GGAATCCCTCTTCTGATCATATCTCTCAAGGAAGTTGACTTCCCATCAAGCTTMAACGA	1543
Dp	1484	GGAATCCCTCTTCTGATCATATCTCTCAAGGAAGTTGACTTCCCATCAAGCTTMAACGA	1543
OY	1544	CTTGATATGTATATTCCTTGATTTAAAGGTGATPACAGGTGCTPACAAAGCAGACAGGGC	1603
Dp	1544	CTTGATATGTATATTCCTTGATTTAAAGGTGATPACAGGTGCTPACAAAGGCGCAGGGC	1603
OY	1604	CCGTGGAGGAAGAGCTTCTGCTATATCATGTTATATGAAAGACAACTCTGGATTTAACGA	1663
Dp	1604	TCGTGGAGGAAGAGCTTCTCTTATATATGTTATATGAAAGACAACTCTGGAGTTTACGA	1663
OY	1664	AGAGATGCTCTTATATCATATCACTTCATGATCAGGGAACGCAATCAGAGAAATTAATTTG	1722
Dp	1664	GGAGATGCTCTTATATCATATCAACGCGATGATCAGTACGTAATCAAGAGATTTAAATTTG	1722
OY	1724	GGAGCTTCTTAAAGCCAGACAA CAGTGTTCCTCATCACTTCCAAAGAACCGCATTTGACAT	1783
Dp	1724	GGAGCTTCTCAAAACAGACATCAATGTTCCTCATCTCGGCGAAGAAACATGCTTTTGAAT	1783
OY	1784	AAGCAGAGTTTGGATCAACGCTTACAGATACCGAGATGGCTACAGCTTTGCCAACCTTGA	1843
Dp	1784	CGCCAGAGCTTTCATTTACGGCTTCAAAATACCGAGAGCGCTACAGCGTTGCCAACCTTGA	1843
OY	1844	AACAAAGAGTTTGGTATGAGAACCGTCATTTGAACCTGTGCTTTGTAAACAACCTTCAA	1903
Dp	1844	AACCAAGAGTTTGGTATCAGAGAACCTTCCTTGAATCTGTGCTTTGTATGCAACAGCTCAA	1903
OY	1904	ATCTTACATATTTAACTGAGATGCGCTTATGGGTATATATGAGGCACAAAAATTAATAT	1963
Dp	1904	ATCTATGCGCTTATGCTATGTCGGGTAAATATATATGAGAGGTATGCGGTGATGTAGA	1963
OY	1964	GGTTGTGTTAGTAAGCTTATTTATGAAAAAATTTAAAAAATTTAAAAA 2013	
Dp	1964	GGATTAAGTTTGTATTAATTTAAATGTTGTAATTTAAAAAATTTAAAAA 2013	

RESULT 3
US-09-398-395A-19
; Sequence 19, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468771, Joseph P.

APPLICANT: Starke, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTBASE
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395A
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(1889)
OTHER INFORMATION: pinene synthase
US-09-398-395A-19

Query Match 64.9%; Score 1306.8; DB 4; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY 68 CAGTCGTCCTCAGTTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCACTCT 127
DB 53 CAAATCGTTGATCGATCTTACCCATGAGCTTACAGCTCTCTCTAGAACAAATCCCACTCT 112
QY 128 TGGATCTGCAGCGCGGGGAATCCGTGGCATTTCCATTAACATGRTTGAACAAGCT 187
DB 113 AGGATGAGTAGGCGAGGGAATCTATCACTCTTCAACAGCATGAGCTCTCAACCTGT 172
QY 188 CGCATCTACTGATCTGTACAGAGACGCGTGGCACTATCATTTCCAACTGTGGAGCA 247
DB 173 TGTAAACGATATGGTGTACGAAGACGATGGGCAATTCATTCACCTCTGGAGCA 232
QY 248 TGAATTCATACAGTCTGATCTCAAGCCCTTATGAGACACCTGATTACGGGAACGTGC 307
DB 233 TGAATGCTACAGTCTCT--TTACCAACGCTTATGAGAAAAATGTAACCTGAGCGTGC 289
QY 308 TGACAGACTTATTTGGGGAAGTAAAGATATATGTTCAATTTCAAGTGCCTGGAAGATG 367
DB 290 TGAAGAACTGATCGGGGAAGTAAAG--AACTGTTCAATTCGATGTATTAAGAAATG 346
QY 368 AG-----GCAATGATCTCTTCAACGACTTTTGTGATGATGAAGTGA 412
DB 347 AGAGTTAATGAGTCCGCTCAATGATCTCATTCACGCTTTGGATGTGCAAGCCTTGA 406
QY 413 ACCTTTGGGAATCGACAGGCAATTTCAAAAAAGATAAAAACGGACCTGCAATATGTTAA 472
DB 407 ACGTTTGGGGAATCATAGACATTTCAAAAGATGAATAAATCGGGCTGTGATTAAGTTTA 466
QY 473 CAGTTATTTGAACGAAAAAGCATTTGATTTGGGAGGAGAGTGTGATGACTGCA 532
DB 467 CAGTTATTTGGGCGCAAAATGGCATGCGATGCGGAGGAGAGTGTGTTACTGATCTAA 526
QY 533 CTCAACCGCTTTGGGCTTTCGAACCTTCGACTACACGAGATACATGTGTCTTCAGATGT 592
DB 527 CTCAACTGCGTTGGGGCTTTCGAACCCCTACGACTACACGAGATACCGGAGTCTTCAGATGT 586
QY 593 TTTGAACCTTTTAAAGCAAAAAATGGCAATTTTCTCCACTGCAATATTCAGATGA 652
DB 587 TTTTAAAGCTTTCAAAAGGCAAAATGGGAGTTCCTGCTCTGAAAAATATTCAGACGA 646
QY 653 GGGAGAGTTAGAGCGCTTCTCAATTTATTCAGGGGCTCCCTGCTGCTTTTCCGGGCA 712
DB 647 TGAAGAGATCAGAGCGCTTCTGAAATTTATTCGGGGCTCCCTCATATGCTTTTCCAG 706
QY 713 GAAAGTTATGAGATGAAGCTGAACATTCCTTACAAAATATTTAAGAGAAAGCCCTGCAAA 772

DB 707 GAAATATATGATGAGCTGAAAATCTTCTACCAAAATATTTAAAGAGCCCTGCAAAA 766
QY 773 GATTCGGCAATCCGATATCTTCACTAGAGATACGGGAGCTTCTGAAATATGTTGGCA 832
DB 767 GATTCGGCTCCCACT--CTTTCGCAAGATCGGGAAGCTTTTGGAAATATGTTGGCA 823
QY 833 CACCAATTTGCAAGCTTTGAGAGCAAGAAATTAATGAGACGTCTTTGAGACGACACTAA 892
DB 824 CACATATTTGCGGAGATTTGAGAGCAAGAAATTAATCAAGTCTTTGAGACGACACTGA 883
QY 893 AAATTAAGAACG-----CGCGAGAACTTTTGAACCTTTGCAAAATTTGAATTCAA 943
DB 884 GAACAGCAAGCATATGTGAAGAGCAAAAACTTTTGAACCTCCGCAAAATTTGAGTTCAA 943
QY 944 TATATTTCACTCCCTTAAGAGAGAGGTTAAACATGTTTCCGAGTGGAGAAAGCTC 1003
DB 944 CATCTTCAATCTTTACAAAAGAGGAGTTAAGAAAGTGTGCTGAGATGGAAGAAATC 1003
QY 1004 GGGTTCTCTGAGATGACCTTCTGTGCAATCTGACGTGGAATTAACGCTTTGGCTTC 1063
DB 1004 GGGTTTCTGAGATGACCTTCTGTGCAATCTGACGTGGAATTAACACTTTGGCTTC 1063
QY 1064 CTGCATTCGCTTGAGGCTTCAACATTCGATTCAGACTCGGCTTTGCCAAGACGTGTCA 1123
DB 1124 TCTTATACGCTTTTGAACGATGTAAGATTCGATTCAGACTCGGCTTTGCCAAGACGTGTCA 1123
QY 1184 CTTCACAGCGCAATTAAGAGATGAGATCGTCCGCGATGGAATGCTTCAGAAATATAT 1243
DB 1184 CTTCACAGCGCAATTAAGAGATGAGATCGTCCGCGATGGAATGCTTCAGAAATATAT 1243
QY 1244 GAAAGAGTGTACATGATGTTTATCAACCCGTAATGAATGCTGAGTGGCAGAGAA 1303
DB 1244 GAAAGAGTGTACATGATGTTTATCAACCCGTTTACGACCCGTAATGAATGCTGAGTGGCAGAGAA 1303
QY 1304 GGCCTAAGGCGGAGACACGCTCACTAATGCAAGACAGGCTTGGAGGCGTGTGATTC 1363
DB 1304 GGCCTAAGGCGGAGATACGCTCACTAATGCTCGGGAAGCTTGGAGGCTTATATGATTC 1363
QY 1364 GTATATGACAGAAACAAAGTGAATGCGCACTGTTATCTGCCAAGTTTGAAGATCTT 1423
DB 1364 GTATATGACAGAAACAAAGTGAATGCGCACTGTTATCTGCCAAGTTTGAAGATCTT 1423
QY 1424 GGAAGAGGGAAGTATGCTGCTCATTCGCCATGCGCACTGCAACCCATTTGAGAGTT 1483
DB 1424 GGAAGAGGGAAGTATGCTGCTCATTCGCCATGCGCACTGCAACCCATTTGAGACAT 1483
QY 1484 GGAATCCCTTTCTGATCAATCTCAAGGAAGTTGACTTCCATGGAAGCTCAATGA 1543
DB 1484 GGAATCCCTTTCTGATCAATCTCAAGGAAGTTGACTTCCATGGAAGCTCAATGA 1543
QY 1544 CTGTATATGATATCACTCTGATTAAGAGTGAATACAGGTGCTTCAAGGCGACAGGCG 1603
DB 1544 CTGTGATATGATATCACTCTGATTAAGAGTGAATACAGGCGGCTTCAAGGCGACAGGCG 1603
QY 1604 CCGTGGAGAAAGACTTCTGCTATATATGATTAATGAAGACAACTCTGATTAAGCA 1663
DB 1604 TCGTGGAGAAAGACTTCTCTATATATGATTAATGAAGACAACTCTGAGATACGA 1663
QY 1664 AGAAGATGCTCTGAATATATCACTTCATGATCAGGGAAGCAATTCAGAAATTAATTTG 1723
DB 1664 GGAAGATGCTCTGAATATATCACTTCATGATCAGGGAAGCAATTCAGAAATTAATTTG 1723
QY 1724 GGAAGATGCTCTGAATATATCACTTCATGATCAGGGAAGCAATTCAGAAATTAATTTG 1783
DB 1724 GGAAGATGCTCTGAATATATCACTTCATGATCAGGGAAGCAATTCAGAAATTAATTTG 1783
QY 1784 AAGCAGATTTGGCATCAGGTTACAGATACAGATGCGCTACAGCTTTGCCAAGCTTGA 1843

Accession	Sequence	Year
Db	CGCCAGACCTTCCATTACGGTACAATPACGAGACGGCTACACGCTTGCCAACTGTGA	1843
Db	1784 CGCCAGACCTTCCATTACGGTACAATPACGAGACGGCTACACGCTTGCCAACTGTGA	1843
Qy	1844 AACAAAGATTTGGTGATGAGAACCGTCATTGAACTCTGTCCTTTGTAAACAACACTTCAA	1903
Db	1844 AACAAAGATTTGGTGATGAGAACCGTCATTGAACTCTGTCCTTTGTAAACAACACTTCAA	1903
Qy	1904 ATCTACATATTTAACTGAGATGCCCTTATGGGTGATATATAGGGCACACMAAATTAATAT	1966
Db	1904 ATCTATGCCCTATGCTATGTGCGGTTAAATATATGTGGAAGGTGCGCGTTGGATGTAGA	1963
Qy	1964 GCTGTGTTAGTAAAGCTGTAATTATGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTT	2013
Db	1964 GGATTAAGTTGTATTAATTTAATAAAGTTGTATTTAATAAATTTTTTTTTTTTTTTTTT	2013

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RESULT 4
US-09-887-586A-19
: Sequence 19, Application US/09887586A
: Patent No. 6495354
: GENERAL INFORMATION:
: APPLICANT: Chappell, Joseph
: APPLICANT: No. 64953541, Joseph P.
: APPLICANT: Stark, Courtney M.
: APPLICANT: Manna, Kathleen R.
: TITLE OF INVENTION: SYNTHASS
: FILE REFERENCE: 07678-025001
: CURRENT APPLICATION NUMBER: US/09/887,586A
: CURRENT FILING DATE: 2001-06-22
: PRIOR APPLICATION NUMBER: 09/398,395
: PRIOR FILING DATE: 1999-09-17
: PRIOR APPLICATION NUMBER: 60/110,628
: PRIOR FILING DATE: 1999-04-22
: PRIOR APPLICATION NUMBER: 60/150,262
: PRIOR FILING DATE: 1999-08-23
: NUMBER OF SEQ ID NOS: 58
: SOFTWARE: Pastedq for Windows Version 3.0
: SEQ ID NO 19
: LENGTH: 2018
: TYPE: DNA
: ORGANISM: Abies grandis
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (6)...(1889)
: OTHER INFORMATION: pinene synthase
US-09-887-586A-19

```

Query Match	64.9%	Score 1306.8	DB 4	Length 2018
Best Local Similarity	81.0%	Pred. No. 0		
Matches 1595; Conservative	0	Mismatches 342	Indels 33	Gaps 5

QY	68	AAGGTGCGCTCAAGTCTTCTTCATGAGATTAAGGCTCCGGTAACAACTCCAACT	127
Db	53	CAATTCGTTGATCACTTCTTACCAGAGCTTAAGGCTCTCTTAAGAACATTCACGCTCT	112
QY	128	TGGAATCTGCAGGCCGGGAAAATCCGTCGCGCATTTCCATPAACATGTGTGGACAAGCGT	187
Db	113	AGGATGAGTAGGCGACGGGAAATCATCACTCTTCATCAGCAAGAGCTTACACACGT	172
QY	188	CGCATCTACGATTTCTGTACAGAGCGGGTGGGCAACATATCTTCCCAACTGTGGAGCA	247
Db	173	TGTAAACGATATGTGTATGACAGACGCAATGGGCAATTTCCATTCACACTTGGGAGCA	232
QY	248	TGATTTCTACAGTCTCGATCTCAAGGCTTATGAGACCACTGATTAACGGGAACGTGC	307
Db	233	TGATGCTCATACAGTCT--TTACCAACGGCTTATGAGAAAATGTAACCTGGACGCTGC	289
QY	308	TGACAGATTTATTTGGGGAAGTAAAGATATATATGTTCAATTCACGCTCGGAAGATGG	367
Db	290	TGAGAACTGATCGGGGAAGTAAAG--AACATGTTCAATTCGATGTCAATTAAGAAATGG	346
QY	368	AG-----GCATGATCTCTCTTCAACGACTTTTGTGTGTGATGACGTTGA	412
Db	347	AGAGTTATGATCGCTCAATGATCTATTTCAACGCTTTGGATTTGTGCAACGCTTTGA	406

OY	413	ACGTTGGGAATCGACAGGCACTTTCAAAAGAGATTAAGAAACGGCACTCGATTATGTTAA	472
Db	407	ACGTTGGGGATCCATATGACATTTCCAAAGATGAGATTAATAATCGGCGCTTGATTATGTTTA	466
OY	473	CAGTTATTTGGAACCAAAAAGGCATTGATGTGGAGGGAGAGAGTGTGACTGACCTTCA	532
Db	467	CAGTTATTTGGGGCCAAAATGGCATCGGATGGGAGGGAGAGTGTGTTA CTGATCTGAA	526
OY	533	CTCAACCGCCCTTGGGGCTTGGAACTCTCCCACTACAGGATATCACTGTCTTTCAAGATGT	592
Db	527	CTCAACCTGCGCTTGGGGCTTGGAACTTACACCTTACAGCTACAGGATATCCCGGTCTTCAAGATGT	586
OY	593	TTTGAACGTTTTTAAAGACAAAATATGGGCAATTTCTCCCACTGCCAATATTCAGATAGA	652
Db	587	TTTCAAAGCTTTGAAAGGCCAAAATGGGCAATTTCTCTGCTCTGAAAATATTCAGACAGA	646
OY	653	GGGAGAGATTGAGAGCGCTTCTCAATTTATTCAGGAGCTCCCTCGTCCGCTTTCCCGGCGA	712
Db	647	TGAAGAGATCAGTGGCGCTTCTGAAATTTATTCGGGCGCTCCCTCATTTGCTTTCCAGGGGA	706
OY	713	GAAAGTATATGGAATGAGACTGAAACATCTCTACAAAATTTTAAGAGAGCCCTGCAAAA	772
Db	707	GAAATATATGGAATGAGGCTGAAATCTTCTCTACAAAATTTTAAGAGAGCCCTGCAAAA	766
OY	773	GATTCGGGCAATCGAGTATTAATCTTCTCATTAGAGATACGGGAGCGTTCTGGAATATGTGTGGCA	832
Db	767	GATTCGGGCTCTCAAGT---CTTTGGCAGAGATCGGGGAGCGTTTGGAAATATGTGTGGCA	823
OY	833	CACCAATTTTGGCCAGCTTTGGAAGCAGAGAAATTATATGAGCGTCTTTGGACAGCACACTAA	892
Db	824	CACATATTTTGGCCGAGATTTGGAAGCAGAGAAATTATATCAATCTTTTGGACAGCACACTGA	883
OY	893	AAATATAGACGC-----CGCCGAGAACTTTTGAACCTTTCAAAATTTGAATTCAA	943
Db	884	GAAACAGAAATCTATGTGAAGAGCAAAAACCTTTAGAACTCGCBAATTTGAGACTTCA	943
OY	944	TATATTTCACTCTTACAGAGAGAGATTAAACATGTTTCCGATGTGGAAGACTC	1003
Db	944	CATCTTTCATATCTTACAAAAGAGGAGATTAGAAAGTCTGGTCAGATGTGGAAGAAATC	1003
OY	1004	GGGTTCTCCTGAGATGACCTTTCTGTGCAATCGTCAGTGGGAATACTAACGCTTTGGGCTTC	1063
Db	1004	GGGTTTCTCTGAGATGACCTTTCTGTGCAATCGTCAGTGGGAATACTAACCTTTGGGCTTC	1063
OY	1064	CTGCAATTCGCTTCAGGCTCAACATCTTGATTCAGACTCGGCTTTGACCAAGATGTCTCA	1123
Db	1064	CTGCAATTCGCTTCAGGCTCAACATCTTGATTCAGACTCGGCTTTGACCAAGAGCTGTCA	1123
OY	1124	TCTTATCACGGTTTGTGACGACATGTACGAGTCTTTGGGCAAGTAAACGAGCTGTGAACT	1183
Db	1124	TCTTATCACGGTTCTTGACGATATGTACGACACTTTGGGCAAGTAAACGAGCTGTGAACT	1183
OY	1184	CTTCACAGCGCAATTAAGAGATGGATCCGTCGCGATGGAAATGCTTCAGAAATATAT	1243
Db	1184	CTTCACAGCGCAATTAAGAGATGGATCCGTCCTCATATGATTTGCTTCCAGAAATATAT	1243
OY	1244	GAAAGAGGTGTACATGATGGTTTATCAACCTGTAATGAATGGCTCGAGTGCGAGAA	1303
Db	1244	GAAAGAGGTGTACATGATGGTTTATCAACCTGTAATGAATGGCTCGAGTGCGAGAA	1303
OY	1304	GGCTCAAGGCTTCAGACAGCTCAACTATGCAAGACAGGCTTTGGGAGGCGTATTGATTC	1363
Db	1304	GGCTCAAGGCTTCAGACAGCTCAACTATGCTCGGGAAGCTTTGGGAGGCGTATTGATTC	1363
OY	1364	GTATATGCAAGAGCAAAAGTGAATCGCACATGTTATCTGCCACGTTTGAAGAGTACTT	1423
Db	1364	GTATATGCAAGAGCAAAAGTGAATCGCACATGTTATCTGCCACGTTTGAAGAGTACTT	1423
OY	1424	GGAGAAACGGGAAGTTAGCTCTGTCTATCGGCCATGGGCACTGCAACCAATTCAGAGTT	1483
Db	1424	CGAAATATGGGAAGTTAGCTGTGTCTATCGCATATCGCAATTCGCAACCAATTCAGACAT	1483

QY	713	GAAAGTTATGAGTAGAGCTGAAACATTCTCTACAAAAATTTTAAAGAGAGCCCTTGCAAAA	772
Db	707	GAAATATTATGGAATGAGCTGAAATCTTCTTACCAAAATATTTAAAGAGAGCCCTGCAAAA	766
QY	773	GATTCGGGCAATCGATATACCTTTTACATAGAGATACGGGACGTTCTGGAAATATGTTGGCA	832
Db	767	GATTCGGGCTCTCCAGT---CTTTGCGAAGAGATGGGGAACCTTTTGGAAATATGTTGGCA	823
QY	833	CACCAATTTGGCCACGTTTGGAGCAAGAAATTAATGAGACGCTCTTGGACAGCACACTAA	892
Db	824	CACATATTTTGGCCGAGATTGGAGAGAGAAATTAATCAACAGTCTTTTGGACAGCACACTGA	883
QY	893	AAATAAGAACGC-----CGCGAGAACTTTTGAACCTTGCAAAATTTGAATTCAA	943
Db	884	GAAACACAGATCATATGTGAAGAGCAAAAACTTTTGAACCTCCCAAAATTTGAGTTCAA	943
QY	944	TATATTTCACTCCCTTAAGAGAGAGATTAAACATGTTTCCGATGGTGGAAAGCTC	1003
Db	944	CATCTTTCATCTTACAAAGAGGGAGTTGAAAGTCTGGTCAGATGGTGGAAAGATC	1003
QY	1004	GGGTTCTCTGAGATGACCTTCTGTGCACATCGTCAAGTGAATACTACGCTTTGGCTTC	1063
Db	1004	GGGTTTCTGAGATGACCTTCTGTGCACATCGTCAAGTGAATACTACGCTTTGGCTTC	1063
QY	1064	CTGCATTGCGTTCGAGCCTCAACATTTGGAATTCAGACTGGGCTTTACCAAGATGTCTCA	1123
Db	1064	CTGCATTGCGTTCGAGCCTCAACATTTGGAATTCAGACTGGGCTTTACCAAGATGTGTCA	1123
QY	1124	TCTTATACGGTCTTGAGCAACATGTAACGACGCTTGCGGACAGATAGACGAGCTGGAAC	1183
Db	1124	TCTTATACGGTCTTGAGCAATGTAAGACACCTTGCGGACAGATAGACGAGCTGGAAC	1183
QY	1184	CTTCACAGCGCAATTAATGAAGATGGATCCGTCGCGAGTGAATGCCCTTCAGAAATAT	1243
Db	1184	CTTCACAGCGCAATTAATGAAGATGGATCCGTCGAGTATGATTTGCCCTTCAGAAATATAT	1243
QY	1244	GAAAGAGGTGTCATGATGCTTTTATCACACCGTAAATGAAGATGCTGAGTGGCAGAGAA	1303
Db	1244	GAAAGAGGTGTCATTAACCGTTTACGACACCGTAAATGAAGATGCTGAGAGGCGAGAGAA	1303
QY	1304	GGCTCAAGGCCAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGGTGTTTGATTC	1363
Db	1304	GGCTCAAGGCCAGATACGCTCACATATGCTCGGGAAGCTTTGGAGGCTTATATGATTC	1363
QY	1364	GTAATATCAGAAAGCAAGTGAATCGCACATGTTTACCTGGCCCTCTTATGATGATGACTA	1423
Db	1364	GTAATATCAGAAAGTGAATGCTGTCTATCGCCCATGGGCACTGCAACCCATTTGAGAGCTT	1483
QY	1424	CGAAATATGGAAGATTATGCTGTGTATCGCATATCGCAATTCGCAACCTTCTGCAACAT	1483
Db	1424	CGAAATATGGAAGATTATGCTGTGTATCGCATATCGCAATTCGCAACCTTCTGCAACAT	1483

QY	1484	GGAATCCTCCCTTCTGTGATCAATCCCTCAAGAAAGTTGACCTCCATGAGAGCTCAATGA	1543
Db	1484	GGAATCCTCCCTTCTGTGATCAATCCCTCAAGAAAGTTGACCTCCATGAGAGCTCAATGA	1543
QY	1544	CTGTATATGATCAATCTTGCATTAAAGAGTGATACAGGTGCTTCAAGGACGACAGGCG	1603
Db	1544	CTGTGCAATGTGCCATCTTCCATTACGAGGAGTAAACGGGTGCTAACAGGCGGACAGGCG	1603
QY	1604	CCGTGGAGAAAGAGCTTGCTATATCAATGTTATATGAAAGACATCCTGGATTAAACGGA	1663
Db	1604	TCGTGGAGAAAGAGCTTCTTATATCAATGTTATATGAAAGACATCCTGGAGTATACGA	1663
QY	1664	AGAAAGTCTCTGATCATATCAACTTCATGATCAGGACCGCAATCAGAGATTTAAATTG	1723
Db	1664	GGAAGATGCTCTGATCATATCAAGCCATGATCAGTACGTAACGTAATCAAGATTTAAATTG	1723
QY	1724	GGAGCTTCTTAAAGCCAGACAAACAGTGTCCCATCACTTCAAGAAACAACGATTGACAT	1783
Db	1724	GGAACTTCTTAAACAGACATCAATATGTTCCATCTCGCGAAGAAACAATGCTTTTGACAT	1783
QY	1784	AAGCAGAGTTTGGCATCAAGGTTACAGATACCGAGATGGCTTACAGCTTTGCCAAGTTGA	1843
Db	1784	CGCCAGAGCTTTCCATTACGGCTCAAAATACCGAGAAGGCTTACAGCGTTGCCAAGTTGA	1843
QY	1844	AACCAAAGTTTGGTGAAGAAACCGCATTTGAACCTGTGGCTTTGTAAACAACCTTCAA	1903
Db	1844	AACGAAAGTTTGGTCAAGAAACCCCTCTTGAAATCTGTGCTTTGTAGCAACAGCTCAA	1903
QY	1904	ATCTTACAATATTAACGAGATGCCCTATGGGTGTATATAGGGCAACAACAAATATTAATAT	1963
Db	1904	ATCTATGCCCTATGCTATGTATGTCGGGTAAATATATATGTGAAGGTAAAGCGCTTGATGTAGA	1963
QY	1964	GGTTGTGTAGTAAAGCTGTATTTATGAAAAAATTTAAAAAATTTAAAAA 2013	
Db	1964	GGATTAAGTTGTATTAATTTATTAAGTTGTATTTAAAAAATTTAAAAA 2013	

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RESULT 5
US-09-895-752-19
Sequence 19, Application US/098955752
Patent No. 6559297
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 65592971, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/895,752
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(1889)
OTHER INFORMATION: phenase synthase
US-09-895-752-19

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Query Match	64.9%	Score	1306.8	DB	4	Length	2018
Best Local Similarity	81.0%	Pred. No.	0				
Matches 1595; Conservative	0	Mismatches	342			Indels	33
						Gaps	5

OY	68	CAGGTGCGGCGTCAGTCTCTTCATGATTAAGGCTCTCGTGTGAACAAATCCCACTCT	127
Db	53	CAATTCGTTGATCAGTTCTCACTTCAACCATGAGCTTTAAGGCTCTCTCTGAAACAAATTCAGCTCT	112
OY	128	TGGAATCTGCAGGCGCGGGGAAATCCGTCGCGCATTTCCATAAACATGTGTTGACAAGCGT	187
Db	113	AGGAATGAGTAGTGGCGAAGGAAATCTATCACTCTTCATCAGCATGAGCTCTACACCGT	172
OY	188	CGCATCTACGATCTCTGTACAGAGACGCGTGGGGAATATCATCTTCCAAACCTGTGGGACGA	247
Db	173	TGTACACGAGTAGATGTGTACGAAACGCAATGAGGAGATTTCCATTCCAACCTGTGGGACGA	232
OY	248	TGATTTTCATACAGTCTCTGATCTCTCAAGCGCTTATGAGACGACTGATTAACGGGAACGTGC	307
Db	233	TGATGTCTATACAGTCT---TTACCAACGCGCTTATGAGAGAAAATCGTACCTGTGAGCGTGC	289
OY	308	TGACAGACTTATTTGGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGGAAGATGG	367
Db	290	TGAGAAACTGATCGGGGAGATAAAG---AACAATGTTCAATTCGATATGATAGAAAGATGG	346
OY	368	AG-----GCAATGATCTCTTCCAAACGACTTTTGCTGGTGCATGACGTGA	412
Db	347	AGAGTTATGATGATCCGCTCAATGATCTCATTTCAACGCTTTGAGTTGTCCAGACGCTTTGA	406
OY	413	ACGTTTGGGAATGCACAGGACTTTCAAAAAAGATTAATAACGGCACTGCATTAATGTATA	472
Db	407	ACGTTTGGGGATTCATGACACTTTCAAAAGATGAGATTAATAACGGCGCTTATTAATGTATA	466
OY	473	CAGTTATTTGGAACGAAAAGGCAATGGAATGTGGGAGGGAAGATGTTGACTGACCTCA	532
Db	467	CAGTTATTTGGGGCCAAAATGGCAATCGGATCGGGAGGAGAGATGTATATCTGATCTGAA	526
OY	533	CTCAACCGCCTGTGGGGCTTGCAGACTCTCCGACTACACGATATACCTGTGTTCCAGATGT	592
Db	527	CTCAACCTGCGTTGGGGCTTGCAGACCTCAACGACTACACGATATCCGGATGTTCCAGATGT	586
OY	593	TTTGAACGTTTAAAGACAAAATGGGCAATTTTCTCCACTGSCAAATATTCAGATAGA	652
Db	587	TTTCAAAAGCTTTCMAAGGCCAAAATGGGCAAGTTTCTGCTCTGMAAAATATTCAGACAGA	646
OY	653	GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCGCTCCTCGTGCCTTTCCGGGCGA	712
Db	647	TGAAGAGATCAGAGCGCTTCTGAAATTTATTCGCGGCTCCTCCTCACTGCTTTCCAGGGGA	706
OY	713	GAAAGTTATGATGAGAGCTGAAAACATTTCTACAAAATATTTAAGAGAGCGCTGCAAAA	772
Db	707	GAAATATATGATGAGAGCTGAAAACCTTCTTCACAAATATTTAATAAAGAGCGCTGCAAAA	766
OY	773	GATTCGGGCATCCGATATACCTTTCACTAGAGATACGGGAGGTTCTGTGAATATGTGTGGCA	832
Db	767	GATTCGCGTCTCCAGT---CTTTGCGAGAGATCGGGAGCGTTTGGAAATATGTGTGGCA	823
OY	833	CACCAATTTTGCACAGCTTGGAGCAAGAAATTAACATGAGAGCTCTTTGGACAGCACATAA	892
Db	824	CACATATTTTGCOCGAGATTGGAGCAAGAAATTAACATCAAGTCTTTGGACAGCACATGA	883
OY	893	AAATTAAGACGC-----CGCCGAGAACTTTTGAACCTTGCAAAATTTGGAATTCCA	943
Db	884	GAAACACAAAGTCATATGTATGAAAGACAAAACCTTTTGAACCTGCAAAAATTTGAGTTCCAA	943
OY	944	TATATTTCACTCCCTTACAGAGAGAGAGTTAAAAACATGTTCCCGATGGTGGAAAGACTC	1003
Db	944	CATCTTTTCATCTCTTACAAAAGAGGAGTTTGAAGATCTGTCAGATGTGTGGAAAGATC	1003
OY	1004	GGGTTCTCTGAGATGACCTTTCTGTGACATCGTCAAGTGAATATCTACGCTTTGGCTTC	1063
Db	1004	GGGTTTTCTGAGATGACCTTTCTGCGACATCGCAAGTGAATATCTACACTTTTGGCTTC	1063
OY	1064	CTGATATTCGCTTGCAGGCTCAACCTTGTGATTTCAAGCTCGGCTTTTCCAAAGATGTCTCA	1123
Db	1064	CTGATATTCGCTTGCAGGCTCAACCTTGTGATTTCAAGCTCGGCTTTTCCAAAGATGTCTCA	1123

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QY 1124 TCTATACGCGTTCTTGAAGATGTACAGCGCTTTCGACAGTAGACGAGCTGAACT 1183
DB 1124 TCTATACGCGTTCTTGAAGATGTACAGCGCTTTCGACAGTAGACGAGCTGAACT 1183
QY 1184 CTTCAACAGCGCAATTAAGATGGATCCGTCGCGATGGAATCCCTCCAGAAATATAT 1243
DB 1184 CTTCAACAGCGCAATTAAGATGGATCCGTCGCGATGGAATCCCTCCAGAAATATAT 1243
QY 1244 GAAAGAGATGTACATGATGTTTATACACCGCTAAATGATGCTCGATGCGAGAGA 1303
DB 1244 GAAAGAGATGTACATGATGTTTATACACCGCTAAATGATGCTCGATGCGAGAGA 1303
QY 1304 GAGCTCAAGCGGAGACAGCTCAACTATGACAGAGAGCTGGAGGCTGTTTATGATTC 1363
DB 1304 GAGCTCAAGCGGAGATGAGCTCAACTATGAGCTGGAGGCTGTTTATGATTC 1363
QY 1364 GTATATGCAAGAGAGAGATGATGCGACATGCTGTTATGCTCCAGCTTGAAGATGATTC 1423
DB 1364 GTATATGCAAGAGAGAGATGATGCGACATGCTGTTATGCTCCAGCTTGAAGATGATTC 1423
QY 1424 GAGAGACGCGAAAGTATGATGCTGCTCATGCGCCATGCGACATGCAACCCATTCGACGTT 1483
DB 1424 GAGAGATGCGAAAGTATGATGCTGCTCATGCGCATGCGCATGCAACCCATTCGACAT 1483
QY 1484 GAGACATCCCTTCTCTGATCATCTCTCAAGAGAGATGATCCCATGGAAGCTCAATGA 1543
DB 1484 GAGACATCCCTTCTCTGATCATCTCTCAAGAGAGATGATCCCATGGAAGCTCAATGA 1543
QY 1544 CTTGATATGATCATCTCTCTGATTAAGAGTGTATCACGCTGCTCAAGGCGAGACAGGCGC 1603
DB 1544 CTTGATATGATCATCTCTCTGATTAAGAGTGTATCACGCTGCTCAAGGCGAGACAGGCGC 1603
QY 1604 CCGTGAGAGAGAGATGCTGCTATATCATGTTATATGAAGCAATCCTCGATTAACGA 1663
DB 1604 CCGTGAGAGAGAGATGCTGCTATATCATGTTATATGAAGCAATCCTCGAGTATCAGA 1663
QY 1664 AGAGATGCTCTGATCATCATCACTTATGATGATGAGGAGCGCAATCAGAGATTAATTTG 1723
DB 1664 AGAGATGCTCTGATCATCATCACTTATGATGATGAGGAGCGCAATCAGAGATTAATTTG 1723
QY 1724 GAGAGCTTCAAGCGAGACAAAGTGTCCCATCTCACTTCAAGAAACAGCATTTGACAT 1783
DB 1724 GAGAGCTTCAAGCGAGACAAAGTGTCCCATCTCACTTCAAGAAACAGCATTTGACAT 1783
QY 1784 AAGCAGATTTGGCATCAAGCTGTTACATATCCGAGATGCTACAGCTTCCCAAGCTTGA 1843
DB 1784 AAGCAGATTTGGCATCAAGCTGTTACATATCCGAGATGCTACAGCTTCCCAAGCTTGA 1843
QY 1844 AACAAAGATTTGGATGAGAGAGCGGATGATGAGCTGATGAGCTTGTAAACAACACTTGA 1903
DB 1844 AACAAAGATTTGGATGAGAGAGCGGATGATGAGCTGATGAGCTTGTAAACAACACTTGA 1903
QY 1904 ATCTACATATTAATCTGAGATGCGCTATGAGTGTATATAGGCGACAGAAATTAATAT 1963
DB 1904 ATCTATGCGCTATGCTATGCTGAGTAAATATATGAGAGTATGAGCGGATGAGTGA 1963
QY 1964 GCTTGTGTATTAAGCTGATTTATTAAGAAAAAATTAATTAATTAATTAATTAATTAAT 2013
DB 1964 GATTAAGTGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2013

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RESULT 6

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US-09-903-012B-19
Sequence 19, Application US/09903012B
Patent No. 6569656
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 6569656, Joseph P.
APPLICANT: Starke, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903, 012B

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CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/100, 993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130, 628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150, 262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(1889)
OTHER INFORMATION: pinene synthase
US-09-903-012B-19

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Query Match 64.9%; Score 1306.8; DB 4; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

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QY 68 CAGGTCGCGCTTCACTTCTCATGATTAAGGCTCTCGTAGAACAATCCCAACTCT 127
DB 53 CAATCGTTGATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 112
QY 128 TGAATCTGACAGCGCGGAAATCGTGGCGCATTCATTAACATGTTGACAGCGT 187
DB 113 AGAATGATGATGAGCGAGAAATCATCATCTTCCATCAGATGAGCTTACACCGT 172
QY 188 CGCATCTCATGATCTGTACAGAGACGCTGGGCACTATCATTCACACTGTGGAGAGA 247
DB 173 TGTAAACGATATGTTGATGAGAGAGCGATGCGATTTCAATTCACACTGTGGAGAGA 232
QY 248 TGATTTCAATCACTCTCATCTCACTCAACGCTTATGAGACACTGATTAACCGGAAAGCTGC 307
DB 233 TGATGTCATCACTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 289
QY 308 TGACAGACTTATGAGGAGATTAAGATTAATGTTCAATTTCAATGCTGGAAGATGG 367
DB 290 TGAGAAATGATCGGGAGATTAAG---ACATGTTCAATTCATGATTAAGATGG 346
QY 368 AG-----GCATGATCTCTCACTCACTCACTTTCGCTGCGATGAGAGCTTGA 412
DB 347 AGAGTAAATGATCGCGCTCAATGATCTCACTCACTTTCGATGATGCGACAGCTTGA 406
QY 413 ACGTTGGAAATGACAGAGCAATTTCAAAAAAAGATTAAGAGCGACATCGATTTATGTTAA 472
DB 407 ACGTTGGGAAATGACATGACATTTCAAAAGATGAGATTAATTCGCGCTTATGTTAA 466
QY 473 CAGTTATTTGAGCGAAAAAGCATTTGATGAGGAGAGAGATGTTGATGACTGCA 532
DB 467 CAGTTATTTGAGCGAAAAAGCATTTGATGAGGAGAGAGATGTTGATGACTGCA 526
QY 533 CTCAACGCGCTTGGGCGCTTGAACCTTCGCACTCAAGGATTAACCTGCTTCAAGATG 592
DB 527 CTCAACGCGCTTGGGCGCTTGAACCTTCGCACTCAAGGATTAACCTGCTTCAAGATG 586
QY 593 TTGAACGCTTCTTAAAGCAAAAAATGAGCAATTTTCCTCACTGCACTATTCAGATAGA 652
DB 587 TTTCAGAGCTTTCAGAGCGCAAAATGAGCACTTTTCCTGCTCTGAAATATTCAGAGAGA 646
QY 653 GGGAGAGATTAAGCGCTTCTCAATTTATAGGCGCTCTCGCTGCTTCCGCGGCA 712
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QY 713 GAAAGTATGATGAGATGAGCAATTCCTCAAAATATTTAAGAGAGCGCTGCAAAA 772
DB 707 GAAATTTATGATGAGATGAGCAATTCCTCAAAATATTTAAGAGAGCGCTGCAAAA 766
QY 773 GATTCGCGCATCGATTAATCTTCACTAGAGATACGGGACGCTTGTGAATATGTTGCA 832

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Db 767 GATTCGGTCTCCAGT---CTTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCA 823
Qy 833 CACCAATTTGGCAGCTTGAAGCAAGGAAATTAATGAGACGCTTTGGACAGCACTAA 892
Db 824 CACATATTTGGCGGATTTGAGAGCAAGGAAATTAATGAGACGCTTTGGACAGCACTGA 883
Qy 893 AAATAGAACCC-----CGCCGAGAACTTTTGAAGCTTTGCAAAATTTGAATTCAA 943
Db 884 GAACACGAGCATATATGTAAGAGCAAAAACCTTTTAAACCTCGGAAAATTTGAGTTCAA 943
Qy 944 TATATTTCACTCTTCAAGAGAGAGATTAACATGTTTCCGATGTTGAAAGACTC 1003
Db 944 CATCTTTCATCTTCAAAAAGAGGAGTGAAGTCTGTGATGATGTTGAAAGATTC 1003
Qy 1004 GGGTTTCCTGAGATGACCTTCTGCGACATGTCAGTCAGTGAATCTAGCTTTGGCTTC 1063
Db 1004 GGGTTTCTTGAATGACCTTCTGCGACATGTCAGTCAGTGAATCTAGCTTTGGCTTC 1063
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Db 1064 CTGCAATTCGCTTCAAGCTTCAACATTTGATTCAGACTCGGCTTTACCAAGATCTCA 1123
Qy 1124 TCTTATACGCTTTTGAAGCATGTAAGAGCTTTGGCAGCATGAGAGCTGGAAT 1183
Db 1124 TCTTATACGCTTTTGAAGCATGTAAGAGCTTTGGCAGCATGAGAGCTGGAAT 1183
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Db 1184 CTTCACAGCGCAATTAAGAGATGAGATCGGTCGCGAGTGAATGCTTCCAGAAATAT 1243
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Db 1304 GGGTCAAGCGCGAGACAGCTTCACTAATGAGAGAGAGCTTTGGAGGCTTTTGAATC 1363
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Db 1364 GTATATGAGAGAGAGAGATGAGATGCGCATGTTATCTGCCAGCTTTGAGAGATCTT 1423
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Db 1484 GGAATATCCCTTTCTGATGATCATCTGATGAGAGAGTTGATCTCCATGAGATCTCAAT 1543
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Db 1544 CTGTATATGATCATCTTCTGATTAAGAGTATCAAGCTGCTTCAAGAGAGAGAGGCT 1603
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Db 1604 CCGTGAAGAGAGAGCTTCTGATTAATGATGATTAAGAGAGAGAGCTTGAATTCAGGA 1663
Qy 1664 AGAAGATGCTGATGATCATCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1723
Db 1664 AGAAGATGCTGATGATCATCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1723
Qy 1724 GGAAGATGCTGATGATCATCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1783
Db 1724 GGAAGATGCTGATGATCATCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1783
Qy 1784 AAGCAGAGATTTGAGATCAAGCTTCAAGATGAGATGAGATGAGATGAGATGAGATG 1843
Db 1784 AAGCAGAGATTTGAGATCAAGCTTCAAGATGAGATGAGATGAGATGAGATGAGATG 1843
Qy 1844 AACCAAGATTTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1903
Db 1844 AACCAAGATTTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 1903

Qy 1904 ATCTACATATTTAATGAGATGCGCTTATGAGATGAGAGAGAGAGAGAGAGAGAT 1963
Db 1904 ATCTATGCGCTTATGAGATGCGCTTATGAGATGAGAGAGAGAGAGAGAGAGAT 1963
Qy 1964 GGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2013
Db 1964 GGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2013

RESULT 7
US-09-900-797-19
; Sequence 19, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6645762, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06, 797
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-900-797-19

Query Match 64.9%; Score 1306.8; DB 4; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

Qy 68 CAGGTGCGCTCAGTCTTCTCATGATTAAGGCTCTCGTGAACAATCCCACTCT 127
Db 53 CAATCGTTGATCAGTTCTTACCATGAGCTTAAGGCTCTCTTGAACAATCCCACTCT 112
Qy 128 TGAATCTGACGCGCGGAGAAATCGTGGCATTCATTAACATGTTTGAACAGCT 187
Db 113 AGAATAGTAGGAGGAGAAATCTATCACTCTTCATGAGATGAGCTTACACCGT 172
Qy 188 CGCATCTACTGATCTGTAAGAGAGAGCGGCGCAATCATCATTCGAACCTGAGAGCA 247
Db 173 TGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 232
Qy 248 TGATTTCAATCAGCTCTGATCTCAAGCGCTTATGAGAGAGAGAGAGAGAGAGAGT 307
Db 233 TGATGATACAGTCT---TTACCAAGCGCTTATGAGAGAGAGAGAGAGAGAGAGT 289
Qy 308 TGACAGATTAATGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 367
Db 290 TGAAGATGATGAGT 346
Qy 368 AG-----GCATGATCTCTTCAACGAGCTTTTGTGATGATGATGATGATGATG 412
Db 347 AGAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 406
Qy 413 AGCTTTGAGATGAGT 472
Db 407 AGCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 466

146 TGAGATGAGTTTGAGCAGCCGAGCTCTGATGATCATGTGATCAAGAGCAGATAGTCG 205
QY 223 ACTATCATTCACCTGTGGAGCAGATGATTTTCAATACAGTCTCTGATCTCAAGCCTTATG 282
Db 206 AGTTTCATTCACATCTGGAGACGACGATTTCAATCAATCTC--TATCAACGGCTTATG 262
QY 283 GAGACCTGATTTACCGGAGAGTGCTGACAGACTTATGGGAGTAAGTAATATATGT 342
Db 263 GGGACCTTCATACCGGTGACGTGTGATAGCTTTATGTGGAATTAAGGATATAT--T 319
QY 343 TCAATTTCAAGTCCGTGAGAGATGAG-----GCATGATCTCTTCAAC 387
Db 320 TCACCTTCATTTTACCGGAGATGAGAACTAATCATCCCTCAATGATCTCATTTCAAC 379
QY 388 GACTTTTGTGTGATGATGAGTGAACCTTTGGAAATGACAGGATTTCAAAAAAGGA 447
Db 380 GCGTTTATATGATGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 439
QY 448 TAAAAACGGACCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
Db 440 TAAAAACGGACCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
QY 508 GGGAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 567
Db 500 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 559
QY 568 ACGGATACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 624
Db 560 ACGGATACAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 619
QY 625 TTTCCCTCAGTCCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684
Db 620 AGTTTGTATGTTGGCCATCCAAACAGAGAGATGATGATGATGATGATGATGATGATGATG 679
QY 685 GGGGCTCCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 744
Db 680 GGGGCTCCCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 739
QY 745 CAAATATTTTAAAG 804
Db 740 AAATATATTTTAAAG 796
QY 805 TACGGGAGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 864
Db 797 TAGAGTACGTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 856
QY 865 ACATGAGAGCTTGTGAGACGACACTTAAATATAG-----AACGCCGCCGAGAAAC 915
Db 857 ACATGAGAGATGATGAG 916
QY 916 TTTTGAAGCTTGCAGAAATTTGGAATTCATATATTTTCACTCCCTTACAGAGAGAGATTA 975
Db 917 TTTTGAAGATTTGCAAAATTTGAGTTTCAATATTTTCACTCCCTTACAGAGAGAGATTA 976
QY 976 AACATGTTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1035
Db 977 AAGACCTCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1036
QY 1036 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1095
Db 1037 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
QY 1096 TCAGAGCTGGGCTTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1155
Db 1097 TCAGAGCTGGGCTTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1156
QY 1156 TCTTTCGAGCAGTACAG 1215
Db 1157 CTTTTCGAGCAGTACAG 1216
QY 1216 CCGGATGAGATGCTTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1275

1217 CTGCCACAGATTTGCTTCCAGATATATGAAAGGTTGTACATGATGATGATGATGATGATG 1276
QY 1276 TAAATGAATGGCTCGAGTGGCAG 1335
Db 1277 TAAATGAATGGCTCGAG 1336
QY 1336 GACAGGCTTGGAG 1395
Db 1337 GACAGGCTTGGAG 1396
QY 1396 GTTATCTGCCAGCTTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1455
Db 1397 GTTATCTGCCAGCTTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1456
QY 1456 CATGCGACCTGCAACCCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1515
Db 1457 TATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1516
QY 1516 AAGTTGACTTCCATGCAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1575
Db 1517 AATATGACTTTCATGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1576
QY 1576 ATACAGGCTGATACAG 1635
Db 1577 ACCTTCCCTGCTACAG 1636
QY 1636 ATATGAAG 1695
Db 1637 ATATGAAG 1696
QY 1696 TCAGGAG 1755
Db 1697 TCAATATCTTATCAAG 1756
QY 1756 TCATCTTCAG 1815
Db 1757 TTGCTTTCAG 1816
QY 1816 GAGATGCTACAGCTTGTGCAACGTTGAAACAAAGAGTTGATGATGATGATGATGATGATG 1875
Db 1817 GAGATGCTACAGCTTGTGCAACGTTGAAACAAAGAGTTGATGATGATGATGATGATGATG 1876
QY 1876 AACCTGTGCTTTG 1889
Db 1877 AGTCTGTGCTTTG 1890

RESULT 9
US-09-360-545-66
Sequence 66, Application US/09360545
Patent No. 6429014
GENERAL INFORMATION:
APPLICANT: Croceau, Rodney B
APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REFERENCE: wu13885
CURRENT APPLICATION NUMBER: US/09/360,545
EARLIER FILING DATE: 1998-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 66
LENGTH: 2186
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(1923)

US-09-360-545-66

Query Match 53.3%; Score 1072.4; DB 4; Length 2186; 177
Best Local Similarity 76.4%; Pred. No. 2.4e-306;
Matches 1428; Conservative 0; Mismatches 391; Indels 51; Gaps 7;

QY TTTCTTCATAGATTAGGCTCTCCGTAGAACAACTCCCACTCTTGAATCTGACAGCC 142
DB TTTCTTCATAGATTAGGCTCTCCGTAGAACAACTCCCACTCTTGAATCTGACAGCC 149
QY GGGGAAATCCGTCGCGCATTCATTAACATGTGTGACAAAGCGTCGATCTACTGATTC 202
DB AGGGAATCTTCAACACCTTCTGTGACATGTGTGACAAAGCGTCGATCTACTGATTC 209
QY TGTACAGAGAGCGCTGGCACTATCATTTCCACTGTGGAGAGATGATTCATACAGTC 262
DB TCTCAAAAGACGATAGGTGATCATTCCTCAATCTGTGGAGAGATGATTCATACAGTC 269
QY TCTGATCTCAACGCTTTATGAGACCTGATTAACGGGAAAGTGTGACAGCTTATGG 322
DB TC---TATCAACGCTTATGAGAGCTTCTTACCGAAGAGTGTGAGAACTGATTTGG 326
QY GGAAGTAAAGATATATGTTCAATTTCAAGTCGCTGAGAGATGAG----- 369
DB GGAAGTAAAGATATATGTTCAATTTCAAGTCGCTGAGAGATGAGATGATTC 383
QY 327 GGAAGTAAAGATATATGTTCAATTTCAAGTCGCTGAGAGATGAGATGATTC 383
DB 370 --GCAATGATCTCTTCAACGATTTTGTGATGATGATGATGATGATGATGATG 427
QY 384 CCTCAATGATCTTATGAGACGCTTGTGATGATGATGATGATGATGATGATGATG 443
DB 428 CAGGATTTCAAAAGATTAAGATTAAGATGATGATGATGATGATGATGATGATGATG 487
QY 444 TAGACATTTCAAAAGATTAAGATTAAGATGATGATGATGATGATGATGATGATG 503
DB 488 AAAAGCATTTGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 547
QY 504 AAAAGCATTTGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 563
DB 548 GCTTGAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
QY 564 GTTTCGAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 623
DB 608 AGACAAATTTGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 667
QY 624 AGACAAATTTGAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 680
DB 668 GCTTCTCAATTTATCAGGCGCTCTGATGATGATGATGATGATGATGATGATGATG 727
QY 681 GCTTCTCAATTTATCAGGCGCTCTGATGATGATGATGATGATGATGATGATGATG 740
DB 728 AGCTGAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 787
QY 741 GCTGGAATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 800
DB 788 TATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
QY 801 T---CTTCAACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 857
DB 848 CTGGAACGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 893
QY 858 ATTGGAACGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 917
DB 894 AATAAGAGC-----CGCCGAAGATTTTGAAGCTTGAAGATTTGAATTC 943
QY 918 GAAAGAGAGCGATATCTGACAGGAAAGCTTTTGAAGATTCGGAAGATTTGAATTC 977
DB 944 TATATTTCACTCTTCAAGAGAGAGATTAAGATGATTTCCGAGGTGGAAGATTC 1003
QY 978 CATCTTTCACTCTTCAAGAGAGAGATTAAGATGATTTCTTCAAGATGATGATTC 1037
DB 1004 GGGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1063
QY 1038 GGGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1097

QY 1064 CTGATTCGCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1123
DB 1098 TTGATTCGCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1157
QY 1124 TCTTATCAGGCTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1183
DB 1158 TCTTATCAGGCTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1217
QY 1184 CTTCACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1243
DB 1218 CTTCACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
QY 1244 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1303
DB 1278 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1337
QY 1304 GATTCACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363
DB 1338 GATTCACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1397
QY 1364 GTATATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1423
DB 1398 GTATATCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1457
QY 1424 GGAAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483
DB 1458 GGAAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1517
QY 1484 GGAAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1543
DB 1518 GGAAGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1577
QY 1544 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1603
DB 1578 TTTGATATCTTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1637
QY 1604 CCGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1663
DB 1638 CCGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1697
QY 1664 AGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1723
DB 1698 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1757
QY 1724 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1783
DB 1758 GGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1817
QY 1784 AAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1843
DB 1818 AAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1877
QY 1844 AAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1903
DB 1878 AAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1937
QY 1904 ATCTAATTA 1913
DB 1938 TTCTATATA 1947

RESULT 10
US-09-360-545-1
; Sequence 1, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jörg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wbur13385


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? CURRENT APPLICATION NUMBER: US/09/360,545
? CURRENT FILING DATE: 1999-07-26
? EARLIER APPLICATION NUMBER: 60/052,249
? EARLIER FILING DATE: 1997-11-07
? EARLIER APPLICATION NUMBER: PCT/US98/14528
? EARLIER FILING DATE: 1998-07-10
? NUMBER OF SEQ. ID NOS.: 107
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1
? LENGTH: 2196
? TYPE: DNA
? ORGANISM: Abies grandis
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (69)..(1952)
? OTHER INFORMATION: Clone Ag2.2 encoding myrcene synthase
? US-09-360-545-1

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Query Match	53.2%	Score 1071.6	DB 4	Length 2196
Best Local Similarly	75.0%	Pred. No. 4.1e-306		
Matches 1430; Conservative	0	Mismatches 441	Indels 36	Gaps 6

QY	68	AAAGGTGCGGCTCAAGTCTTCTTCATGAGATTAAGGCTCCGGTAAGAAACAATCCCAACTCTC	127
Db	116	CAAGTCGTTGATCAATTTCATTAAGACATATAGGCTCCCTATAGAACAAATCCCAATCT	175
QY	128	TGGAATCTGCAGGCGCGGGAAATCCGTCGCGCATTCATTAACAATGTGTTTGAACAAGCT	187
Db	176	TGGAATGCGTATGGCGAAGGGAATCTGTACGCGCTTCATGAGCATCAGTTTGGCCACCG	235
QY	188	CGCATCTAAGTATTTCTGTACAGAGACGCGTGGGCATATCAATTCCAACTGTGGGACGA	247
Db	236	TGCACCTGATGATGGTGTACAAAGACGCAATAGGTGCTACCAATCCAAATATCGGGACGA	295
QY	248	TGATTTCTATACAGTCTCGATCTCAACGCTTATGAGACACTGAATTAACGGGAAAGTGC	307
Db	296	TGATTTCTATACAGTCTC---TATCAACGCTTATGAGGAAACCTTTACAGGAAGTGC	352
QY	308	TGACAGACTTATTTGGGGAAGTAAAGATTAATGTTCAATTTCAAGTCCGTCGAAAGTGG	367
Db	353	TGAGAGATTAATGTGAGAGTAAABAGTA---TTCAATTCAGATGACTGATGATGG	409
QY	368	AGG-----CAATGATCTCTTCAACGACTTTTGTCTGTGATGACGTTGA	412
Db	410	AAGATTAATGAGTCTCTTAAATGATCTCATGACGCGCTTGGATGATGATGAGCTTGA	469
QY	413	ACGTTTGGGATTCGACAGGCAATTTCAAAAAAABAGATTAABAAACGCACTGATTAATTTAA	472
Db	470	ACGTTTGGGGAATGCTAGACATTTCAAGAACAGATTAACATCAGCTCTGATTAATTTT	529
QY	473	CAGTTAATGGAAACGAAAAAGCATTGAGATGTGGAGGAGAGGTGTGATCAGTCACTCA	532
Db	530	CCGTTTACGGAGAGAAAACGCAATTGGAATGTGGAGAGACAGATTTGTACTGATCTCA	589
QY	533	CTCAACGCGCTTTGGGGCTTGCAGCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT	592
Db	590	CTCAACTCGTTGGGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTTCAGAGGT	649
QY	593	TTTGAACGTTTATAAGACAAAATAGGCGAATTTTCTCCACTGCGCAATATTCAGATAGA	652
Db	650	TTTAAACCTTTTCAAGATCAAAAATGGAACAGTTGTATGCTCCCC--GGTCAAGCA	706
QY	653	GGGAGAGATTAGAGCGGTTCTCAATTTTATTCAGGGGCTCGCTCGTGCCTTTCCGGGCGA	712
Db	707	GGGTGAGATCAGAAAGCTTTCTTAATTAATGCGGCTTCCCTCATTTGCTTCCCTGTGTG	766
QY	713	GAAGATTATGATGAGCTGAACAATCTCTACAAATAATTAAGAAGAACCCCTGCAGAA	772
Db	767	GAAGATTATGAGGAAGAGCTGAATCTTCTCCACAAGATATTTGAAGAAGCTCTACAAA	826
QY	773	GATTCGCGCATCTCAGTATTACTTTCATAGAGATCGGACGTTCTGGAATATGTGTGGCA	832
Db	827	GATTCGATCTCTCCGCT---CTTTCACAAAGATTAAGTGTGTATGGAATATGTGCTGCA	883

OY	833	CACCAATTTCGCACGCTTGGAGCAAGAGAAATTTCATGAGACGTCTTTGGACAGCACATA-	891
Db	884	CACAAATTTCGCAGATTGGAGCAAAATTTACATGACACACTTGAAGAAAGCACACAG	943
OY	892	-----AAATTAAGAACGCCGCCGAGAACTTTTGAACCTTGCAGAAATTTGGAAATTCAA	943
Db	944	TGCATGGCTCAATTAATAATGCTGGGAGGAAGCTTTTGAACCTTGCAGAAATTTGGAGTTCAA	1003
OY	944	TATATTTCACTCTCTTACAAAGAGAGAGTTTAAAACATGTTTCCGATNGTGGAAAGACTC	1003
Db	1004	TATATTTTACCTCTTACAAACAAAGGAATTAACAATCTTTTGGAGTGGGAAAGAGTC	1063
OY	1004	GGGTTTCTCGAGATGACCTTCTGTCACATTCGCACGTGGAAATCTACGCTTTGCGCTTC	1063
Db	1064	GGATTTGGCTTAATTTGACATTTTGGTCGGCATTCGCATGTGGAAATTTCAACCTTTGGCTC	1123
OY	1064	CTGCATTGCGTTCGAGCTTCAACATTTCTGAAATTCAGCTCGGCTTTTACAGAGATGTCTCA	1123
Db	1124	TTGTATTGCCATTGACCCAAAACATTCCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCA	1183
OY	1124	TCTTATACGGTTCTTBAACACATGTACAGAGCTTTGGGACAGTAAACGACGTGGAACT	1183
Db	1184	TCTTGTCAAGTTTGGACGATATTTCAGACACTTTTGGAAACGATTAACGAGCTTGAACCT	1243
OY	1184	CTTCACAGCGCAATTTAAGATGGATTCGCTCCGCATGGAAATGCCCTTCAGAAATATAT	1243
Db	1244	CTTCACATCTGCAATTTAAGATGGAAATTCATCAGAGATGAAACACCTTCAGAAATATAT	1303
OY	1244	GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAAATGCTGTGAGTGGCAGAGAA	1303
Db	1304	GAAATGTGTGTACATGTGTGTGTGTGAACTGTAAATGAACCTGACAGAGAGCGGAGAA	1363
OY	1304	GGCTCAAGGCGCGAAGACGCTCAACTATGCAAGACAGCTTGGGAGGCGTGTTTGATTC	1363
Db	1364	GACTCAAGGAGAAACACTCTCAACTATGTTCCGAAAGCTTTGGAGGCTTATTTTGAATTC	1423
OY	1364	GTATATSCAGAGAACAAATGGATTCGCCACTGTTATCTGCCCACGTTTGAAGAGTACTT	1423
Db	1424	ATATATGGAAGAAACAAATGSAATCTCTAATGTGTTATCTGCCAATGTTTGAAGAGTACCA	1483
OY	1424	GGAAACAGGGGAAATTTAGCTCTGTCTCATGCCCCACAGGCACTGCAACCCATTTGAGAGTT	1483
Db	1484	TGAACAAATGGGAAATGTAGCTCTGCATATTCGGTGAACAACTTGGAACCCATCTCACTTT	1543
OY	1484	GGACATCCCCCTTCTCTATCACTACCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGA	1543
Db	1544	GAAATGCATGGCTTCTGATTACATCTTGAAGGGAATTTGATTTTCCATCCAGTTCAATGA	1603
OY	1544	CTTGATATGTATCATCTCTTGATTTAAGAGTGTATCACCGTGTCAACAGGCACAGGCG	1603
Db	1604	TTTGGCATTCGCTCTTCTTCGGCTACGAGGTCACACGCTGTCAACAGGCCGATGAGGA	1663
OY	1604	CCGTGGAGGAAGACCTTCGTATATATGTTTATATGAAGACAATCTGTGATTTAAGGA	1663
Db	1664	TCGTGTGTAAGACCTTCGTATATATGTTTATATGAAGACAATCTGTGATTAACCGA	1723
OY	1664	AGAAATGCTCTGATCATATCAACTTCATGATCAGGACGCAATCAAGAAATTTAAATTC	1723
Db	1724	AGAAATGCTCTCAATCATATCAATGCAATGCTCAATGAACATATCAAGAAATTTAAATTC	1783
OY	1724	GGACCTTTAAGCGCAGACAACTGTTCCTCATCACTTCCAGAAACACCATTTGACAT	1783
Db	1784	GGAACTTTAAGATCCAAACGACAAATTTCCAAATCTGGCCAAAGAACATGTCTTTTGACAT	1843
OY	1784	AAGCAGATTTGGCATCAGCGTTACATATCCGAGATGGCTACAGCTTTGCCAACGTTCGA	1843
Db	1844	AACAAGAGCTTCCACCATCTCTACATATATCGAGATGGCTTTATGTTTGCACAAAGGA	1903
OY	1844	AACAAGATTTGGTATGAGAACCGTCACTTGAACCTGTGCTTTGTATCAACACTTTCAA	1903
Db	1904	AACAAAAAATTTGGTATGAGAACCTCTTGAATCTATGCTTTTATTAACATATACATA	1963

Oy 1904 ATCTACATATTAACTGAGCATGCCCTATGGGTATATATAGGCACA 1950
| | | | | | | | |
Db 1964 TCCATAATAAATAGCTCATTAATGCTAAATTATTTGGCCTTAGACATA 2010

RESULT 11
116-09-396

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US-09-398-395A-29
Sequence 29, Application US/09398395A
Patient No. 6468772
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 6468772, Joseph P.
APPLICANT: Scarke, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASS
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/398,395A
CURRENT FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/110,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: ParseSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69)..(1949)
OTHER INFORMATION: myrcene synthase
US-09-398-395A-29

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Query Match	53.2%	Score 1071.6	-DB 4	Length 2196
Best Local Similarity	75.0%	Pred. No. 4.1e-306		
Matches 1430	0	Mismatches 441	Indels 36	Gaps 6

Qy	68	CAGGTCGGGCTCAGGTCCTTTCATGAGATTAAAGGCTCCGGTAGAACAATCCCACTC	127
Db	116	CAGTCGGTATCAAGTTCATTCAATGACATATAGGCTCCCTTATGACAATCCCAATCT	175
Qy	128	TGGAATCTGCAGGCCGGGAAATCCGTCCGCATTCATTAACATGCTGTGTGAACAGCT	187
Db	176	TGGAATGGGTAGGCGAAGGAAATCTGTCAAGCCCTTCATGAGCATCAGTTTGGCCACCG	235
Qy	188	CGCATCTACTGATTTCTTACAGAGACGGCTGGGCACTTACATTCCAACTGTGGGACGA	247
Db	236	TGCACCTGATATGCTGTACAAAGACGATTAAGTGTACTACATTCCAATATCTGGGACGA	295
Qy	248	TGATTTCTTACAGTCTCTGATCTCAACGCCCTTATGAGCACCCTGATTAACGGGAAAGTGC	307
Db	296	TGATTTCTTACAGTCTC---TATCAACGCCCTTATGAGGAAACCTCTTACACAGGAAGTGC	352
Qy	308	TGACAGACTTATTTGGGGAAATTAAGATTAATGTTTCAATTTCAAGTCCGTGGAATGG	367
Db	353	TGAGAGATTAATTTGGAGGTAAAGATGA---TTCAATTTCAATGTACTCGATGATATGG	409
Qy	368	AGG-----CAATGATCTCCCTTCAACGACTTTTGTCTGTCGATGACCTTGA	412
Db	410	AAGATTAATGAGTTCTCTTAATGATCTCATGCAAGCCCTTGGATATGTGATAGCCTTGA	469
Qy	413	ACGTTTGGGAATTCGACAGGCACTTCAAAAAAGATTAATAAAGGCACTCGATTATGTTAA	472
Db	470	ACGTTTGGGGATAGCTAGACATTTCAAGAACAGATTAACATCAGCTCTGGAATTAATTTTTT	529
Qy	473	CAGTTATTTGGAACGAAAAAGCAATTTGATGTGGAGGAGAGATGTGTACTGACCTCAA	532
Db	530	CCGTTTACTGGGAGGAAAAACGCAATTTGATGTGGAGAGACAGTATTTGTTACTGATCTCAA	589
Qy	533	CTCAACCGCCTTGGGGCTTGCAGACTCTCCGACTACAGGATACAGTGTCTTCAGATGT	592

Db	590	CTGAACGCGGTGCGGTTTGGAACCTTCCTGCATACACGGGTAACAGTATCTCCAGAGT	649
Oy	593	TTTGAAGCTTTTAAAGCAAAAATGGGCAATTTTCCCTCCACTGCCAATATTCAGATGA	652
Db	650	TTTAAAGCTTTTCAAGTCAAAAATGGAACAGTTGTATGCTCCCC---GGTCAAGACGA	706
Oy	653	GGGAGAGTTAGAGCGGCTTCATTTATTCAGGGGCGCCCTCGTGCCTTCCCGGGGA	712
Db	707	GGGGAGATCAGAGCGCTTCTTAATTATATCGGGCTTCCCTCAATGCTTCCCTGGTGA	766
Oy	713	GAAAGTTATGATTAAGCTGAAGCAATTTCTACAAAATATTTAAGAGAGCCCTGCAAAA	772
Db	767	GAAAGTTATGGAAGAAGCTGAATCTTCCACAAGATATTTGAAGAAGCTTACAAA	826
Oy	773	GATTCCGGCATCCAGTATCTTTCACTAGATACGGGACCTTCCGAATATGTTGGCA	832
Db	827	GATTCAGATCCTCCCT---CTTTCACAAGAGATTAAGTTGTTATGGAATATGCTGGCA	883
Oy	833	CACCAATTTGGCAAGCTTGGAAGAAGAAATTAATAGAGCGTCTTTGGACAGCACATA-	891
Db	884	CACAAATTTGCAAGATTGAAGCAAGAAATTAATATGACACACTTGAAGAAACACACAG	943
Oy	892	-----AAAATTAAGAACCGCCGCGAGAACTTTTGAAGCTTCAAAATTTGAATTCAA	943
Db	944	TGCATGGCTCAATTAATAATGCTGGAGAAAGCTTTTGAAGCTTCAAAATTTGAAGTTCA	1003
Oy	944	TATATTTCACTCGCTTACAGAGAGAGAGTTAAAATATGTTTCCGATGCTGAAGACATC	1003
Db	1004	TATATTTAAGCTCTTACACAAAAGAAATTCATATCTTTTGAAGATGCTGAAGAGATC	1063
Oy	1004	GGGTTCTCTGATATGACCTTCTGTCACATCTGTCACGTGGAATATACGTTTGGCTTC	1063
Db	1064	GGATTTGGCTTAATTTGACATTTGCTCGGCACTGTCATGTGGAATTTACATTTGGCTTC	1123
Oy	1064	CTGCATTTGCGTTGAGCGCTCAACATTTCTGATTCAGACTCGGCTTTTACAGATATGCTCA	1123
Db	1124	TTGTATTTGCCATTAACCCAAAACATTTCTGCATTCAGACTAGGCTTCCGCAAAAATGTGCA	1183
Oy	1124	TCTTATACCGGTTCTTGAAGCATGTACGAGCTTTCGGCACAGTATGACAGCTGGAATCT	1183
Db	1184	TCTTGTACAGATTTTGGACGATATTTAGCAACATTTTGAACGATGACGAGCTTGAATCT	1243
Oy	1184	CTTCACAGCGCAATTAAGAGATGGGATCCGTCGGATGGAATGCTTCCAGAAATATAT	1243
Db	1244	CTTCACATCTGCCATTTAAGAGATGAATTCATCAAGATATGAACCTTCCAGAAATATAT	1303
Oy	1244	GAAAGAGTGTACAGATGTTTATTCACACCGTAAATGAATGGCTCGAGTGGCAGAGA	1303
Db	1304	GAAATGTGTACATGTCGTGTTTGAACGTAAATGAATGACCTGACACAGAGCGGAGAA	1363
Oy	1304	GGCTCAAGCGCGGACACGCTCAACTATGCAAGAAGGCTTGGAGGCGGTTTGTATTC	1363
Db	1364	GACTCAAGGGAGAAACACTCTCAACTATGTTGAAAAGGCTTGGAGGCTTATTTTGAATTC	1423
Oy	1364	GTATATGCAAGAGCAAAATGATGCGCATCTGCTTATCTGCCACGTTTGAAGATTAAT	1423
Db	1424	ATATATGGAAGAACAAAATGATCTCTAATGATTAATCTGCCAATGTTTGAAGATTAACA	1483
Oy	1424	GGAAACCGGAAGATTAGCTCTGCTCATTCGCGCCATGGGCACTGGAACCCATTTGACGTT	1483
Db	1484	TGAAGATGGGAAGATGAGCTCTGATATCGGATGCAACATTTGAACCCATCTTCACTTT	1543
Oy	1484	GGACATCCCTTTTCTGTATCATCTCTCAAGAAAGTTGACTTCCATCGAAGCTCAATGA	1543
Db	1544	GAAATGCAATGGCTCTGATTAATCTTTGAAGGAATTAATTTTCATCTCAAGTTCAATGA	1603
Oy	1544	CTTATATATGATTCATCTTGCATTAAGAGTGAATACAGGCTCTACAAAGCAGACAGGCG	1603
Db	1604	TTTGGCAATCTGCTTCTCTTCCGCTACGAGGATGACACGCTGCTTACAAAGCGCATGGGA	1663
Oy	1604	CCGATGGAAGAGACTTCTGTATATGATGTTATATGAAGAACATCTCGATTTAAAGGA	1663

Db 1664 TCGTGGAAGAGCTTGTGTATATCATGTTATATGAAGACAATCTGTGATCAACCGA 1723
Oy 1664 AGAAGATGCTCTGATCATATCAATCTTATGATCAGGAGCCAAATCAGAGAATTAAATTG 1723
Db 1724 AGAAGATGCCCTCATATCATATCAATGTCATGTCATATCAATCAAGAAATTTAAATTG 1763
Oy 1724 GGAGCTTGAAGCCAGACAACAGTGTTCATCACTTCCAGAAACAGCATTTGACAT 1783
Db 1784 GGAATCTTAAGATCCAAACGAATATTCATGCTGGCCAAAGAAACATGCTTTTGACAT 1843
Oy 1784 AAGAGAGTTTGGATCAGGTTACAGATCCGAGATGGCTACAGCTTTGGCAACGTGA 1843
Db 1844 AACAGAGCTCTCCACCTCTTACATATATCGAGATGGCTTTAGTGTGCCAACAGGA 1903
Oy 1844 AACAAAGTTTGGTATGATGAGAACCGTCAATGAACCTTGCTTTGTAACAACCTTCA 1903
Db 1904 AACAAAAAATTGGTATGAGAAACATCTTGAATCTATGCTTTTAACTATACATTA 1963
Oy 1904 ATCTACATATTAATGAGATGCCCTTATGGGTATATAGGGCACA 1950
Db 1964 TCCATATATATAGCTCATATGCTAAATTTATTTGGCCTTATGACATA 2010

RESULT 12
US-09-887-586A-29
Sequence 29, Application US/09887586A
Patent No. 6495354
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64953541, Joseph P.
APPLICANT: Starke, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHESIS
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69)...(1949)
OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Query Match 53.2%; Score 1071.6; DB 4; Length 2196;
Best Local Similarity 75.0%; Pred. No. 4.1e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;
Oy 68 CAGGTCGCTCAGTCTTCTTCATGAGATTAAGGCTCCGTCGAGAACATCCCAACTT 127
Db 116 CAGTCGTTGATCGTTAAATTCATGAACATTAAGCTCCCTATAGAACAAATCCCAACTT 175
Oy 128 TGAATCTGACGCGGAGAAATCCGTGCGCATTCATTAACATGTGTTGACAAAGCT 187
Db 176 TGAATGCGTGAAGGAGAAATCTGTCAAGCTTCCATGAGCAATCATTTGGCCACCG 235
Oy 188 CGATCTAATGATCTGTACAGAGACGCGTGGCAACTATATTCGAACCTGTGGAGCA 247
Db 236 TGCACCTGATATGTTGTAACAAGACGATAGGTACATACCAATTCATATCTGGAGCA 295
Oy 248 TGATTTCTAAGTCTGATCTCAAGGCTTATGAGACACCTGATTCACGGGAAACGTC 307
Db 296 TGATTTCTAAGTCTC--TATCAAGCTTATGGGAAACCTCTTATCCAGGAACGTC 352

Oy 308 TGACAGACTTATGGGAGATAAAGATATATGTTCAATTTCAAGTCCTGGAAGATG 367
Db 353 TGAAGATTAATGATGAGGTAAGAAAGATAT--TTCAATTCATATGACCTGATGATGG 409
Oy 368 AGG-----CAATGATCTCTTCAACGACTTTTGTGGTCCATGACGTTGA 412
Db 410 AAGATTAATGATTCCTTTATGATCTCATGCAACGCTTTGGATGATGATGACGTTGA 469
Oy 413 ACGTTGGGATGACAGGCACTTTCAAAAAAGATATAAAACGCGACCTCATATATGTTAA 472
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Db 590 CTCAACTGCGTGGGCTTGGAACTCTTCAATTAACAGGGTACCTGTATCTCCAGAGT 649
Oy 593 TTGAAGTTTTTAAAGCAAAAAATGGGCAATTTTCCCACTGCCAATATTCAGATGA 652
Db 650 TTTAAAGCTTTTCAAGATCAAAATGCAAGTTTGTATGCTCCCC--GCTCAGACGA 706
Oy 653 GGGAGATTAAGAGCGCTTCAATTTATTCAGGGCTCCCTGCTGCTTTCCGGCGA 712
Db 707 GGGTGAATGAGAGCGTCTTAACTTATATCGGGCTTCCCTCATGCTCTCCCTGGTGA 766
Oy 713 GAAAGTATGATTAAGCTGAAACATTTCTTACAAATTTTAAAGAAAGCCCTGCAAAA 772
Db 767 GAAAGTATGAAAGAACTGAAATCTTCCCAAGAAATTTGAAAGAGCTTACAAAA 826
Oy 773 GATTCGGGCAATCCAGTATCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA 832
Db 827 GATTCAGTCTCCGCT--CTTTCAAGAGATATAAGTTGTATGAAATATGCTGGCA 883
Oy 833 CACCAATTTGCAAGCTTGAAGCAAGAAATTAATGAGAGCTTTTGACACGACACTA- 891
Db 884 CACAAATTTGCAAGATTTGAAAGCAAGAAATTAATGAGACACACTTGAAGAAACACAG 943
Oy 892 -----AAATTAAGAAACCGCCGAGAAACTTTTGAACCTTGCAAAATTTGCAATTC 943
Db 944 TGCATGCTCAATTAATAATGCTGGAGAAAGCTTTTGAACCTTGCAAAATTTGAGTTCAA 1003
Oy 944 TATATTCACCTCTTACAGAGAGAGATTAACATGTTTCCGATGAGTGAAGACTC 1003
Db 1004 TATATTTAATCTCTTACAGAAAGAAATTAATCTTTTGAAGTGTGAAGAGTGC 1063
Oy 1004 GGGTTCCTGAGATGACCTTCTGTGACATCTGACGTGGAATATACGCTTTGCGCTTC 1063
Db 1064 GGAATTCCTTAATTAATGACATTTGCTCGGACATCGCATGTGGAATTCATCTTTGGCTC 1123
Oy 1064 CTGATGCGCTGCAAGCTCAACATTTGATTCAGACTCGGCTTTACCAAGATGTC 1123
Db 1124 TTGATATGCAATTAACCAAAACATTTGATTAAGACTGAGCTTCCCAAAATGTGTCA 1183
Oy 1124 TCTTATCAGGTTCTTGAACGATGTAAGAGCTTTGGGCAAGTGAAGAGCTGAACT 1183
Db 1184 TCTTGTACAGTTTGAACGATATTTAGACACTTTTGAAGCAATTTGACAGCTGAACT 1243
Oy 1184 CTTCAAGCGCAATTAAGATGGAATCCGTCCGATGGAATGCTTCCAGAAATATAT 1243
Db 1244 CTTCAATCTGCAATTAAGATGGAATTCATCAGATATGAACACCTTCCAGAAATATAT 1303
Oy 1244 GAAAGAGTGAATGATGTTTATCAACCTTAAAGAAATGCTGAGTGGAGAGAA 1303
Db 1304 GAAATGTGTGAACGATGCTGTTTGAACCTGTAATGAAGCTGACAGAGAGGCGAGAA 1363
Oy 1304 GGCCTCAAGGCGGAGACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGTTGATTC 1363
Db 1364 GACTCAAGGAGAAACCTCTCAACTATGTTGCAAGAGCTTGGAGGCTTATTTTGAATTC 1423

QY	1364	GTATATGAGAGAAAGCAAGTGGATATGGCACTGGTATATCGCCACGTTTGGAGAGTACTT	1423
Db	1424	ATATATGGAAAGACAAATATGGATCTTAAATGGTTATCTGGCAATGTTTGAAGAGTACCA	1483
QY	1424	GGAGAACGGGAAAGTTTACTCTGTCTGCATCGCCATGCGCAGCTGCACCCCATTTCTGACGTT	1483
Db	1484	TGAGATATGGGAAAAGTAGAGCTCTGCATATCGGGTATGACAACTTGGAAACCATCTCTCACGTT	1543
QY	1484	GGACATCCCCCTTTTCTGTATCACTATCTTCAAGGAAGTTGACTTTCCCATGGAAGCTCATGA	1543
Db	1544	GAATGCAATGCGCTTCTGTATCACTCTTGAAAGGGAATTAATTTTCCATCTCAGATTCAATGA	1603
QY	1544	CTTATATATGTATCAATCTTGATTAAGAGGTGATACAGGGGTCTACAAAGGAGACAGGGC	1603
Db	1604	TTTGGCATCGTCTTCTTCCTCGGCTTACGGAGGTACACAGCGTCTTCAAAAGCCGATAGGGA	1663
QY	1604	CCGTGAGAAAGAGCTTGTCTATATCATGTATATGAAAGACATCCTGTGATTTAACGGA	1663
Db	1664	TCTGTGTGAAGAGCTTGTGTATATCATATGTTATATGAAAGACATCCTGTATCAACGGA	1723
QY	1664	AGAAATGCTCTGTAATCATATATCAACTTCATGAGGACGCAATCAGAGAAATTAAATTG	1723
Db	1724	AGAAGATGCCCTCAATCATATCAATGCATGTCATATACATTAATCAAAAGATTTAAATTG	1783
QY	1724	GGAGCTTCTAAGCGACGACAACAGTGTCCATCACTTCGAAAGAAACGCAATTGACAT	1783
Db	1784	GGAACTTCTAAGATCTCAACGACAAATATTCGAATGTGCGCAAGAAACATGCTTTTGGACAT	1843
QY	1784	AAGCAGAGTTTGGGATCAACGGTTACAGATACCGAGATGGCTTACAGCTTTGGCCAACTTGA	1843
Db	1844	AACAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTTGTGTGGCAACAAGGA	1903
QY	1844	AACCAAGAGTTTGGTATGAGAACCCGTCATTGAACCTTGTGCTTTGTATACCAACTTCAA	1903
Db	1904	AACCAAAAAAATTTGGTTATGAGAAACATCTCTGGAATCTATGCTTTTAACTATTAACATTA	1963
QY	1904	ATCTACATATTTAACTGAGAGTGCCTTATGGGTATATATAGGGGACA	1950
Db	1964	TCCTAATATATATAGCTCATATATGCTAAATTTATTTGGCTTATAGACATA	2010

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RESULT 13
US-09-895-752-29
? Sequence 29 Application US/09895752
? Patent No. 6559297
? GENERAL INFORMATION:
? APPLICANT: Chappell, Joseph
? APPLICANT: No. 65592971, Joseph P.
? APPLICANT: Starks, Courtney M.
? APPLICANT: Manna, Kathleen R.
? TITLE OF INVENTION: SYNTHASE
? FILE REFERENCE: 07678-025001
? CURRENT APPLICATION NUMBER: US/09/895,752
? CURRENT FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: 09/398,395
? PRIOR FILING DATE: 1999-03-17
? PRIOR APPLICATION NUMBER: 60/100,993
? PRIOR FILING DATE: 1998-09-18
? PRIOR APPLICATION NUMBER: 60/130,628
? PRIOR FILING DATE: 1999-04-22
? PRIOR APPLICATION NUMBER: 60/150,262
? PRIOR FILING DATE: 1999-08-23
? NUMBER OF SEQ ID NOS: 58
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 29
? LENGTH: 2196
? TYPE: DNA
? ORGANISM: Abies grandis
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (69)...(1949)
? OTHER INFORMATION: mycense synthase
US-09-895-752-29

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Query Match	53.2%;	Score 1071.6;	DB 4;	Length 2196;
Best Local Similarity	75.0%;	Pred. No. 4.1e-306;		
Matches 1430;	Conservative 0;	Mismatches 441;	Indels 36;	Gaps 6;

QY	68	CAGGTGCGGCTCAAGTCTTCTCATGAGATTAAAGCTCTCGGTGAAACAATCCCAACT	127
Db	116	CAAGTCGTGATCAAGTTCATTCAATTCAATGAACATTAAGCTCTCTATGAAACAATCCCAACT	175
QY	128	TGGAATCTGCAGGCGCGGGAAATCCGTCGCGCAATTCCTATAACATGTGTTGACAAAGT	187
Db	176	TGGAATCGTAGGAGGAGAAATCTGCACGCCCTTCATGAGCATCAATTTGGCCACCGC	235
QY	188	CGCATCTACTGATCTGTACAGAGACCGGTGGGCAATCATATTCACCACTGTGGAGCA	247
Db	236	TGCACCTGATGATGGTGTACAAABAACGATAGTGATCTACCATTCGAATATCTGGAGCA	295
QY	248	TGATTTCAATACGTCCTGATCTCAAGCGCTTATGAGACACCTGATTAACGGGAACGTGC	307
Db	296	TGATTTCAATACAGTCCTCTTATCAAGCGCTTATGAGGAAACCTCTTAACAGGAACGTGC	352
QY	308	TGACAGACTTATTTGGGGAATGAAGATATATATGTTCAATTCAAAGTCGTGAAGATGG	367
Db	353	TGAAGATTAATTTGTGAGAGTGAAGAAAGATATTTCAATTCATATGTAACCTGAGTATGG	409
QY	368	AGG-----CAATGATCTCTTCAACGACTTTGCTGTGATGACCTTGA	412
Db	410	AAGATTAATAGTTCCTTATATGATCTTCAAGCAACGCTTTGATGATGATCGATACCTTGA	469
QY	413	ACGATTTGGGAATGACACAGCATTTCAAAAAAGATTAATAAACCGCACCTGATATGTTAA	472
Db	470	ACGTTTGGGATGCTGACATTTCAAGAACGATATAATCACTGACTCTGATATATGTTT	529
QY	473	CAGTTATTTGAAGGAAAAAGCATTTGATGAGGAGAGATGTTGTGACTGACCTCAA	532
Db	530	CCGTTACTGGGACGAAAAACGGCATTTGATGAGGAGAGACAGTATTTGTTACTGATCTCAA	589
QY	533	CTCAACCGCCTTGGGGCTTGGAACTCTCCGACATCAAGGATACACTGTGCTTCAGATGT	592
Db	590	CTCAACTGCGTTGGGGTTTGCACATCTTCGATTCACAGGATACACTGTATCTCAGAGGT	649
QY	593	TTTGAACGTTTAAAGACAAAAATGGGCAATTTCTCCACATCCCAATATTCAGATGA	652
Db	650	TTTAAAGCTTTTCAMATCAAAATGACAGTTGTATGCTCCCC--GCTCAGACAGA	706
QY	653	GGGAGATTAAGAGCGCTTCTCATTTATTCAGGGCTCCCTGATGCTTCCCGGGA	712
Db	707	GGGAGATTAAGAGCGCTTCTCATTTATTCAGGGCTCCCTCATGCTTCCCTGATGA	766
QY	713	GAAAGTATGATGMAAGCTGMAACATTCCTACAAAAATTTTAAAGAGAGCCCTGCAAA	772
Db	767	GAAAGTATGATGMAAGCTGMAACATTCCTACAAAAATTTTAAAGAGAGCCCTGCAAA	826
QY	773	GATTCGGGCACTGAGTATCTTTCACTTGAAGATACGGGACGTTCTGAAATATGATGGCA	832
Db	827	GATTCGAGTCGCGCT--CTTTCACAAAGATTAAGATTTGTATGGAATATGCTGGCA	883
QY	833	CACCAATTTTGCACAGCTTGGAGAGCAAGAAATTCATGAGACGCTCTTTGGACAGCACATTA	891
Db	884	CACCAATTTTGCACAGATTTGGAGAGCAAGAAATTCATGAGACACTTTGGAAGAAGACAG	943
QY	892	-----AAATTAAGAACGCCCGGAGAACTTTTGAAGACTTGCAGAAATTTGGAATTCAA	943
Db	944	TGCATGCTCAATTAATAATGCTGGAGAAAGCTTTTGAAGACTTGCAGAAATTTGAGTTCAA	1003
QY	944	TATATTTCACTCTTACAGAGAGAGAGATTAAAACATGTTTCCGATGCTGGAAGAAGCTC	1003
Db	1004	TATATTTCACTCTTACAGAGAGAGAGATTAAAACATGTTTCCGATGCTGGAAGAAGCTC	1063
QY	1004	GGGTTCTCTGAGATGACCTTGTGTGACATCTGACAGTGAATATATACGTTTGGCTTC	1063
Db	1064	GGATTTGCTTAATTTGACATTTTGTCTGGCAATCTGCAATGTGAATTTCTACACTTTTGGCTTC	1123

QY	1064	TTGCATTGCGTTCGAGCCTCAACAACTTCGATTCAGATCTCGGCTTTACCAAGATGCTCA	1123
Db	1124	TTGTATTGCCATTGATCCCAAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTGTCA	1183
QY	1124	TCCTTATCACGGTTCTTGACGACATGTACGACGCTCTTCGGCAACAGTACGAGCTGGAAT	1183
Db	1184	TCCTGTCCACATTTTGTGACGATATTTTACGACACTTTTGGAAACGATTCGAGCTTGAAC	1243
QY	1184	CTTCACAGCCGCAATTTAAGATGGGATCCGTCGCGCATGTGAATGCTTCAGAAATATAT	1243
Db	1244	CTTCACATCTGCATTTAAGATGGAATTCATCGAGATGAAACCTTCCAGAAATATAT	1303
QY	1244	GAAGAGAGTGTACATGATGTTTATCAACCCGTAATGAAATGCTTCAGTGGCAGAGAA	1303
Db	1304	GAATATGTGTATCANTGTCGTGTTGAAACGTAAATGAACTGACACGAGAGCGGAGAA	1363
QY	1304	GGCTTCAGAGCCGAGACACGCTCAACTATTCAGAAACAGGCTTGGAGGCGTGTGTTGATTC	1363
Db	1364	GACTCAAGGGGAAACACTCTCAACTATATGTTTCGAAAGGCTTGGAGGCGTGTATTTTGAATTC	1423
QY	1364	GTATATGACGAGAGCAAGTGGATCGCACTGCTATCTGCCCAGCTTTGAGAGTACTT	1423
Db	1424	ATATATGGAAGAGCAAAATGATATCTTAATGCTTATCTGCCAATGTTTGAAGAGTACCA	1483
QY	1424	GGAGAACGGGAAAGTTAGCTCTGCTCATGCGCCATGCGCACTGCACACCATTTGACGTT	1483
Db	1484	TGAGAATGGGAAAGTAGACTCTGCATATCGGCTGAGCAACATTGCAACCCATCTTCACCTT	1543
QY	1484	GGACATCCCTCTTCTCTGATCAATCCCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGA	1543
Db	1544	GAATGCAATGCGCTTCTGTATCATCTTGAAGAGAAATGATTTTCCATCAAGTTCATTAATGA	1603
QY	1544	CTTGATATGTATCATCTCTTCGATTTAAGAGTGATACACGCTGCTTACAAAGCAGACAGGGC	1603
Db	1604	TTTGGCAATCGTCTTCTTCCTGCGCTACGAGGTGACACAGCTGTACAAAGCCGATAGGGA	1663
QY	1604	CCGTGAGAAAGAAAGCTTGTCTATATATCTGTTATATGAAAGCAATCCTGGATTTAACGGA	1663
Db	1664	TCGTGTGGAAGAAAGCTTGCTGTATATCATGTTATATGAAAGCAACATCTGATCAACCGA	1723
QY	1664	AGAAGATGCTCTGAATCATATCACTTCAATGATCAAGGACCAATCAAGAAATTTAAATTTG	1723
Db	1724	AGAAATGCTCCCTCATCATATCATATGCAATGCTGTCAATGACATTAACAAAGATTTAAATTG	1783
QY	1724	GAGCTTCTAAAGCCAGACAAACAGTGTTCCTCATCACTTCAAGAAACACGATTTGACAT	1783
Db	1784	GGAATCTTCAAGATTCACCAACGAAATATTCGAATGCTGCGCAAGAAACATGCTTTTGGACAT	1843
QY	1784	AAGCAGATTTTGGCATCACGGTTACAGATPCCAGATGGGCTACAGCTTTGGCAACGTTGA	1843
Db	1844	AACAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGGCAACAGGA	1903
QY	1844	AACAAAGAGTTTGTGATGAGAACCGTCATTTGAACCTGTGCTTTGTAAACAACCTTCAA	1903
Db	1904	AACAAAAAATTTGTTATGAGAAACACTCCTGAATCTATGCTTTTAACTATTAACATA	1963
QY	1904	ATCTACATATTTAATCTAGGATGCCCTATGGGTATATTAAGGACACA	1950
Db	1964	TCCATTAATTAATAGCTCATTAATGCTAAATTAATGGCCTTATGACATA	2010
RESULT 14			
US-09-903-012B-29			
Sequence 29 Application US/09903012B			
Patent No. 6569656			
GENERAL INFORMATION:			
APPLICANT: Chappel, Joseph			
APPLICANT: No. 65696561, Joseph P.			
APPLICANT: Starks, Courtney M.			
APPLICANT: Manna, Kathleen R.			
TITLE OR INVENTION: SYNTASES			
FILE REFERENCE: 07678-025001			
CURRENT APPLICATION NUMBER: US/09/903.012B			

	CURRENT FILING DATE:	2001-07-11
	PRIOR APPLICATION NUMBER:	60/100,993
	PRIOR FILING DATE:	1998-09-18
	PRIOR APPLICATION NUMBER:	60/130,628
	PRIOR FILING DATE:	1999-04-22
	PRIOR APPLICATION NUMBER:	60/150,262
	PRIOR FILING DATE:	1999-08-23
	NUMBER OF SEQ ID NOS:	58
	SOFTWARE:	FastSeq for Windows Version 3.0
	SEQ ID NO 29	
	LENGTH:	2196
	TYPE:	DNA
	ORGANISM:	Abies grandis
	FEATURE:	
	NAME/KEY:	CDS
	LOCATION:	(69)...(1949)
	OTHER INFORMATION:	myricene synthase
	US-09-903-012B-29	
Query Match	53.2%; Score 1071.6; DB 4;	Length 2196;
Best Local Similarity	75.0%; Pred. No. 4,1e-306;	
Matches 1430; Conservative	0; Mismatches 441; Indels	36; Gaps 6;
Oy	68 CAGGTGCTGCCTCAGTTCCTCTCATGTAGATTAAAGCGCTCTCCGTGGAACCAATCCCAACTCT	127
Db	116 CAATCTCTTGATCATGGTTCAATTCATGAAACAATAAGCCCTCCCTAATGAAACAATCCCAATCT	175
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Db	176 TGGAAATCGTAAGCGGAGGAATCTGTACAGCCCTTCATATGACATCAAGTTTGGCAACGC	235
Oy	188 CGCATCTACTGATTTCTGTACAGAGACGCGTGGCAACTATCATTCATCACTGTGGAGCA	247
Db	236 TGCACTCGTAGATGTGTACAAAAGACCATAAGGTGATCACCATTCCAATATCTGGAGCA	295
Oy	248 TGATTTATATPACAGTCTGTGATCTCAAGCCCTTAATGAGACCTGATTAACCGGGAACGNGC	307
Db	296 TGATTTATACAGTCTC--TATCAACGCTTAATGGGAAACCTCTTAACAGAACCTGC	352
Oy	308 TGAAGAATTATTTGGGAGTAAGATATATATGTTCAATTTCAAGTCTGTGAAGATGG	367
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1964 TCCATATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2010

RESULT 15
US-09-900-797-29
Sequence 29, Application US/09900797
Patent No. 6645762
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph P.
APPLICANT: No. 66457621, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTASES
FILE REFERENCE: 07678-023001
CURRENT APPLICATION NUMBER: US/09/900,797
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq For Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69)...(1949)
OTHER INFORMATION: myrcene synthase
US-09-900-797-29

Query Match 53.2% Score 1071.6; DB 4; Length 2196;
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Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

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 Job time : 174 secs

OM nucleic - nucleic search, using sw model

2664.540 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 6432934

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/pdatata/2/pubnpa/PCT_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Query Match	Score	length	DB	ID	Description
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1	2013	100.0	2013	15	US-10-025-145A-64	Sequence 64, Appl
2	1306.8	64.9	2018	9	US-09-887-586A-19	Sequence 19, Appl
3	1306.8	64.9	2018	9	US-09-903-012-19	Sequence 19, Appl
4	1306.8	64.9	2018	10	US-09-900-797-19	Sequence 19, Appl
5	1306.8	64.9	2018	13	US-09-893-820-19	Sequence 19, Appl
6	1306.8	64.9	2018	14	US-10-041-007-21	Sequence 21, Appl
7	1306.8	64.9	2018	15	US-10-025-145A-3	Sequence 3, Appl
8	1092.4	54.3	1890	15	US-10-025-145A-77	Sequence 77, Appl
9	1072.4	53.3	2186	15	US-10-025-145A-66	Sequence 66, Appl
10	1071.6	53.2	2196	9	US-09-887-586A-29	Sequence 29, Appl
11	1071.6	53.2	2196	9	US-09-903-012-29	Sequence 29, Appl
12	1071.6	53.2	2196	10	US-09-900-797-29	Sequence 29, Appl
13	1071.6	53.2	2196	13	US-09-893-820-29	Sequence 29, Appl
14	1071.6	53.2	2196	14	US-10-041-007-25	Sequence 25, Appl

45	390.2	19.4	1735	9	US-09-903-012-9	Sequence 49, Appl
44	390.2	19.5	1735	14	US-09-887-566A-49	Sequence 13, Appl
43	391.6	19.5	2528	14	US-10-041-007-15	Sequence 13, Appl
42	391.6	19.5	2424	15	US-10-025-145A-15	Sequence 15, Appl
41	391.6	19.5	2424	14	US-10-041-007-14	Sequence 14, Appl
40	391.6	19.5	2424	13	US-09-883-820-45	Sequence 45, Appl
39	391.6	19.5	2424	10	US-09-900-070-45	Sequence 45, Appl
38	391.6	19.5	2424	9	US-09-903-012-45	Sequence 45, Appl
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31	429.6	21.3	1967	15	US-10-025-145A-17	Sequence 17, Appl
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25	471	23.4	696	15	US-10-025-145A-5	Sequence 5, Appl
24	925.4	46.0	2089	15	US-10-025-145A-5	Sequence 5, Appl
23	925.4	46.0	2089	14	US-10-041-007-23	Sequence 23, Appl
22	925.4	46.0	2089	13	US-09-883-820-57	Sequence 57, Appl
21	925.4	46.0	2089	9	US-09-900-070-57	Sequence 57, Appl
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19	925.4	46.0	2089	9	US-09-887-566A-57	Sequence 57, Appl
18	929.4	46.2	2429	15	US-10-041-007-27	Sequence 27, Appl
17	929.4	46.2	2429	14	US-10-041-007-27	Sequence 27, Appl
16	1071.6	53.2	2205	15	US-10-025-145A-31	Sequence 31, Appl
15	1071.6	53.2	2205	15	US-10-025-145A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

; Sequence 64, Application US/10025145A

; GENERAL INFORMATION:

APPLICANT: Bohlmann, Joerg

APPLICANT: Phillips, Michael A.

FILE REFERENCE: WSUR116414

CURRENT FILING DATE: 2002-06-28

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1998-07-10

PRIOR FILING DATE: 1997-07-11

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; NUMBER OF SEQ ID NOS: 14/
; SOFTWARE: PatentIn version 3.11

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LENGTH: 2013

ORGANISM: *Abies Grandis*

NAME/KEY: CDS

OTHER INFORMATION:

US-10-023-143A-05

Query Match	Score	DB	Version
100.0%	2013	13	2013
100.0%	Pred. No. 0		

Matches 2013; Conservative v; Mismatched v; Under v; Gap v

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Db ATCATCTCTCAAGGAAGTTGACTTCCCATGCAAGCTCAATGACTGATATGATCATCC 1560
Qy 1561 TTGATTAAGAGGTGATACACGCTGCTTACAGGCAACAGGCGCTGAGAGAAAGCTT 1620
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Qy 1621 CGCTATATGATGTTATATGAAGAACAATCCTGATTAACGAGAAAGATGCTCTGAATC 1680
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Qy 1681 ATATCACTTCATGATCAGGAGCGCAATCAAGAAATTAATTTGGAGCTTCTAAAGCCAG 1740
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Db ACGGTTACAGTACCGAGATGAGGCTTGGCAAGTTGAAACAAAGATTGGTGA 1860
Qy 1861 TGAGAACCGTCAATTTGAACCTGTGCTTGTGAACAACCTTCAATCTACATATTAATG 1920
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Qy 1921 AGAGTGCCTTATGAGGTGTATATAGGAGCACAAATAATATGTTGTGTATTAAGC 1980
Db AGAGTGCCTTATGAGGTGTATATAGGAGCACAAATAATATGTTGTGTATTAAGC 1980
Qy 1981 TGTAAATTTATGAATAAAAAAAAAAAAAAAAAAAAAA 2013
Db TGTAAATTTATGAATAAAAAAAAAAAAAAAAAAAAAA 2013

RESULT 2
US-09-887-586A-19
; Sequence 19, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-02501

Db 1844 AACGAGATTGGTCACGAGAACCCCTCTGAACTGTGCTTTGTAGCAACAGCTCAA 1903
QY 1904 ATCTACATATATTAATCTGAGATGCGCCCTATGGGTGATATAGGGCACAACAAAATATATAT 1963
Db 1904 ATCTATGCCCTATGCTATGTGCGGTTAAATAATATGTGAGAGGTAGCCCTTGATGTAGA 1963
QY 1964 GGTGTGTTAGTAAAGCTGTATATTATGAAAAAATATATATATATATATATATATATATAT 2013
Db 1964 GGATAGATTGTTGTTAT 2013

RESULT 3

US-09-903-012-19
; Sequence 19, Application US/09903012
; Patent No. US20020094557A1
GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 05/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-903-012-19

Query Match 64.9%; Score 1306.8; DB 9; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;
QY 68 CAGGTGCTGCTCACTTCTTCATGAGATTAAAGGCTCTCCGTAGAACATCCCACTCT 127
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Dp	1184	CTTCAACGCGCAATGAAAGATGGGATCGCTCCTCGATGAATGCTCTCCAGAAATATAT	1243
QY	1244	GAAGAAGGTATACATGATGTTTATCAACCCGTAAATGAAAATGCGCTCGAGTGGCAGAGAA	1303
Dp	1244	GAAGAAGGTATACATGAGCGTTTACGACACCGTAATGAAATGCGCTCGAGGCGCAGAGAA	1303
QY	1304	GGCTCAAGGCGGAGACACGCTTCAACTATATGCAAGACAGGCTTTGGGAGGGGTGTTTGAATTC	1363
Dp	1304	GGCTCAAGGCGGAGATAGCTCAACATATAGCTGGGAACCTTTGGGAGGCGTTATATATGATTC	1363
QY	1364	GTATATGACGAGAACCAAAAGTGGATCGCACATGTTATATGCCCCAGTTCGAGAGTACTT	1423
Dp	1364	GTATATGACGAGAACGAAAGTGGATCGCACATGTTATATGCCCCAGTTCGAGAGTACTA	1423
QY	1424	GGAGAACGGGAAAGTTAGCTCTGCTCATCGGCCATGCGGCACTGCACGCAACCATTTGACGTT	1483
Dp	1424	CGAAGATGGGAAAGTTAGCTGTGGCTCATCGCATATTCGCGATTCGCAACCATTTGACCAAT	1483
QY	1484	GGACATCCCTTTCTGTATCAATTCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA	1543
Dp	1484	GGACATCCCTTTCTGTATCAATTCCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAAACGA	1543
QY	1544	CTTATATATGATTCATCCCTCCATTAAAGAGTGAATACACGCTGCTTACAAGCAGACAGGGC	1603
Dp	1544	CTTGGCATTGTCCTCCTTCGATTTACAGAGTGAATACGCGGTGCTTACAAGGCGGACAGGGC	1603
QY	1604	CGGTGAGAGAGAAGCTTCGTATATATCATGTTATATGGAAGACAATCCTGGAATTAACGA	1663
Dp	1604	TCTGTGAGAGAAAGCTTCCTTATATATCATGTTATATGGAAGACAATCCTGGAAGTATACGA	1663
QY	1664	AGAAGATGCTCGAATCATATCAACTTCATGATACAGGAGCGCATTCAGAGAAATTAATGTG	1723
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QY	1724	GGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCACTTCCAAAGAAACAACGATTTGACAT	1783
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QY	1784	AAGCAGAGTTTGGCATCAACGGTTACAGATATCCGAGATGGCTTACAGCTTTGCCAAGTTGA	1843
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QY	1904	ATCTACATATTAATCTAGAGATGCCCTATAGGGTGTATATATGAGGCAACAAAAATTAATAT	1963
Dp	1904	ATCTATGCCCTATGCTATGTGCGGGTTAAATATATATGGAAGGTATAGCGTGTGATGTAGA	1963
QY	1964	GCTTGTGTATTAAGCTGTATATTTATCAAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAA	2013
Dp	1964	GGATTAAGTTTGTATTAATTTTAAATTAAGTTGTATTTTAAAAAATTTTAAAAAATTTTAAAA	2013

RESULT 5
US-09-893-820-19
Sequence 19, Application US/09893820
Publication No. US20040053386A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20040053386A1, Joseph P
APPLICANT: Stark, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/893,820
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US/09/398,395A
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 86/100,993

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: PRIOR FILING DATE: 1996-09-18
: PRIOR APPLICATION NUMBER: 60/130,628
: PRIOR FILING DATE: 1999-04-22
: PRIOR APPLICATION NUMBER: 60/150,262
: PRIOR FILING DATE: 1999-08-23
: NUMBER OF SEQ ID NOS: 58
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 19
: LENGTH: 2018
: TYPE: DNA
: ORGANISM: Abies grandis
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (6)...(1889)
: OTHER INFORMATION: piene synthase
: OS-09-893-820-19

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Query Match	64.9%	Score 1306.8;	DB 13;	Length 2018;
Best Local Similarity	81.0%;	Pred. No. 0;		
Matches 1595;	Conservative	0;	Mismatches 342;	Indels 33; Gaps 5;

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OY	128	TGGAATCGACGCCGGGAAATCCGTGCGCATTCCTAATAACATGTGTTGACAAGCT	187
Db	113	AGGAATGAGTGGCGAGGGAATCTATCACTCTCTCATCAGATGAGCTCTACCAACGT	172
OY	188	CGCATCTACGATTCGTGACAGACACGCTGGGGAACTATCATTCGAACTGTGGGACGA	247
Db	173	TGTAAACGAGATGCTGTGACAAACGATGAGGAGATTCATTCGAACTCTTGAGACGA	232
OY	248	TGATTTCAATACGCTCTGATCTCAACGCCCTTATGAGACCTGATTAACGGGAAACGTGC	307
Db	233	TGATGTCATACAGTCT---TTACCAACGCTTATGAGAAAATATGTAACCTGGAGCGTGC	289
OY	308	TGACAGACTTATTTGGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGGAAATGG	367
Db	290	TGAGAACTGATCGGGGAAGTAAAG---AACATGTTCAATTCGATGTCTATTGAAGAATGG	346
OY	368	AG-----GCATGATCTCTTCCAAACGACTTTTGCCTGCGATGACGTGA	412
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OY	413	ACGTTTGGGAATCGACACGACATTTCAAAAAAGATTAATAACGGCACCTGCATTAATGTAA	472
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OY	773	GATTCGGGATCCAGTATATCTTTCACTAAGAGATACGGGAGCTTCTGGAATATGTGTTGGCA	832
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1904 ATCTAATATTTAATGAGATGCGCTTATGAGGTTATATGAGGACACAAATTAATAT 1963

1904 ATCTAATATTTAATGAGATGCGCTTATGAGGTTATATGAGGACAGCTTGAATTTGA 1963
1964 GGTGTGTGTATTAAGCTTAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 2013
1964 GGTGTGTGTATTAAGCTTAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 2013
RESULT 6
US-10-041-007-21
; Sequence 21, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081051
; CURRENT APPLICATION NUMBER: US/10/041.007
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandie
US-10-041-007-21
Query Match 64.9%; Score 1306.8; DB 14; Length 2018;
Best Local Similarity 61.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;
68 CAGGTGCTGCTGAGTCTTCTCATGAGATTAAGGCTCTCGTGAACATCCAACTCT 127
53 CAAATCGTGTATGATTTCTTACCATGAGCTTAAGGCTCTCTTGAACATTCAGCTCT 112
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DB 1184 CTTCACAGCGCACAATTAAGAGATGGATCGCTCGCGATGGAATGCTTCAGAAATATAT 1243
QY 1244 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
DB 1244 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
QY 1304 GGCTCAAGGCGGAGACGCTCAATATGACAGAGAGCTTGGAGGCGTGTGATGATTC 1363
DB 1304 GGCTCAAGGCGGAGATGACCTCAATATGATGATGATGATGATGATGATGATGATGATTC 1363
QY 1364 GTATATGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
DB 1364 GTATATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
QY 1424 GGAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
DB 1424 GGAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
QY 1484 GGACATCCCTTCTCTGATCAATCTCAAGAGAGATGATGATGATGATGATGATGATGATGAT 1543
DB 1484 GGACATCCCTTCTCTGATCAATCTCAAGAGAGATGATGATGATGATGATGATGATGATGAT 1543
QY 1544 CTGATATGATATCATCTTTCATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 1603
DB 1544 CTGATATGATATCATCTTTCATTAAGAGATGATGATGATGATGATGATGATGATGATGAT 1603
QY 1604 CCGTGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
DB 1604 CCGTGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
QY 1664 AGAAGATGCTGATCATATCAATCTTCAAGAGAGATGATGATGATGATGATGATGATGATGAT 1723
DB 1664 AGAAGATGCTGATCATATCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1723
QY 1724 GGAGCTTCAAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1783

DB 1724 GGAATCTCTCAAAACAGACATCATATGTTCCATCTCGCGAGAGAGAGATGCTTTGACAT 1783
QY 1784 AAGAGAGTTTGGATACAGGTTTACAGATCCGAGATGAGCTTGCAGCTTTGCAAGTTGA 1843
DB 1784 CGCAGAGCTTTCATTAACGCTTACAAATATCCGAGAGCTTACAGCTTTGCAAGTTGA 1843
QY 1844 AACAAAGAGTTTGGTATGAG 1903
DB 1844 AACAAAGAGTTTGGTATGAG 1903
QY 1904 ATCTAATATATTAAG 1963
DB 1904 ATCTAATATATTAAG 1963
QY 1964 GGTGTGTTGTAAG 2013
DB 1964 GGTGTGTTGTAAG 2013

RESULT 7
US-10-025-145A-3
; Sequence 3, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoclonal Syntheses from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1892)
; OTHER INFORMATION:
US-10-025-145A-3

Query Match 64.9%; Score 1306.8; DB 15; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY 68 CAGGTGCTCCTCAAGTTCTTCTCATGATTAAGGCTCTCCGTAAGAAACAATCCCACTCT 127
DB 53 CAATTCGTGATCAGTTCTTCAATGAGCTTAAGGCTCTCTCTGAAACAATCCAGCTCT 112
QY 128 TGAATCTGACAGGCGGGGAAATCCGTCGCGCATTTCCATAAACATGTGTTGAACAAGCT 187
DB 113 AGAATGAGTAGGAGAGAGAAATATATCACTCTTCATACGATGAGAGCTTACACCGT 172
QY 188 CGCATCTACTGATCTGTACAGAGAGCGTGGCAACTATCATTTCCAACTGTGGAGCA 247
DB 173 TGTAAACGATATGCTGTACAGAGAGCGATGAGGAGATTTCAATTCACACTCTGGAGCA 232
QY 248 TGATTTCAATACGCTCTGATCTCAACGCTTATGAGACACTGATTAACGGGAAAGCTGC 307
DB 233 TGATGTCAATACGCTCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
QY 308 TGAACAGCTTATTTGGGAGAGAGAGATATATGTTCAATTTCAAGTCCGCTGAGAGATG 367

Db 290 TGAGAACTGATCGGGGAAGTAAAG---ACATGTTCAATTCGATGATCATTAAGAAATGG 346
Qy 368 AG-----GCAATGATCTCTTCAAGAACTTTTGTGCTGATGATGAACTTGA 412
Db 347 AGAGTTAATGAGTCCGCTCAATGATCTATTCAGCCCTTGGATGTCAGACGCTTGA 406
Qy 413 AGCTTTGGGAATCGACAGCACTTTCAAAAAGAGATTAAGAAAGGCACTGATTAATTTA 472
Db 407 AGCTTTGGGAATCGATGATCTTCAAGATGATTAAGATGAGGCTTGAATTAATTTA 466
Qy 473 CAGTTAATGGAAGCAAAAAAGCATTGATGTTGGAGGAGAGAGTGTGTGACTGACTCA 532
Db 467 CAGTTAATGAGGCGAAATGAGATGCGGAGGAGAGTGTGTGACTGACTGAA 526
Qy 533 CTCAACCGCTTTGGGGCTTCCAACTCTCCGACTCAACGATGATGCTGTCTTCAAGATG 592
Db 527 CTCAACCGCTTTGGGGCTTCCAACTCTCCGACTCAACGATGATGCTGTCTTCAAGATG 586
Qy 593 TTTGAAGCTTTTAAAGCAAAAAATGGGCAATTTTCTCCACTGCAATTAATTCAGATGA 652
Db 587 TTTCAAGCTTTTCAAGGCAAAAAATGGGCAATTTTCTCCACTGCAATTAATTCAGATGA 646
Qy 653 GGGAGAGATTAGAGCGCTTCAATTTATTCAGGCGCTTCCCTGCTGCGCTTTCCCGGGA 712
Db 647 TGAAGAGATCAGAGCGCTTCAATTTATTCGCGGCTTCCCTGCTGCGCTTTCCAGGGGA 706
Qy 713 GAAAGTTATGATGAACTGAAACATTTCTTCAAAATATTTAAGAAAGCCCTTCAAAA 772
Db 707 GAAATATTTGATGAGCTGAATCTTCTTACAAATATTTAAGAAAGCCCTTCAAAA 766
Qy 773 GATTCGGGCTTCCAGTATCTTCACTAGAGTACGGGAGCTTGGAAATATGTTGGCA 832
Db 767 GATTCGGGCTTCCAGTATCTTCACTAGAGTACGGGAGCTTGGAAATATGTTGGCA 823
Qy 833 CACCAATTTGCGACGCTTGAAGCAAGAAATTCATGACGCTTGTGGAACAGCACTTA 892
Db 824 CACATATTTGCGACGCTTGAAGCAAGAAATTCATGACGCTTGTGGAACAGCACTGA 883
Qy 893 AAATTAAGACG-----CGCGAGAACTTTTGAACCTTGGCAAAATTTGAATTTCA 943
Db 884 GAACACGAACTATATGTAAGAGCAAAAACTTTTAAACCTGCAAAAATTTGAGTTTCA 943
Qy 944 TATATTTCACTCTTCAAGAGAGAGAGATTAACATGTTTCCGAGTGGAAAGACTC 1003
Db 944 CATCTTTCAATCTTCAAAAAGAGAGATTAAGAACTTGTGCAATGTTGAAGAACTC 1003
Qy 1004 GGGTTCTCTGAGATGACCTTCTGTGCAATCTGCAAGTGAATCTACGCTTTGGCTTC 1063
Db 1004 GGGTTCTCTGAGATGACCTTCTGTGCAATCTGCAAGTGAATCTACGCTTTGGCTTC 1063
Qy 1064 CTGCAATGCGTTCCAGCTTCAACATTTCTGATTCAGACTCGGCTTTGCAAGACCTGCA 1123
Db 1064 CTGCAATGCGTTCCAGCTTCAACATTTCTGATTCAGACTCGGCTTTGCAAGACCTGCA 1123
Qy 1124 TCTTATCAGCGTTCTTGAAGATGATGAGCACTTCCGACAGTGAAGAGCTGAACT 1183
Db 1124 TCTTATCAGCGTTCTTGAAGATGATGAGCACTTCCGACAGTGAAGAGCTGAACT 1183
Qy 1184 CTTCAAGCGCAATTAAGAGATGGATCGTCCGCGATGGAATGCTTCCAGATATAT 1243
Db 1184 CTTCAAGCGCAATTAAGAGATGGATCGTCCGCGATGGAATGCTTCCAGATATAT 1243
Qy 1244 GAAAGGAGTGAATGATGATGATTAACACCGTAAATGAAATGCTGAGTGGCAGAGAA 1303
Db 1244 GAAAGGAGTGAATGATGATGATTAACACCGTAAATGAAATGCTGAGTGGCAGAGAA 1303
Qy 1304 GGGCTCAAGCGCGAGACAGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTC 1363
Db 1304 GGGCTCAAGCGCGAGATGACCTCAATATGCTGGAGAGCTTGGAGGCGTGTGATTC 1363
Qy 1364 GTATATGAGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
Db 1364 GTATATGAGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423

Qy 1424 GGAGAACGGGAAATTTACTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGAGCTT 1483
Db 1424 CGAGATGGGAAATTTACTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGAGCTT 1483
Qy 1484 GGACATCCCTTTCTGATCATCTCTCAAGAAAGTATCTTCCATCGAAAGCTCAATGA 1543
Db 1484 GGACATCCCTTTCTGATCATCTCTCAAGAAAGTATCTTCCATCGAAAGCTCAATGA 1543
Qy 1544 CTTGATATGATCATCTTGTGATTAAGAGTGAATCAAGTGTCTTCAAGGAGAGAGG 1603
Db 1544 CTTGATATGATCATCTTGTGATTAAGAGTGAATCAAGTGTCTTCAAGGAGAGAGG 1603
Qy 1604 CCGTGAAGAAAGAGTGTCTTATATCATGTTATATGAAAGATCTTGTGATTAACGA 1663
Db 1604 TCGTGAAGAAAGAGTGTCTTATATCATGTTATATGAAAGATCTTGTGATTAACGA 1663
Qy 1664 AGAAGATGCTCTGATCATATCACTTCAATGATGATGAGGAGCCATCAAGAAATTAAT 1723
Db 1664 GGAAGATGCTCTGATCATATCAAGCCATGATGATGATGATGATGATGATGATGAT 1723
Qy 1724 GGAAGCTTAAAGCGAGCAACAGTGTTCATCACTTCCAAAGAAACAGCATTTGACAT 1783
Db 1724 GGAAGCTTCAAAACAGACATCAATGTTCCCATCTCGGCGAAAGAAACATGCTTTGACAT 1783
Qy 1784 AAGCAGATTTGGCATCAAGCTTCAAGATACCGAGATGCTTCAAGCTTTGA 1843
Db 1784 CGCAGAGCTTTCATTAAGCTTCAATGAGCTTCAAGATACCGAGATGCTTCAAGCTTTGA 1843
Qy 1844 AACAAAGATTTGATGATGAGAAACGCTTGAATGAACTTGTGTAACAACTTGA 1903
Db 1844 AACAAAGATTTGATGATGAGAAACGCTTGAATGAACTTGTGTAACAACTTGA 1903
Qy 1904 ATCTATGCTTAAAGCTGTAATTTATGAAAAAATTTGAAAAAATTTGAAAAAAT 2013
Db 1904 ATCTATGCTTAAAGCTGTAATTTATGAAAAAATTTGAAAAAATTTGAAAAAAT 2013
Qy 1964 GGTGTGTGATTAAGCTGTAATTTATGAAAAAATTTGAAAAAATTTGAAAAAAT 2013
Db 1964 GGTGTGTGATTAAGCTGTAATTTATGAAAAAATTTGAAAAAATTTGAAAAAAT 2013

RESULT 8
US-10-025-145A-77
; Sequence 77, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Crocneau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; TITLE OF INVENTION: Monocleptene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025, 145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360, 545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052, 249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1890)
; OTHER INFORMATION:
US-10-025-145A-77

Query Match 54.3%; Score 1092.4; DB 15; Length 1890;
Best Local Similarity 76.8%; Pred. No. 8.6e-313;
Matches 1439; Conservative 0; Mismatches 396; Indels 39; Gaps 7;

QY TTTCTATTACTCCGCTGGTTTCCAGGTGTCCTCAGTCTTCTTCTCATGAGTTAAGGCTC 105
DB TTTCTATTACTCCGCTGGTTTCCAGGTGTCCTCAGTCTTCTTCTCATGAGTTAAGGCTC 105
26 TGTCTCCAAATCGGTCTCGCAAAATCGTGAATCGTTTCTATGATGAGATTAAGGCTA 85
QY TCCGTAGAACAAATCCCAATCTTTGGAATCTGCAGCGCGGGGAAAATCCGTCGCATTC 165
DB TCAGTAGAACAAATCCCAATCTTTGGAATCTGCAGCGCGGGGAAAATCTGTGACATTC 145
QY TAAACATGTGTTGACAAGCGTCGATCTACTG---ATTCTGTCAGAGACGCGTGGCA 222
DB TGAGATGAGTTTGAACAACGAGCTCTGATGATCATGTGTACAAAGACGCAATAGTCG 205
QY ACTATCATTTCAACTGTGGAGACATGATTTGATACAGTCTCTGATCTCAACGCTTATG 282
DB AGTTTCATTTCAATCTGTGGAGACGACATTTCAATACATCTC---TATCAACGCTTATG 262
QY GAGACCTGATTTACCGGGAGCGTGCTGACAGATTTATGGGAAAGTAAAGATTAATGT 342
DB GGGACCTTCATACCGGTGACGCTGCTGATGACATTAATGGAAGTAAAGGCTATA---T 319
QY TCAATTTCAAGTCGCTGGAAGATGAG-----GCATGATCTCTTCAAC 387
DB TCACCTCAATTTGACCGGAGATGGAATATCACTCCCTCATGATCTCATTTCAAC 379
QY GACTTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447
DB GCCCTTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 439
QY TAAAAACGCGACTCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507
DB TAAAGACGCGACTCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499
QY GGGAGAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
DB GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 559
QY ACCGATACACTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 624
DB ACCGATACACTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
QY TTTCTCCACTCGCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 684
DB AGTTTGTATGTTCCGCGCATCCAAACAGAGAGATGATGATGATGATGATGATGATGATGAT 679
QY GGGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
DB GGGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
QY CAAATATTTTAAAGAAAGCCCTGCAAAAGATTTCCGGCATCCAGTATCTTTCACTAAGA 804
DB AAAATATTTTAAAGAAAGCCCTTCAAAATATGCTGCTCCAGT---CTTTTCAAGAGA 796
QY TACGGGACGTTCTGGAATATGTTGGACACCAATTTGCCAGCGCTTGGAGCAAGAAAT 864
DB TAGAGTACGTTCTGAGAGATGTTGGCAACCAATATGCTCAAGATTTGGAACCAAGAACT 856
QY ACATGACGCTTTTGGACAGACACTTAAATTAAG-----AACGCCCGGAGAAAC 915
DB ACATGACGTTTGGAGAGAGACATGCTGATGAGACGTTTATATGAAATGAGAAAC 916
QY TTTTGAAGAACTTGGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 975
DB TTTTGAAGAACTTGGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 976
QY AACATGTTTCCGAGTGTGAAAGACTGGGTTCTCTGAGATGACCTTGTGCAATC 1035
DB AAGACCTCTCCAGATGTGAGAAAGATTTGGGTTCTCTCACTGACATTTTCTCGGCACTC 1036
QY GTCAAGTGAAATTAAGCTGTTGGCTTCTGCAATGTCGTTGAGCTTCAACATTTCTGGAT 1095

DB TTTTGAAGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 1037
QY TCAGACTCGGCTTTACCAAGATGCTCATCTTATCAAGCTTCTTGAAGACATGTAGACAG 1155
DB TCAGACTCGGCTTTGCAAAATGTGTATCTTATCAAGCTTGTGAGACATGTATACACA 1156
QY TCTTCGGCACAAGTACAGACTGGAACTTTCACAGGCACAATTTAAGATGGGATCCGT 1215
DB CTTTGGAAACATGAGAGACTGGAACTTTCACAGCTGACATTTAAGATGGGATCCGT 1216
QY CCGGATGAGATGCTTTCAGATATTTGAAAGAGTGTACATGATGTTTATACACCG 1275
DB CTGCCACAGATTTGCTTTCAGAGATTTGAAAGGTTGTACATGTTGTTTACAAACCG 1276
QY TAAATGAAATGCTCGAGTGGCAGAGAGAGGCTCAAGGCGGAGACAGCTCAACTATGCAA 1335
DB TAAATGAAATTTGCTGAGAGGCAACAAGTCTCAAGGCGGAGAGAGCTTCAACATGCTC 1336
QY GACAGCTTGGAGGCGTGTGTTGATTCGATATGACAGAAAGCAAGTGTATGCGCACTG 1395
DB GACAGCTTGGAGGCGCTATCTTGTATGATATGAAAGAAAGTGAATGATTCGAGTGT 1396
QY GTTATCTGCCACGTTTGAAGATGATTTGAGAAACGGAATGTTAGCTTGTCTATGCC 1455
DB GTTATCTGCCACGTTTGAAGATGATTTGAGAAACGGAATGTTAGTGTGTTATGCGCA 1456
QY CATGGGACTGCAACCCATCTGACGTTTGACATCCCTTCCGATCACAATCTCCAAAG 1515
DB TATTCGATTTGCAACCCATCTGACATGATGATGATGATGATGATGATGATGATGATGAT 1516
QY AAGTTGACTTCCATCCAGAGCTCAATGATGATGATGATGATGATGATGATGATGATGAT 1575
DB AATATGACTTTCATGAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
QY ATACACGCTGTACAGGCAAGACGGCCCGTGGAGAAAGCTTGTCTATATCATGTT 1635
DB ACACCTCGCTGTACAGGCAAGACGGCCCGTGGAGAAAGCTTGTCTATATCATGTT 1636
QY ATATGAAAGCAATCTCGATATTAACGAGAAAGTGTCTGATCATATCAATCAATTCATGA 1695
DB ATATGAAAGCAATCTCGATATTAACGAGAAAGTGTCTGATCATATCAATCAATTCATGA 1696
QY TCAGGAGCGCAATCAGAAATTAATTTGAGAGCTTCTTAAAGCCAGACAAAGTGTCCCA 1755
DB TCAATTAATTAATCAAGAAAGTGAATTTGGAGCTTCCGACAGAGCGCAACGCTCATATA 1756
QY TCACTTCCAGAAACACGCAATTTGACATTAAGCAGAGTTTGGCATCAAGGTTACAGATACC 1815
DB TTGCTTCCAGAAACACGCTTTTGAATCTTCAAAAGGTTCCCTTCAAGGCTTCAAGAAATACC 1816
QY GAGATGCTACAGCTTGGCCAAAGTTGAAACAAAGAGTTGATGATGAGAAACGCTCATTTG 1875
DB GAGATGCTTACAGCTTGGCCAAAGTTGAAACAAAGAGTTGATGATGAGAAACGCTCATTTG 1876
QY AACCTGTGCTTTG 1889
DB AGTCTGTGCTTTG 1890

RESULT 9
US-10-025-145A-66
; Sequence 66, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bonlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monocarpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: NSUR118414
; CURRENT APPLICATION NUMBER: US/10/025, 145A
; CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US 09/360,545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052,249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 2186
TYPE: DNA
ORGANISM: Abies Grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(1923)
OTHER INFORMATION:
US-10-025-145A-66

Query Match 53.3%; Score 1072.4; DB 15; Length 2186;
Best Local Similarity 76.4%; Pred. No. 8.2e-307;
Matches 1428; Conservative 0; Mismatches 391; Indels 51; Gaps 7;

83 TTCTTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCACTTGGATCTGAGGCC 142
90 TACTCATATGAGCTCAAGCCCTCTGCGAAGCAATCCCACTTGGATGTAAGGG 149
143 GGGGAATCCGTCGGCATTCATTAACATGTTTGGACAGCGTCGACTTACTGATTC 202
150 AGGGAATCTTTCACACCTTCTGTAGACATGATTTGACACCGCTGATCTGATGATCG 209
203 TGTACAGAGAGCGCGGAGCACTATCATTTCCAACTGGGAGCATGATTTGATGATC 262
210 TCTACAAAGACGATAGTACTATCATTTCAATCTGAGAGCGAGTTTATATACATC 269
263 TCTGATCTCAACGCTTATGAGACACTGATTAACCGGGAACGTGCTGACAGACTTATGG 322
270 TC---TATCAACGCTTATGAGGAGCTTCTTACGAGAACGTGCTGAGAACTGATTTGG 326
323 GGAAGTAAAGATATATGTTCAATTTCAAGTCCGTGAGATGAG----- 369
327 GGAAGTAAAGATATGTTCAATTTCAAGTCCGTGAGATGAG----- 383
370 --GCAATGATCCTTCAACGACTTTGTGGTGAATGCGTTGAACGTTGGGAATCGA 427
384 CTTCAATATCTTATTAAGACGCTTTGATGATGATGATGATGATGATGATGATGATGATG 443
428 CAGGATTTCAAAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 487
444 TAGACATTTCAAAAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 503
488 AAAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547
504 AAAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 563
548 GCTTGAACCTCTCCGATCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 607
564 GTTTCGAACTCTTCCGCTCAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623
608 AGACAAAATGAGGCAATTTTCTCCACTGCGCAATTAAGATTAAGATTAAGATTAAGATTAAGAT 667
624 AGACAAAATGAGGCAATTTTCTCCACTGCGCAATTAAGATTAAGATTAAGATTAAGATTAAGAT 680
668 GCTTCTCAATTTATTAAGAGGCTCTCTGCTGCTTCTTCCGCGAGAAAGTTATGATGA 727
681 GCTTCTCAATTTATTAAGAGGCTCTCTGCTGCTTCTTCCGCGAGAAAGTTATGATGA 740
728 AGTGAACATTTCTCTACAAAATATTTAAGAGAACCTTGCAAAAGATTTCCGCGATCCAG 787
741 GCGTGAATTTTCTCTTCAAGATATTTGAAGAACCTTGCAAAAGATTTCCGCGATCCAG 800
788 TATATCTTCACTAGATAGGAGCGTTCTGGAATATGATGATGATGATGATGATGATGATGATGAT 847
801 T---CTTTCACAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 857

848 CTTGAACGAGAGATTTATCATGACGCTTTTGAACAGACACTA-----AA 893
858 ATTGAACGAGAGATTTATCATGACGCTTTTGAACAGACACTA-----AA 917
894 AATAAGAGCG-----CGCGAAGAACTTTAAGAACTTGAAGATTTGAATTC 943
918 GAAAGAGCGCAATATCTGAGACAGGAGAAAGCTTTTGAAGAACTTGAAGATTTGAATTC 977
944 TATATTTCACTCTCTTCAAGAGAGAGATTAAGATTTTCCGAGTGTGAAGACTC 1003
978 CATCTTCACTCTCTTCAAGAGAGATTAAGATTTTCCGAGTGTGAAGACTC 1037
1004 GGGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1063
1038 GGGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1097
1064 CTGATTCGCTTCAAGAGAGATTTTGAAGATTTTCCGAGTGTGAAGACTC 1123
1098 TTGATTCGCTTCAAGAGAGATTTTGAAGATTTTCCGAGTGTGAAGACTC 1157
1124 TCTTATCAGGCTTCTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
1158 TCTTATCAGGCTTCTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1217
1184 CTTCACAGGAGATTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
1218 CTTCACAGGAGATTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1277
1244 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
1278 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1337
1304 GCTTCAAGGCGGAGACGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1363
1338 GACACAGGCGGAGACGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1397
1364 GTATATGAGAGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
1398 GTATATCAAGAGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1457
1424 GAGAGAGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
1458 AGAGAGCGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1517
1484 GAGACATCCCTTCTGATCAATCTTCAAGAGATGATGATGATGATGATGATGATGATGATGAT 1543
1518 GAGACATCCCTTCTGATCAATCTTCAAGAGATGATGATGATGATGATGATGATGATGATGAT 1577
1544 CTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603
1578 TTTGGCATCTTCTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1637
1604 CCGTGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
1638 CCGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1697
1664 AGAGAGCTCTTATCATATCAATCTTCAAGAGATGATGATGATGATGATGATGATGATGAT 1723
1698 GGAAGATGCTCTATCATATCAATCTTCAAGAGATGATGATGATGATGATGATGATGATGAT 1757
1724 GGAAGATGCTCTATCATATCAATCTTCAAGAGATGATGATGATGATGATGATGATGATGAT 1783
1758 GGAAGATGCTCTATCATATCAATCTTCAAGAGATGATGATGATGATGATGATGATGATGAT 1817
1784 AAGCAGAGATTTGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1843
1818 AACAGAGATTTGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1877
1844 AACAGAGATTTGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1903
1878 AACAGAGATTTGATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1937

QY 1904 ATCTACATA 1913
| | | | |
Db 1938 TTTCTATATA 1947

RESULT 10

US-09-887-586A-29
; Sequence 29, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASE
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Query Match 53.2%; Score 1071.6; DB 9; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTGCGCTCACTTCTTCATGAGATTAAAGCTCCGTAGAAACAAATCCCACT 127
| | | | |
Db 116 CAACTGCTGTAATCAAGTTCAATTCATGAACATTAAGCTCCCTATTAACAAATCCCAATCT 175
| | | | |
QY 128 TGAATCTGACGCGCGGGAATCCGTGCGCATTCATTAACATGTGTTGACAAAGCGT 187
| | | | |
Db 176 TGAATGCGTAGCGGAGGAATCTGTACGCTTCATGAGCATGATTTGGCCACCGC 235
| | | | |
QY 188 CGCATCTACTGATTTCTGTACAGAGCGCGTGGCAACTATCATTCGAACTGTGGAGCA 247
| | | | |
Db 236 TGCACCTGATGATGTGTACAAAGCGATAGTGACTACCATTCGAAATCTGGGAGCA 295
| | | | |
QY 248 TGAATTCATAGTCTGATCTCAAGCGCTTATGAGACACTGATTAACCGGGAACGTCG 307
| | | | |
Db 296 TGAATTCATAGTCTC---TATCAAGCGCTTATGAGGAACTCTTACCAAGGAACGTCG 352
| | | | |
QY 308 TGACAGACTTATGGGGAAGTAAAGATATATGTTCAATTCAGAGCTGGAAGATG 367
| | | | |
Db 353 TGAAGATATATTTGTGAGAGTAAAGATA---TTCAATTCAGATGCTGAGATG 409
| | | | |
QY 368 AGG-----CAATGATCTCTTCACAGCACTTTGCTGTGATGAGCTTGA 412
| | | | |
Db 410 AAGATTAATGAGTCTCTTAATGATCTCATCAAGCGCTTGAATGATGAGTGTGA 469
| | | | |
QY 413 ACGTTTGGGATTCGACAGGCAATTCGAAAGAGATTAAGACGACCTGATTAATGTTAA 472
| | | | |
Db 470 ACGTTTGGGATGCTGACATTCGAAAGAGATTAACATGAGCTGAGATTAATGTTT 529
| | | | |
QY 473 CAGTTATTTGAGCAAGAAAAGCATTTGATGAGGAGAGATGTTGATGACCTGAA 532
| | | | |
Db 530 CCGTTACTGGAGAGAAAAGCATTTGATGAGGAGAGATGTTGATGATGATCTGAA 589
| | | | |
QY 533 CTCAACCGCTTTGGGCTTCGAACTCTCCGACTACAGGATTAAGTGTCTTCAGATGT 592
| | | | |

Db 590 CTCAACTGCGTTGGGCTTCGAACTCTTCGATTAACAGGAGTACATGATCTCCAGAGT 649
| | | | |
QY 593 TTTGACGTTTTTAAAGCAAAAATGGGCAATTTCCCTCACTGCAATATATGATAGA 652
| | | | |
Db 650 TTTAAAGCTTTTCAAGATTAAGAAATGACAGTTTGTATGCTCCCC---GGTCAACAGA 706
| | | | |
QY 653 GGGAGATTAAGAGCGCTTCATTTATTCAGGGCTCCCTCGTCGCTTTCCGGGGA 712
| | | | |
Db 707 GGGTGAATGAGAGCGTCTTATTAATTAATCGGGCTTCCCTCATGCTGCTCCCTGGTGA 766
| | | | |
QY 713 GAAAGTATGATTAAGCTGAAACATTTCTTACAAAATTTTAAGAGAAGCTTCGCAAA 772
| | | | |
Db 767 GAAAGTATGAGAAAGCTGAAATCTTCTCACAAGATATTTGAAAGAGCTTACAAA 826
| | | | |
QY 773 GATTCGGCATCGATTAACCTTCACTAGAGATACGGGAGCTTCGGAATATGATGAGCA 832
| | | | |
Db 827 GATTCAGTCTCCCT---CTTCAAGAGATTAAGTTGTTATGGAATATGGCTGGCA 883
| | | | |
QY 833 CACCAATTTGCGCAGCTTGGAGCAAGAAATTAATGAGAGCTTTTGGACACACTA- 891
| | | | |
Db 884 CACAAATTTGCGCAGATTTGGAGCAAGAAATTAATGAGACACTTGAAGAAAGCACAG 943
| | | | |
QY 892 -----AAATTAAGAACGCGCCGAGAACTTTTGAACCTTGCAAAATTTGAAATTCAA 943
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Db 944 TGCATGCTCAATTAATAATGCTGGAGAAAGCTTTTGAACCTTGCAAAATTTGAGTTCAA 1003
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QY 944 TATATTTCACTCCCTTACAGAGAGAGATTAACATGTTTCCGATGTTGGAAGATC 1003
| | | | |
Db 1004 TATATTAATCTCTTACCAAGAAAGAAATTAATTAATCTTTTGAATGATGAGAAAGATC 1063
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QY 1004 GGGTTCTCTGAGATGACCTTCTGTGCAATCTGACAGTGGAAATTAACGTTTGCTTC 1063
| | | | |
Db 1064 GGATTTGCTTAATTAATGACATTTGCTCGGCAATCGTCAATGGAATTTACACTTTGGCTC 1123
| | | | |
QY 1064 CTGATTCGCTTGAAGCTTCAACATTTTGATTAAGACTGGCTTTTACCAAGATGCTCA 1123
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Db 1124 TTTGATTTGCCATTAACCAAAACATTTGCACTGAGCTGAGCTTCGCAAAATGTGCA 1183
| | | | |
QY 1124 TCTTATACAGGTTCTTGAAGCATGTAAGAGCTGTCGGCAGCTAGAGAGCTGAACT 1183
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Db 1184 TCTTGTACAGTTTGAAGCATATTTAGACACTTTTGAAGCATTAAGAGCTTGAAC 1243
| | | | |
QY 1184 CTTTCAAGCGCAATTAAGAGATGAGATCCGTCCGATGGAATGCTTCCAGAAATAT 1243
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Db 1244 CTTTCAATCTGCAATTAAGAGATGGAATTCATCAGAGATTAAGAACCTTCCAGAAATAT 1303
| | | | |
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCTTAATGAATGGCTGAGTGGAGAGAA 1303
| | | | |
Db 1304 GAAATGTGTGTACATGATGTTTGAATGTAATGAAGTGAACAGAGAGGCGAGAA 1363
| | | | |
QY 1304 GGTCAAGGCGGAGACAGCTCAACTATGCAAGACAGAGCTTGGAGGCGTGTGATTC 1363
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Db 1364 GACTCAAGGAGAAACACTCTCAACTATGTTGCAAGAGCTTGGAGGCTTATTTGATTC 1423
| | | | |
QY 1364 GTATATGAGAGAACAAAGTGAATGCGCACTGTATCTGCCAGCTTTGAGAGTACT 1423
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Db 1424 ATATATGAGAGAACAAATGAGATCTTAATGTTATCTGCCAATGTTTGAAGAGTAC 1483
| | | | |
QY 1424 GGAAGAGGGAATATGATGCTCTGCTCATGCGCCATGCGCACTGGAACCCATTCGAGATT 1483
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Db 1484 TGAATAGGGAATATGAGCTCTGATATCGGTGAGCAACATGGAACCAATCTCACTTT 1543
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QY 1484 GGAATCCCTTTCTGATGACATCTCAAGAGAGTTGACTTCCCATGGAAGCTCAATGA 1543
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Db 1544 GAAATGATGATGATCTCTGATTAATCTGGAAGAGATTTTTCATTCAGGTTCAATGA 1603
| | | | |
QY 1544 CTTGATATGATATCACTCTTGATTAAGAGTATGATACAGGTTCAAGAGCAGAGGCG 1603
| | | | |
Db 1604 TTTGGCATGCGCTTCTCTTGGCTAGAGGAGTACACAGCTGCTTACAAAGCGGATAGGA 1663
| | | | |
QY 1604 CCGTGGAGAGAGCTTCTCTATATCATGTTAATGAAGACAAATCTGGAATTAAGGA 1663
| | | | |

Db 1664 TCGTGTGAAGAGCTGTGTATATATGTAATGAAGCAATCCGTGATCAACGA 1723
Qy 1664 AGAAGATGCTGTAATCATATTAATTAATGATCAAGGACGAATCAGAAATTAATTG 1723
Db 1724 AGAAGATGCTGTAATCATATTAATTAATGATCAAGGACGAATCAGAAATTAATTG 1783
Qy 1724 GGAGCTGTAAGGACGAAGAGTGTCCCATCACTTCCAGAAACGCGATTGACAT 1783
Db 1784 GGAATCTTAAGATCAACGAATATTTCAATGCTGGCCAAAGAAACGCTTTTGACAT 1843
Qy 1784 AAGCAGATTTGGCATCAAGTTAAGATACCGAGATGCTACAGCTTTGGCCAGTTGA 1843
Db 1844 AACAAGAGCTCTCCACATCTTACATATATGAGATGCTTTAGTTGCCAACAAGA 1903
Qy 1844 AACAAAGATTGTTGATGAGAACCGCTCATGACCTGCTTTGTAACAACACTTCAA 1903
Db 1904 AACAAAAAATTTGTTATGAGAAACACTCCTGTAATCTATTTTAACTTAACATA 1963
Qy 1904 ATCTAATATTAATGATGAGATCCCTAATGAGTGTATATAGGCA 1950
Db 1964 TCCATTAATTAATGCTCATTAATGCTTAATTTATTTGCTTATGACATA 2010

RESULT 11

US-09-903-012-29
Sequence 29, Application US/09903012
Patent No. US2002094557A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US2002094557A1, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69)...(1949)
OTHER INFORMATION: myrcene synthase
US-09-903-012-29

Query Match 53.2%; Score 1071.6; DB 9; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

Qy 68 CAGGTGCGCTCACTTCTTCATGAGATTAAAGCTCCGTAAACAATCCCAACT 127
Db 116 CAGGTGCTTGAATCAATTCATGAAACATTAAGCTCCCTAATAACAATCCCAACT 175
Qy 128 TGAATTCGACAGCCGGGAAATCCGTGCGCATTCATTAACATGTGTTGACAAGCT 187
Db 176 TGAATGCGTGGGCGAAGGAAATCTGTACCGCTTCATGACATCAAGTTGGCAACGC 235
Qy 188 CGCATCTACTGATTCTTGTACAGAGACGCGTGGCAACTATCTTCCAACTGTGGAGCA 247
Db 236 TGCACCTATGATGTGTATCAAAAGACGATAGGTATCAACATTCCTCAATTCGGAGCA 295
Qy 248 TGATTTCATACAGTCTGTGATCTCAACGCGCTTATGAGACCTGATTAACCGGAAAGTGC 307

Db 296 TGATTTCATACAGTCTCTCTTATCAACGCTTATGAGGAAACCTCTTACAGAAACGTC 352
Qy 308 TGACAGACTTATTTGGGAGATTAAGATATATGTTCAATTTCAAGTCGCTGGAAGATG 367
Db 353 TGAGAGATTAATTTGGAGATTAAGAGATA---TTCAATTCATATGCTGATGATG 409
Qy 368 AGG-----CAATGATCTCTTCAACGACTTTTGTGCTGTGATGAGTGA 412
Db 410 AAGATTAATGAGTCTCTTAAATGATCTATGCAACGCTTTGAGATGATGAGGCTTGA 469
Qy 413 AGCTTTGGGAATTCGACAGCAATTTCAAAAAGATTAATAACGCACTGATTAATGTA 472
Db 470 AGCTTTGGGATGCTTACATCTTCAAGAAAGATTAATCAGCTGATTAATGTTT 529
Qy 473 CAGTATTTGAACGAAAAAGCATTTGATGAGGAGAGAGTGTGATGACTGACCTCAA 532
Db 530 CCGTTACTGGGAGGAAACGCGATTTGATGAGGAGACAGTATTTGATGATCTCAA 589
Qy 533 CTCAACCGCTTTGGGCTTGGAACTCTCCGACTACAGGATACATGCTGTCTTGATGT 592
Db 590 CTCAACGCTGTTGGGTTGCAACTCTTCGATTAACGCGGATACATGATCTCCAGAGT 649
Qy 593 TTTGAACGTTTTTAAAGCAAAAATGGGCAATTTCTCCACTGSCCAATTAATCAGATGA 652
Db 650 TTTAAAGCTTTTCAAGATCAAAATGACAGTTTGTATGCTCCCC---GGTCAACAGA 706
Qy 653 GGGAGAGATTAAGGCGCTTCAATTTATTAAGGCGCTCTCGTGGCTTTCCGCGCA 712
Db 707 GGGTGAATCAGAGAGCGTTCTTAATCTTATTCGGGCTTCCCTCATGCTTCCCTGGA 766
Qy 713 GAAATTTGATGATGAGAGTGAACATTTCTTCAAAAATTTTAAGAGAAAGCTTCAAAA 772
Db 767 GAAAGTTATGAGAGAGCTGAATCTTCCACAAAGATTTGAAGAGCTTCAAAA 826
Qy 773 GATTCGCGCATCTCAATATCTTCACTAGATACGAGACGTTCTGAAATATGTTGCA 832
Db 827 GATTCAGTCTCGCT---CTTCAAGAGATTAAGTTGTATGAAATATGCTGGCA 883
Qy 833 CACCAATTTGCCAGCGCTTGAAGCAAGAAATTAATGACGCTTTTGAACAGACATA- 891
Db 884 CACAAATTTGCCAGATGGAAGCAAGAAATTAATGACACACTTGAAGAAAGACACAG 943
Qy 892 -----AAAATGAACGCGCGCGAAGAACTTTTAACCTTGAAGAAATTTGA 943
Db 944 TGCATGCTCAATTAATAATGCTGGAGAACCTTTTAACCTTGAAGAAATTTGA 1003
Qy 944 TATATTTCACTCTTACAAAGAGAGATTAACATGTTTCCGATGCTGGAAGACTC 1003
Db 1004 TATATTTAATCTCTTACAAAGAGATTAACATGTTTCTTTGAGATGCTGGAAGACTC 1063
Qy 1004 GGGTCTCTGAGATGACCTTCTGTGACATGTCACGCTGAATTAACGCTTTGGCTTC 1063
Db 1064 GGAATTTGCTAATTAATGACATTTGCTCGGATGTCATGTAATTTCACTTTGGCTTC 1123
Qy 1064 CTGATTTGCTGAGCTCAACATTTGATGATGAGATCTGCGCTTTACCAAGATCTCA 1123
Db 1124 TTTGATTTGCCATTTGACCCAAACATTTGACATGAGCTTGGCTTGGCAAAATGTGCA 1183
Qy 1124 TCTTATCAAGGTTCTTGAAGACATTTGACAGCTTTGGCAAGTGAAGTGA 1183
Db 1184 TCTTGTCAAGTTTGGAGCATTTTACGACACTTTTGAACGATGACAGCTTGA 1243
Qy 1184 CTTCACAGCAAAATTAAGATGAGATCGCTCGCGATGGAATGCTTCCAGAAATAT 1243
Db 1244 CTTCACATCTCAATTAAGATGGAATTTCAAGAGATTAAGAACCTTCCAGAAATAT 1303
Qy 1244 GAAAGAGATTTAATGATGTTTATCAACCGTAAATGAATGCTGAGTGGAGAGAA 1303
Db 1304 GAAATGTGTACATGCTGTGTTGAACGTAAATGAATGACGACAGAGGCGAGAA 1363
Qy 1304 GGGCTCAAGGCGAGACAGCTCAATATGCAAGACAGCTTGGAGGCGTGTGATTC 1363

Db 1364 GACTCAAGGAGAAACACTCACTATATGTTGAAAGGCTTGAGGCTTATTTGATTC 1423
Qy 1364 GTATATGAGAGAGAAAGATGATGCGCACTGTTATGCGCCAGCTTTGAGAGTACTT 1423
Db 1424 ATATATGAGAGAGAAAGATGATGCGCACTGTTATGCGCCAGCTTTGAGAGTACTT 1483
Qy 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGACGTT 1483
Db 1484 TGAGATGGGAAAGTAGCTCTGCAATATCGGATGCAACATTTGCAACCCATCTTCACTTT 1543
Qy 1484 GGACATCCCTTTCTGATCATCTCTCAAGAAAGTTGACTTCCCATGAAAGCTCATGA 1543
Db 1544 GAAATGATGCTCTGATCATCTCTCAAGAAAGTTGACTTCCCATGAAAGCTCATGA 1603
Qy 1544 CTGATATGATCATCTCTGATTAAGAGTATGATCAAGGCTTCAAGAGGACAGGGC 1603
Db 1604 TTGGCATGCTCTCTGCTGCGCTGACGAGTGCACACGCTGCTACAAAGGCGGATAGGGA 1663
Qy 1604 CCGTGAGAGAAAGCTTGTCTATATCATGTTATATGAAAGCAATCTTGATTTAAACGA 1663
Db 1664 TCGTGAGAGAAAGCTTGTCTATATCATGTTATATGAAAGCAATCTTGATTTAAACGA 1723
Qy 1664 AGAAGATGCTTGAATCATATCACTTATGATGAGGAGCGCAATCAGAGATTTAATTG 1723
Db 1724 AGAAGATGCTTGAATCATATCAATGCGCATGCTCATGATCAATCAAAAGATTTAATTG 1783
Qy 1724 GGAGCTTCAAGGACGACAGTGTCCCATCACTTCAAGAAAGGAGATTTGACAT 1783
Db 1784 GGAATCTTCAAGATCAAGCAATATTCATGCTGCGCAAGCAATGCTTTTGAAT 1843
Qy 1784 AAGCAGATTTGGCATCAAGCTTACAGATACGAGATGCTTACAGCTTTGCCAAGTTGA 1843
Db 1844 AACAAGAGCTCCACACATCTCTATATATGAGATGCTTTAGTGTGCAACAAGGA 1903
Qy 1844 AACCAAGATTTGGATGAGAGAACCGTATTTGACCTTGTGTTAACAACCTTAA 1903
Db 1904 AACCAAAATTTGGTATGAGAAACACTCTTGAATCTTGTGTTTAACTATTAACATA 1963
Qy 1904 ATCTACATATTTAAGTGAAGTGGCTTATGGGTATATAGGAGCA 1950
Db 1964 TCATATATTAAGCTCATTAATGCTAAATTTATTTGCTTATGACATA 2010

RESULT 12
US-09-900-797-29
Sequence 29, Application US/09900797
Publication No. US20030087406A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20030087406A1, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/900,797
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
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US-09-900-797-29

Query Match 53.2%; Score 1071.6; DB 10; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1,46-306;
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Qy 68 CAGGTGCTGCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTGAAACATCCCACTCT 127
Db 116 CAAGTCTGATGATGATTCATTAATGATGAAATAGCCCTCTATGAAACAATCCCAATCT 175
Qy 128 TGGATCTGACGCGCGGGAATCCGTGCGCATTCATTAACAATGTTTGAACAAGGT 187
Db 176 TGGATGCTGAGCGGGAATCTGATGCGCTTCAAGATGACATGTTTGGCACCGC 235
Qy 188 CGCATCTACTGATCTGTACAGAGACCGGTGGCACTATCATATTCACACCTGTGGAGCA 247
Db 236 TGCACCTGATGATGTTGTAACAAGACCATATGATGATCATACATTCGAATATCTGGAGCA 295
Qy 248 TGATTTCAATACGCTCTGATCTCAACGCTTATGAGACCTGATTAACGGGAACGTGC 307
Db 296 TGATTTCAATACGCTC---TATCAACGCTTATGAGGAAACCTCTTACAGGAACGTGC 352
Qy 308 TGACAGACTTATGGGGAAGTAAGATATATGTTCAATTCAGTCTGAGAGATGG 367
Db 353 TGACAGATTAATGTTGAGAGTAAGAAAGATA---TTCATTCATTAATGCTGAGATGG 409
Qy 368 AGG-----CAATGATCTCTTCAACGACTTTTGGCTGATGAGCTTGA 412
Db 410 AAGATTAATGATGCTCTTATATGATCTCATGCAACGCTTTGATGATGATGATGATG 469
Qy 413 ACGTTGGGAATGACAGGCACTTCAAAAAGATTAATAAGGCACTCGATTTATGTTAA 472
Db 470 ACGTTGGGATGATCTGATGATTAACAAGATTAACAATCACTGATGATTTATGTTT 529
Qy 473 CAGTTATTTGAAGCAAAAGGCAATTTGATGAGGAGGAGATGTTGATGATGATGATG 532
Db 530 CCGTTACTGGAGGAAACGCAATTTGATGAGGAGGAGATGTTGATGATGATGATGATG 589
Qy 533 CTCAACGCTTGGGCTTGCAGACTCTCCGACTACAGATACATGCTGCTTCAAGATG 592
Db 590 CTCAACGCTTGGGCTTGCAGACTCTCCGACTACAGATACATGCTGCTTCAAGATG 649
Qy 593 TTTGAAGCTTTTAAGACAAAATGGGCAATTTCTCCACTGCTCCAAATATTCAGATGA 652
Db 650 TTTAAAGCTTTTCAAAATGCAAAATGAGCAATTTGATGCTCCCTC---GGTCAAGACA 706
Qy 653 GGGAGATTAAGAGGCTTCTCATTTATTCAGGCGCTCCCTGCTGCTTCCCGGGA 712
Db 707 GGGAGATTAAGAGGCTTCTCATTTATTCAGGCGCTCCCTGCTGCTTCCCGGGA 766
Qy 713 GAAATTAAGATGAGCTGAAACATTTCTTCAAAAATTTTAAGAGAGCCCTGCAAAA 772
Db 767 GAAATTAAGATGAGCTGAAACATTTCTTCAAAAATTTTAAGAGAGCCCTGCAAAA 826
Qy 773 GATTCGGCATCCATTAATCTTCACTAGAGATCCGGAAGCTTCTGGAATATGTTGGCA 832
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Qy 833 CACCAATTTGCGACGCTTGAAGCAAGATTAATCATGACGCTTTTGAACAGCACATA- 891
Db 884 CACCAATTTGCGACGCTTGAAGCAAGATTAATCATGACGCTTTTGAACAGCACATA- 943
Qy 892 -----AAATTAAGAACGCGCGGAAACCTTTTGAACCTTGAACATTTGAATTCAA 943
Db 944 TGATGCTGATTAATAAATGCTGGAAGAGCTTTTGAACCTTGAACATTTGAATTCAA 1003
Qy 944 TATATTTCACTCTCTTCAAGAGAGAGTTTAAACATGTTTCCGATGCTGGAAGACTC 1003
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Qy 1004 GGGTTCTCTGAGATGACCTTCTGTCAGATCTGACGATGATGATGATGATGATGATG 1063
Db 1064 GGAATTTGCTTAATTAATGACATTTGCTGCGATGCTGATGATGATGATGATGATG 1123

QY 1064 CTGATGCGCTGAGCTCAACATTCGTGATGAGACTGGCTTTACCAAGATGCTCA 1123
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QY 1124 TCTTATCAGCGTTCTTGACGACATGACAGCTCTTCCGACAGTAGAGAGCTGAACT 1183
DB 1184 TCTTGTCAAGTTTGGACGATATTTAGACACTTTTGAACGATGACGAGCTGAACT 1243
QY 1184 CTTCACAGCGAATTAAGATGGGATCCGTCGCGATGGAATGCTTCCAGATATAT 1243
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QY 1244 GAAAGAGTGATCAATGATGTTTATCAACCGTAAATGAATGCTGAGTGGCAGAGAA 1303
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QY 1304 GAGTCAAGCGCGACAGACGCTCAATGACAGAGCTTGGAGGCGTGTGTTGATTC 1363
DB 1364 GACTCAAGGAGAAACCTCTCACTATGTTGAAAGGCTTGGAGGCTTATTTGATTC 1423
QY 1364 GTATATGAGAGAGCAAGATGATGCACTGTTATTCGCCACGTTTGAAGATCTT 1423
DB 1424 ATATATGAGAGAGCAAGATGATCTTAATGTTATCTGCCAATGTTGAAGATCA 1483
QY 1424 GAGAAACGCGAAAGTATGCTGCTCATGCGCCACGCGCACTGCAACCATTTGAGCTT 1483
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QY 1484 GAGATATCCCTTCTGATCATCTCTCAAGAAAGTTGACTTCCCATGAACTCAATGA 1543
DB 1544 GAAATGATGCTTCTGATCATCTCTCAAGAAAGTTGACTTCCCATGAACTCAATGA 1603
QY 1544 CTGATATGATATCTCTGATTAAGAGTGATACAGCGTGCTCAAGAGCAGACAGGC 1603
DB 1604 TTTGAGATGCTCTCTCTGATTAAGAGTGATACAGCGTGCTCAAGAGCAGACAGGC 1663
QY 1604 CCGTGGAGAGAGAGCTTCTGATTAAGAGTGATACAGCGTGCTCAAGAGCAGACAGGC 1663
DB 1664 TCGTGGAGAGAGAGCTTCTGATTAAGAGTGATACAGCGTGCTCAAGAGCAGACAGGC 1723
QY 1664 AGAGATGCTCTGATCATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1723
DB 1724 AGAGATGCTCTGATCATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1783
QY 1724 GAGCTCTTAAG 1783
DB 1784 GAGCTCTTAAG 1843
QY 1784 AAG 1843
DB 1844 AAG 1903
QY 1844 AAG 1903
DB 1904 AAG 1963
QY 1904 ATCTACATATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1950
DB 1964 TCCATTAATTAATGAG 2010

RESULT 13
US-09-893-820-29
; Sequence 29, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Mann, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-02501
; CURRENT APPLICATION NUMBER: US/09/893,820

;; CURRENT FILING DATE: 2001-06-28
;; PRIOR APPLICATION NUMBER: US/09/398,395A
;; PRIOR FILING DATE: 1999-09-17
;; PRIOR APPLICATION NUMBER: 60/100,993
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 29
;; LENGTH: 2196
;; TYPE: DNA
;; ORGANISM: Abies grandis
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (69)...(1949)
;; OTHER INFORMATION: myrcene synthase
US-09-893-820-29

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QY 68 CAGTGTGCTGAGCTTCTGATGATTAAGCTCTCCGTGAACATCCCACTCT 127
DB 116 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 175
QY 128 TGAATCTGACGAGCGGAGAAATCCGTGCGCATTCATTAACATGTTTGAACAGCGT 187
DB 176 TGAATCTGACGAGCGGAGAAATCCGTGCGCATTCATTAACATGTTTGAACAGCGC 235
QY 188 CGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 247
DB 236 TGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 295
QY 248 TGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
DB 296 TGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 352
QY 308 TGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 367
DB 353 TGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 409
QY 368 AGG-----CAATGATCTCTTCAACGACTTTGCTGATGATGATGATGATGATGATGAT 412
DB 410 AAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
QY 413 ACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 472
DB 470 ACCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
QY 473 CAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 532
DB 530 CCGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
QY 533 CTCAACGCTTGGGCTTGGAGCTCTCCGACTCAACGATGATGATGATGATGATGATGATGAT 592
DB 590 CTCAACGCTTGGGCTTGGAGCTCTCCGACTCAACGATGATGATGATGATGATGATGATGAT 649
QY 593 TTTGAAGCTTTTAAAGCAAAATGGGCAATTTCCCTCCACATGATGATGATGATGATGATGAT 652
DB 650 TTTAAAGCTTTTAAAGCAAAATGGGCAATTTCCCTCCACATGATGATGATGATGATGATGAT 706
QY 653 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 712
DB 707 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 766
QY 713 GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 772
DB 767 GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 826

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Qy 773 GATTCGGGATCCAGTATACCTTTCATAGATACGGGACGTTCTGAAATATGTTGGCA 832
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Db 827 GATTCAGTCTCCGCT---CTTTCACAGAGATTAAGTTTGTATGAAATATGCTGGCA 883
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 833 CACCAATTTGGCAGCGCTTGGAAAGCAAGATTTACATGAGCGTCTTTGACACGACATA- 891
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 884 CACAAATTTGGCAAGATTGGAAGCAAGAAATTAACAATACACACTTGGAAAGACACAG 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 892 -----AAATATAGAAAGCGCGGCAAACTTTTAAACCTTGCAAAATTTGAATCAA 943
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Db 944 TGCAATGCTCAATATAAATATGCTGGAGAGAGCTTTTAAAGCTTGCAAAATTTGAGCTTAA 1003
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Qy 944 TATATTTCACTCTTTCACAGAGAGAGATTAACATGTTTCCGATGTTGGAAGACTC 1003
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Qy 1064 CTGCATTTGCTTGGAGCTCAACATTTGGAATTCAGACTCGGCTTTACCAAGATGCTCA 1123
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Db 1124 TTGTATTTGCAATGACCCAAACATTTGCAATTCAGACTGAGCTTGCCAAATTTGTCTA 1183
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Qy 1124 TCTTATCAGGTTCTTGAAGACATGTACAGAGCTTTCCGCAACATGACAGAGCTGGAAT 1183
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Db 1184 TCTTGTGCAATTTTGGACAGATTTTACAGACACTTTTGGAAAGATGACAGAGCTTGAAT 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1184 CTTTCACAGCGCAATTTAAGATGGAGTCCGTCGCGATGGAAATGCTTTCCAAATATAT 1243
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Db 1424 ATATATGGAAGAGCAAAATGGAATCTTAATGTATGTCCAATGTTTGAAGAGTATCA 1483
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Db 1484 TGAGAAATGGGAAAGTACCTCTGCAATTCGCGTAGCAACATTTGCAACCCATCTTCACTT 1543
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Db 1604 TTTGGCATCTGCTCTTCTTGGCTTACAGAGTGAACAAGCTGCTTCAAGGCGAGTAGGGA 1663
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Qy 1604 CCGTGAAGAGAGAGCTCTGCTATATCATGTTATTAAGAAACAATCTGATTTACGGA 1663
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Db 1664 TCGTGTGTAAGAAAGCTTCTGTATATCATGTTATTAAGAAACAATCTGATTTACAGG 1723
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Qy 1724 GAGAGTTTAAAGCGAGCAACAGTGTCCCATCTTCCAAAGAAACGCAATTTGAT 1783
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Db 1784 GGAATCTTAAAGATCAACAGCAATATTCATGCTGCGCAAGAAACATGCTTTTGAAT 1843
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Db 1844 AACAGAGCTCTCCACCACTCTTACATATATGAGATGAGCTTTAGTGTGCGCAACAGGA 1903
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Db 1904 AACAAAAAATTTGGTTGGAACACATCTGATATCATGCTTTTAACTATTAACATA 1963
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Db 1964 TCCTAATTAATTAAGCTCATTAATGCTTAATTAATTTAGCCTTATGACATA 2010
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RESULT 14
US-10-041-007-25
; Sequence 25, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
US-10-041-007-25

Query Match 53.2%; Score 1071.6; DB 14; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

Qy 68 CAGGTGCGCTCGTCTTCTCATGATTAAGAGCTCTCGTAGAACATCCCACTCT 127
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Db 116 CAAGTCGTATCATGTTCAATTCATGAACATTAAGCTCTCTATTAAGAAATCCAAATCT 175
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Qy 128 TGAATCTGACAGCGGAGAAATCGTCGCGCATTCATTAACAATGTGTTGACAGGCT 187
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Db 176 TGAATGCGTAGAGGAGAAATCTGTACGCTTCATGACATCACTTTGGCCACCGC 235
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Qy 188 CGCATCTAGATTTCTGTACAGAGACGCGTGGCACTATATTTCCAACTGTGGAGCA 247
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Db 296 TGATTTCAATCAAGCTCT---TATCAAGCGCTTATGAGGAACTCTTACAGAACTGC 352
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Qy 308 TGACAGACTTATTTGGGAGAAATTAATATGTTCAATTTCAAGTCTGGAAGATGG 367
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Qy 368 AGG-----CAATGATCTCTTCAACGACTTTTGTGCTGCTGATGACGTTGA 412
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Db 410 AAGATTAATAGATTCCTTATATGATCTCATGCAACGCTTTGATGATGCTGATGGA 469
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Qy 413 ACGTTTGGAGATGACAGCGCTTCAAAAAAGATTAATAACGCGCATCTGATTAATGTTAA 472
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Qy 473 CAGTTATTTGAACGAAAAAGGCAATTTGATGAGGAGGAGAGTGTGACTGACTCAA 532
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Db 530 CCGTTTACGGAAGAAAAACGCGCATTTGATGAGGAGAGACGATTTGTTACTGATCTCAA 589
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Qy 533 CTCAACCGCTTTGGGCTTGAATCTTCCGACTACAGATTAACGCTGTGCTTCAAGAT 592
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Db 650 TTAAAGGCTTTCAAGATCAAAATGACAGTTTGTATGCTCCCC---GGTCAAGACGA 706
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653 GGAAGATTAAGAGCGCTTCAATTTATTCAGAGCGCTCCCTCGTGGCTTTCCGCGGCA 712
707 GGGTGAATCAGAAAGCGTTCTTAATTTATTCAGAGCGCTCCCTCGTGGCTTTCCGCGGCA 766
713 GAAAGTTATGATGAGTGAAGCAATCTCTACAAATATTTAGAGAGCGCTTCGCAAA 772
767 GAAAGTTATGAGAGAGTGAAGCAATCTCTCCCAAGATATTTGAAAGAGCGCTTCGCAAA 826
773 GATTCGCGCATTCAGATTAATCTTCACTAGAGATACGGAGCGCTTCGGAATATGTTGGCA 832
827 GATTCAGATTCGCGCTCTTTCACAAAGATTAAGTTATGAGATATGAGATATGAGCGTGGCA 883
833 CACCAATTTGCGACGCTTGAAGCAAGATTAATGAGCGCTTTCGAGCAGCAGCTTA 891
884 CACCAATTTGCGACGCTTGAAGCAAGATTAATGAGCGCTTTCGAGCAGCAGCTTA 943
892 -----AAATAGAAAGCGCGCGGAGAACTTTAGAACTTTGCAAAATTTGAAATTCGA 943
944 TGCAATGCTCAATAAATATGCTGGAGAGAGCTTTTAGAAGCTTTCGAAATTTGAGATTCGA 1003
944 TATATTTCACTCTTCAAGAGAGAGAGATTAATGATTTCCGATGGTGAAGACTTC 1003
1004 TATATTTAACTCTTCAAGAGAGAGATTAATGATTTCCGATGGTGAAGAGCTTC 1063
1004 GGGTTCCTGAGATGACCTTCTGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1063
1064 GGAATTTGCTCAATTAATGAGATTTGCTGCGATGTCGATGTCGATGTCGATGTCGATGTC 1123
1064 CTGCAATTCGCTTCGAGCTCAACATTTCTGATTCGAGCTTCGCTTTCGCAAGATTCCTCA 1123
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1124 TCTTATACGCGTTCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
1184 TCTTATACGCGTTCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
1184 CTTCAGCGGCAATTAAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1243
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1244 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303
1304 GAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1363
1304 GGGTTCGAGCGGAG 1363
1364 GACTCAAG 1423
1364 GTATATGAG 1423
1424 ATATATGAG 1483
1424 GGAAG 1483
1484 TGAG 1543
1484 GGAATGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
1544 GAAATGCGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603
1544 CTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603
1604 TTGAG 1663
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1664 TCGTGAAG 1723
1664 AGAAG 1723
1724 AGAAG 1783
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1784 GGAAG 1843
1784 AACGAG 1843
1844 AACGAG 1903
1844 AACGAG 1903
1904 AACGAG 1963
1904 AACGAG 1963
1964 AACGAG 2010
RESULT 15
US-10-025-145A-1
Sequence 1, Application US/10025145A
Publication No. US20030175661A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Bohlmann, Joe E.
APPLICANT: Steele, Christopher L.
APPLICANT: Phillips, Michael A.
TITLE OF INVENTION: Monoclonal Syntheses from Grand Fir (Abies Grandis)
FILE REFERENCE: WSOR11841
CURRENT APPLICATION NUMBER: US/10/025, 145A
CURRENT FILING DATE: 2003-06-28
PRIOR APPLICATION NUMBER: US 09/360,545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052,249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies Grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69) (1952)
OTHER INFORMATION:
US-10-025-145A-1
Query Match 53.2%; Score 1071.6; DB 15; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;
68 CAGGTGCTGCTCAAGTCTTCTCATGAGATTAAAGGCTCTCGTGAAGCAATCCCACTCT 127
116 CAGGTGCTGCTCAAGTCTTCTCATGAGATTAAAGGCTCTCGTGAAGCAATCCCACTCT 175
128 TGAATCTGAGAGCGCGGAGAAATCCGTCGCGCATTCATTAACATGCTTGAAGAGGT 187
176 TGAATGCTGAGAGCGCGGAGAAATCCGTCGCGCATTCATTAACATGCTTGAAGAGGT 235
188 CGCATCTGATTCATTCATGAG 247
236 TGAACCTGATATGCTGATCAAG 295
248 TGAATCTGAGAGCGCGGAGAAATCCGTCGCGCATTCATTAACATGCTTGAAGAGGT 307
296 TGAATCTGAGAGCGCGGAGAAATCCGTCGCGCATTCATTAACATGCTTGAAGAGGT 352
308 TGAACCTGATATGCTGATCAAG 367
353 TGAACCTGATATGCTGATCAAG 409
368 AGG-----CAATGATCTCTTCAAG 412

Db 410 AAGATTAATGAGTTCCTTAATGATCTCATGCAACGCCCTTGGATGATGATGACGTTGA 469
Qy 413 ACGTTGGGAATGACAGGCAATTCCTCAAAAAAGATTAATAAAGCGCACTGCATTAATGTTAA 472
Db 470 ACGTTGGGATGATGACATTCATGACGAGATTAATCATCACTGCTGGAATTAATGTTTT 529
Qy 473 CAGTTATTTGAACAAAAAGGCATTTGATGAGGAGGAGATGTTGATGATGACCTCAA 532
Db 530 CCGTTACTGGAGGAAAAAGCGCATTTGATGAGGAGACAGTATTTGTTATCTGATCTCAA 589
Qy 533 CTCAACGCCCTTGGGGCTTGCAGACTCTCCGACTACAGGATACATGCTGTTCAAGATG 592
Db 590 CTCAACTGCGTTGGGGTTCGAACTCTTCGATTAACAGGGTACCTGATCTCCAGAGGT 649
Qy 593 TTTGACGTTTTTAAGACAAAAATGGGCATTTTCCCTCACTGCGCAATATTCAGATGA 652
Db 650 TTTAAAGACTTTTCAAGATCAAAAATGACAGTTTGTATGCTCCCC--GGTCAAGACGA 706
Qy 653 GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCCCTCCCTGCTGCTTCCCGCGA 712
Db 707 GGGTGAATCAGAAAGCGTTTAACTTATATCGGGCTTCCCTCATGCTTCCCTGGTGA 766
Qy 713 GAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 772
Db 767 GAAAGTTATGGAAGAAAGCTGAATCTTCCCAAGATATTTGAAGAAAGCTTCAACAAA 826
Qy 773 GATTCGGGCATCCAGTATCTTCACTAGATACGGAAGCTTCTGAAATATGTTGGCA 832
Db 827 GATTCAGATCTCCCT--CTTTCAAGAGATTAAGTTGTTGATGAAATATGCTGCA 883
Qy 833 CACCAATTTGCGACGCTTGAAGAGAAATTAATGATGATGATGATGATGATGATGATGAT 891
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Qy 1364 GTATATGCAAGAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1423
Db 1424 ATATATGGAAGAAAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1483
Qy 1424 GGAAGAGCGGAAAGTTAGCTCTGCTCATCGGCCATGCGCACTGGAACCAATTTGACGTT 1483
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Qy 1484 GGAATCCCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
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Qy 1544 CTTGATATGATATCACTCTTGAATTAAGAGTATGATGATGATGATGATGATGATGATGAT 1603
Db 1604 TTTGGCATGCTCTTCTTCTGCGCTACGAGGTGACACAGCTGCTTCAAGAGCCGATTAAGGA 1663
Qy 1604 CCGTGAAGAAAGCTTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
Db 1664 TCGTGTGAAGAAAGCTTCTGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1723
Qy 1664 AGAAGATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1723
Db 1724 AGAAGATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1783
Qy 1724 GGAAGCTTGAAGGAGCAAGCAAGTGTTCATGATGATGATGATGATGATGATGATGATGAT 1783
Db 1784 GGAATCTTAAGATCCAAAGCAATATTTCCAAATGCTGGCCAAAGAAATGCTTGTGACAT 1843
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Db 1904 AACAAAGATTTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1963
Qy 1904 ATCTAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1950
Db 1964 TCCATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2010

Search completed: July 26, 2004, 16:33:40
Job time : 3703 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:57 ; Search time 7588 Seconds

(without alignments)
11498.356 Million cell updates/sec

Title: US-10-025-145A-64

Perfect score: 2013
Sequence: 1 ttctgacgtcctctcctc.....aaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pac: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hg_hum: *
31: em_hg_inv: *
32: em_hg_other: *
33: em_hg_mus: *
34: em_hg_pln: *
35: em_hg_rtd: *
36: em_hg_mam: *
37: em_hg_vrt: *
38: em_ay: *
39: em_hg_hum: *
40: em_hg_mus: *
41: em_hg_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2013	100.0	2013	6	AR222136
2	2013	100.0	2013	8	AGU87910
3	1306.8	64.9	2018	6	BD227661
4	1306.8	64.9	2018	6	AR222097
5	1306.8	64.9	2018	6	AR240696
6	1306.8	64.9	2018	6	AR266971
7	1306.8	64.9	2018	6	AR316320
8	1306.8	64.9	2018	6	AR338463
9	1306.8	64.9	2018	6	AR429869
10	1306.8	64.9	2018	6	AGU87909
11	1273.6	63.3	1958	8	AY237645
12	1178.4	58.5	2062	8	AF543527
13	1155.6	57.4	2162	8	AF543529
14	1103.2	54.8	2166	8	AF461460
15	1101.4	54.7	2168	8	AF369918
16	1095.4	54.4	1853	8	AF139206
17	1093.4	54.3	1850	6	AR222146
18	1085.8	53.9	2150	8	AF369919
19	1072.4	53.3	2186	6	AR222137
20	1072.4	53.3	2186	6	AF139205
21	1071.6	53.2	2196	6	BD227666
22	1071.6	53.2	2196	6	AR222096
23	1071.6	53.2	2196	6	AR240701
24	1071.6	53.2	2196	6	AR266976
25	1071.6	53.2	2196	6	AR316325
26	1071.6	53.2	2196	6	AR338468
27	1071.6	53.2	2196	6	AR429874
28	1071.6	53.2	2196	6	AGU87908
29	1071.6	53.2	2205	6	AR222116
30	1040.2	51.7	2100	8	AF543530
31	971.4	48.3	1960	8	AF543531
32	929.4	46.2	2439	8	AR222138
33	929.4	46.2	2439	8	AF139207
34	925.4	46.0	2039	6	BD227677
35	925.4	46.0	2039	6	AR222098
36	925.4	46.0	2039	6	AR240712
37	925.4	46.0	2039	6	AR266987
38	925.4	46.0	2039	6	AR316336
39	925.4	46.0	2039	6	AR338479
40	925.4	46.0	2039	6	AR429885
41	925.4	46.0	2039	8	AF006193
42	889.4	44.2	2094	8	AF543528
43	807.4	40.1	1513	6	BD272958
44	805.8	40.0	1634	6	BD273051
45	623.6	31.0	1173	6	BD273050

ALIGNMENTS

RESULT 1
LOCUS AR222136 2013 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 64 from patent US 6429014.
ACCESSION AR222136
VERSION AR222136.1 GI:23329510
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2013)
AUTHORS Steele,C.V., Kohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (Abies grandis)
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;
FEATURES Location/Qualifiers

source 1. . 2013
/organism="unknown"
ORIGIN /mol_type="genomic DNA"

Query Match 100.0%; Score 2013; DB 6; Length 2013;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TTTTGACGTCCTCTTATCTGATGAGCAAGCTGAATGCGTCTTCTTCTATCTACTCCG 60

QY 61 TGTGTTCCAGGTCGCTCAGTCTTCTCATGAGATTAAAGCTCTCCGTAACAATCC 120
DB 61 TGTGTTCCAGGTCGCTCAGTCTTCTCATGAGATTAAAGCTCTCCGTAACAATCC 120

QY 121 CAACCTTTGAATCTGACAGCGCGGGAAATCCGTCGCGCATTCATTAACAATGTGTTGA 180
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QY 181 CAAGCGTGCATCTAATCTGATCTGACAGACGCGTGGGCAACTATATCCAACTCTGT 240
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QY 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCTTTATGAGACACTGATTTCCGG 300
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QY 301 AAGCTGTGACAGACTTATGCGGGAAGTAAAGATATATGTTCAATTTCAAGTCGTGG 360
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QY 361 AAGATGAGGGAATGATCTCCTTCAACGACTTTGCTGCTGATGACGTGAACGTTTGG 420
DB 361 AAGATGAGGGAATGATCTCCTTCAACGACTTTGCTGCTGATGACGTGAACGTTTGG 420

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QY 1681 ATATCAACTTCATGATCAAGGAGCCCAATCAGAGAAATTTAAATTTGGAGCTTCTAAAGCCAG 1740
DB 1681 ATATCAACTTCATGATCAAGGAGCCCAATCAGAGAAATTTAAATTTGGAGCTTCTAAAGCCAG 1740

QY 1741 ACAACAGTGTCCCATCACTTCCAAAGAAACAGGATTTGACATAGACAGATTTGGCATC 1800
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QY 1801 ACGGTTACAGATACCGAGATGCTACAGCTTTGCGCAACGTTGGAACAAAGAGTTTGGTGA 1860
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QY 1861 TGAGAACCGTCAATGAACTGTGCTTTGTGAACAACCTTCAAAATCTTCAATATTTAACTG 1920
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QY 1921 AGGATGCCCTATGGGTGATATAGGGAACAAAAATTAATATGTTGTGTTAAGC 1980
DB 1921 AGGATGCCCTATGGGTGATATAGGGAACAAAAATTAATATGTTGTGTTAAGC 1980

QY 1981 TGTATTTATGAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 2013
DB 1981 TGTATTTATGAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAAATTTAAAAA 2013

RESULT 2	LOCUS	ACU87910	2013 bp	mRNA	linear	PLN 10-AUG-2001
DEFINITION	Abies grandis (-)-camphene synthase (Ag6.5) mRNA, complete cds.					
ACCESSION	U87910					
VERSION	U87910.1	GI:2411484				
KEYWORDS						
SOURCE	Abies grandis					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Coniferopsida; Coniferales; Pinaceae; Abies.					
REFERENCE	1 (bases 1 to 2013)					
AUTHORS	Bohlmann, J., Steele, C.D. and Croteau, R.					
TITLE	Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase					
JOURNAL	J. Biol. Chem. 272 (35), 21784-21792 (1997)					
MEDLINE	J. Biol. Chem. 272 (35), 21784-21792 (1997)					
PUBMED	9268308					
REFERENCE	2 (bases 1 to 2013)					
AUTHORS	Bohlmann, J., Phillips, M., Ramachandiran, V., Katoh, S. and Croteau, R.					
TITLE	cDNA cloning, characterization, and functional expression of four new monoterpene synthase members of the tpsd gene family from grand fir (Abies grandis)					
JOURNAL	Arch. Biochem. Biophys. 368 (2), 232-243 (1999)					
MEDLINE	Arch. Biochem. Biophys. 368 (2), 232-243 (1999)					
PUBMED	99373092					
REFERENCE	3 (bases 1 to 2013)					
AUTHORS	Bohlmann, J., Steele, C.L. and Croteau, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (31-JAN-1997) Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340, USA					
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	/gene="Ag6.5"					
	36..1892					
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	/note="terpene synthase; monoterpene synthase; terpene cyclase"					
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	/product="(-)-camphene synthase"					
	/protein_id="AAB70707.1"					
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ORIGIN						
Query Match	100.0%;	Score 2013;	DB 8;	Length 2013;		
Beet Local Similarity	100.0%;	Pred. No. 0;				
Matches 2013;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
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Db	1	TTTGGAGTGCTTCTTATCTGATAGCAAGCTGAATGCTCTTTCTATTACTCCGC	60			
Oy	61	TGCTTTCCAGGTCTGCTCAGCTTTCTTCATGAGATTAAAGCTCTCCGTGAACAATCC	120			
Db	61	TGCTTTCCAGGTCTGCTCAGCTTTCTTCATGAGATTAAAGCTCTCCGTGAACAATCC	120			

QY	121	CAACTCTTGGAACTCTGCAAGCGCGGGGAAATCCGCTCGGCATTCCATTAACAGTGTTTGA	180
Db	121	CAACTCTTGGAAATCTGCAAGCGCGGGGAAATCCGCTCGGCATTCCATTAACAGTGTTTGA	180
QY	181	CAAGCGTCGCACTCTAGTATCTGTACAGAACCGCTGGGCAACTATCTTCCAACCTGT	240
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QY	241	GGGACGATGATTTCAATACAGTCTGTGATCTCAAGCCCTTAAGAGCACCTGATTAACGGG	300
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QY	301	AACGTGCTGACAGACTTAATGGGGAGTAAAGATATTAATGTTCAATTTCAAGTCGCTGG	360
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QY	361	AAGATGAGGCAATGATCTCCTTCAACGACTTTTGTCTGTGATGACGTTGAACGTTTGG	420
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QY	481	GGAAAGAAAAAGGCAATGGATGTGGGAGGAGATGTTGTGACTGACCTCAACTCAACCG	540
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QY	541	CCTTGGGGCTTCGAACTCTCCGACTACACGGATACCTGTGTCTTCAGATGTCTTTGAAACG	600
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QY	601	TTTTTAAAGACAAAAATGGGCAATTTTCTCCACATGCGCAATATTCAGATAGGAGGAGAG	660
Db	601	TTTTTAAAGACAAAAATGGGCAATTTTCTCCACATGCGCAATATTCAGATAGGAGGAGAG	660
QY	661	TTAAGGCGCTTCGAAATTTATTCAGGGCTTCCTGTGTGCGCTTTCGCGGAGAAAGTTA	720
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QY	721	TGATGAAAGCTGAAACATCTCTCAAAATATTTAAAGAAAGCCCTGCAAAAGATTCGGG	780
Db	721	TGATGAAAGCTGAAACATCTCTCAAAATATTTAAAGAAAGCCCTGCAAAAGATTCGGG	780
QY	781	CATCCAGTATACCTTCACTAGAGATACGGGCGTTCTGGAAATATGTTGGACACCAATT	840
Db	781	CATCCAGTATACCTTCACTAGAGATACGGGCGTTCTGGAAATATGTTGGACACCAATT	840
QY	841	TGCCACGCTTGGAGACAAAGAAATTAACATGACGCTTTGGACACACACCTAAAAATTAAG	900
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Db	901	ACGCGCGCGAAGAACTTTTAGAACCTTGCAAAATGGAATTCATATATATTTCACTCCTTAC	960
QY	961	AAGAGAGAGATTAACATATGTTTTCCGATGTTGAAAAGACTCGGGTCTCTCTGAGATGA	1020
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QY	1021	CCTTCTGTGCACTGTCACGTTGGAATCTACGCTTTGGGCTTCCGCACTTGCCTTTCGAGC	1080
Db	1021	CCTTCTGTGCACTGTCACGTTGGAATCTACGCTTTGGGCTTCCGCACTTGCCTTTCGAGC	1080
QY	1081	CTCAACATTTCTGATTCAGACTCGGCTTTTACCAAGATGTCTCATCTTATCCGCTTCTTG	1140
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QY	1141	ACGACATGTACAGCTCTTGGGCAACGATGACGAGCTGGAACTCTTCAACGCGACCAATTA	1200
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Qy	1321	CGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTGTTGATTCGTATATGCAAGAACGA	1380
Dp	1321	CGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTGTTGATTCGTATATGCAAGAACGA	1380
Qy	1381	AGTGGATCGCACATGATTAATCTGCCCAAGCTTGAGAGATCTTGAGAGAACGGAGAAAGTTA	1440
Dp	1381	AGTGGATCGCACATGATTAATCTGCCCAAGCTTGAGAGATCTTGAGAGAACGGAGAAAGTTA	1440
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Dp	1441	GCTCTGCTCATGCGCCATGCGGCACTGCACACCCATTTCTGACGTTGGACATCCCTTCTCTG	1500
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Dp	1501	ATCACATCCCAAGAAAGTTGACCTTCCATGGAAGCTCAATGACTGTATATGATCAATCC	1560
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Dp	1561	TTCCATTAAAGAGTGATACACGCGTGCTACAAAGGACGACGGGCCCGTGGAGAAAGACCTT	1620
Qy	1621	CGTCTATATCATGTTTATATGAAAGCAATCCTCGATTAAACGAAAGAGATGCTCTGAATC	1680
Dp	1621	CGTCTATATCATGTTTATATGAAAGCAATCCTCGATTAAACGAAAGAGATGCTCTGAATC	1680
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Dp	1681	ATTATCAACTCATGATCAGGAGCGCAATCAGAGAATTAAATTGGAGGCTTCTAAAGCCAG	1740
Qy	1741	ACAAACAGTGTCCCATCACTTCCAAAGAAACAGCAATTTGACATTAAGCAGAGTTTGGCATC	1800
Dp	1741	ACAAACAGTGTCCCATCACTTCCAAAGAAACAGCAATTTGACATTAAGCAGAGTTTGGCATC	1800
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Dp	1801	ACGGTTACAGATACCGAGATGGGCTAAGGCTTGGCAACGTTGAAACAAAGAGTTTGGTGA	1860
Qy	1861	TGAGAACCGTCATTGGAACCTGTGCTTGTGTAAACAACCTTCAAAATCTACAAATATTAACTG	1920
Dp	1861	TGAGAACCGTCATTGGAACCTGTGCTTGTGTAAACAACCTTCAAAATCTACAAATATTAACTG	1920
Qy	1921	AGGATGCCCTATGGGTGTATATAGGGCACAAAAATTAATATGTTGTGTATAGTAAAGC	1980
Dp	1921	AGGATGCCCTATGGGTGTATATAGGGCACAAAAATTAATATGTTGTGTATAGTAAAGC	1980
Qy	1981	TGTAATTATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG	2040
Dp	1981	TGTAATTATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG	2040
RESULT 3	BD227661		
LOCUS	BD227661	2018 bp	DNA
DEFINITION	Syntheses.		linear
ACCESSION	BD227661		
VERSION	BD227661.1	GI:33037431	
KEYWORDS	JP 2002526066-A/13.		
SOURCE	Abies grandis		
ORGANISM	Abies grandis		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferoopsida; Coniferales; Pinaceae; Abies.		
AUTHORS	1 (bases 1 to 2018)		
TITLE	Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.		
JOURNAL	Patent: JP 2002526066-A 13 20-AUG-2002; UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR		

BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES									
COMMENT	OS	Adies grandis (giant fir)	PN	JP 200252606-A/13	PD	20-AUG-2002	PR	17-SEP-1999	JP 2000574228
	PF	18-SEP-1998	US	60/100993	22-APR-1999	US	60/130628	PR	23-JUN-1999
	US	60/150262	PI	JOSEPH CHARPELLE, KATHLEEN R MANN, JOSEPH P NOEL, COURTNEY M PI					
FEATURES	source	Location/Qualifiers	1..2018	/organism="Abies grandis"	/mol_type="genomic DNA"	/db_xref="taxon:46611"	Location/Qualifiers	(6)..(1889).	
ORIGIN	Query Match	64.9%; Score 1306.8; DB 6; Length 2018;	Best Local Similarity	81.0%; Pred. No. 0;	Matches 1595; Conservative	0; Mismatches 342; Indels 33; Gaps 5			
OY	68	CAGGTCGCTCAGTCTTCTCATGAGATTAAAGGCTTCGCTAGAACATATCCAACTCT	127						
Db	53	CAAAATCGTGTATGAGTTCTTACCCATGAGCTTAAGGCTCTCTGAMACAAATTCAGACTCT	112						
OY	128	TGGATCTGCAGCGCGGGGAATCCGTGCGCATTCATTAACATGTGTTTGAACAAGCGT	187						
Db	113	AGGAATGAGTATGGCGAGGAATCTATATCTCTTCATCAGCATGAGCTCTACACAGCT	172						
OY	188	CGCATCTACTGATTTCTGTACAGAGACGGGTGGGCAACTATCATTTCCAACTGTGGAGCA	247						
Db	173	TGTAAACGATGATGGTGTACAGAAACGATGGGCGAATTTCCATTTCCAACTTCGGAGACA	232						
OY	248	TGATTTCAATAGTCTCGATCTCAAGCCCTTAATGAGACACCTGATTAACCGGGAACGTGC	307						
Db	233	TGAATGCTAATAGTCT--TTACCAACGGCTTAATGAGAAATATGTAACCTGAGAGTGC	289						
OY	308	TGACAGACTTATTTGGGAGTAAGATATATGTTTCAATTTCAAGTCGCTGGAAGATGG	367						
Db	290	TGAAGAACTGATCGGGGAAGTAAAG--AACTGTCAATTCGATGTCATTAGAAGATGG	346						
OY	368	AG-----GCATGATCTCTTCAACAGACTTTTGTCTGTGTCATGACGTTGA	412						
Db	347	AGAGTTAATAGATCCGCTCAATGATCTCATTTCAACGCCCTTTGATGTGTGACAGGCTTTGA	406						
OY	413	ACGTTTGGGATTCAGACAGGCAATTTCAAAAAAGATATAAAAACGGCACTCGATTATGTTAA	472						
Db	407	ACGTTTGGGATTCATAGACATTTCAAAAGATAGAGATATAAATCGGGCTTGATTAAGTTTA	466						
OY	473	CAGTTATTTGACGAAAAAGGCATTTGATGTGGAGGAGAGTGTGACTGACCTCAA	532						
Db	467	CAGTTATTTGGGCGAAAAATGCGATCGGATGCGGGGAGAGATGTTGTTAATGATCTGAA	526						
OY	533	CTCAACCGGCTTTGGGGCTTGGACATCTCCCGACTACAGGATATACATGTCGTTTCAGATGT	592						
Db	527	CTCAACGCGCTTTGGGGCTTGGACATCTCCCGACTACAGGATATACATGTCGTTTCAGATGT	586						
OY	593	TTTGAACGTTTAAAGCAAAAAATGGGCAATTTTCTCACTGCGCAATATTCAGATAGA	652						
Db	587	TTTCAAGGCTTCAAAAGGCAAAAATGGGCAATTTTCTGCTCTGAAAATATTCAGACAGA	646						
OY	653	GGGAGAGTTTGAAGCGCTTCTCAATTTATTCAGGGGCTTCCTGTCGGCTTTCCCGGCGA	712						
Db	647	TGAAGAGATCAGAGCGCTTGAATTTATTCGCGGCGCTTCCTCATATGCTTTCCAGGGGA	706						

Qy	713	GAAAGTATGAGTAAAGCTGAAACATTCTCTACAAAATATTTAAGAGAGCCCTGCAAAA	772
Db	707	GAAAATTATGAGATGAGCGCTGAAATCTTCTCTACAAAATATTTAAGAGAGCCCTGCAAAA	766
Qy	773	GATTCCGGGCAATCCAGTATACCTTTCACTGAGATACGGGACGTTCTGGAATATGGTGGCA	832
Db	767	GATTCGGGTCTCCAGT---CTTTGGCGAGAGATCGGGGACGTTTGGAAATATGGTGGCA	823
Qy	833	CACCAATTTGCGACGCTTGGAAGCAAGGAATTAATGAGACGCTTTTGGACAGCACACTAA	892
Db	824	CACATATTTGCGCGATTGGAAGCAAGGAATTAATCAATCAAGCTTTTGGACAGCACACTGA	883
Qy	893	AAATAAGAACGC-----CGCCGAGAACTTTTAGAATCTTGCAAAATTTGCAATTCAA	943
Db	884	GAACACGMAAGTCATATGTGAAGAGCAAAAACTTTTAGACTCGMAAATTTGGAGTTCAA	943
Qy	944	TATATTTCACTCCCTTAACAAGAGAGAGTTAAACAATTTCCGATGGTGGAAAGACTC	1003
Db	944	CATCTTTCAATCTTTACAAAGAGGAGATTAAGAAAGTTGGTCAGATGGTGGAAAGATC	1003
Qy	1004	GGGTTCTCTGAGATGACCTTCTGTGCAATCGTCAACGTGAAATACTACGCTTTGGCTTC	1063
Db	1004	GGGTTTTCTGAGATGACCTTCTGTGCAATCGTCAACGTGAAATACTACCTTTGGCTTC	1063
Qy	1064	CTGCATTTGCGTTTCCGACCTCAACATTTCTGATTCAGACTCGGCTTTTACCAAGATGTCTCA	1123
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Qy	1124	TCTTATCACGGTTTCTTGACGCAATGTACAGAGCTTTCCGGCACAGTACGAGCTGGMACT	1183
Db	1124	TCTTATCACGGTTTCTTGACGATGTGTAGACACCTTCCGGCACAGTACGAGCTGGMACT	1183
Qy	1184	CTTCAACAGCGCAATTAAGAGATGGGATCCGTCGCGATGGAATGCTTCCAGAAATATAT	1243
Db	1184	CTTCAACAGCGCAATTAAGAGATGGGATCCGTCGCGATGGAATGCTTCCAGAAATATAT	1243
Qy	1244	GAAGAAGGTACATGATGATGTTTATCACACCGTAAATGAATGGTCGAGTGGCAGAGAA	1303
Db	1244	GAAGAAGGTGTACATAGCGGTTTATCGAACCGTAAATGAATGGTCGAGAGGCAAGAGCA	1303
Qy	1304	GGCTCAAGCGCCGAGACACGCTCAACTAGTCAAGACAGGCTTGGGAGGGGTGTTTGATTCT	1363
Db	1304	GGCTCAAGCGCCGAGATGAGCTTCAACTATGCTGCGGAGACCTTGGGAGGGCTTATATGATTCT	1363
Qy	1364	GTATATGAGAGAGCAAGATGGATGCGCACTGTTATCTGCCACGTTTGAAGAGTACTT	1423
Db	1364	GTATATGAGAGAGCAAGATGGATGCGCACTGTTATCTGCCCTCTTTGATGAGTACTTA	1423
Qy	1424	GGAGAACGGGAAAGTTAGCTGTGCTCATGCGCCATGCGCACTGCACCAACCATTTTGACGTT	1483
Db	1424	CGAGAAATGGGAAAGTTAGCTGTGCTCATGCGCAATTCGCGCAATTCGCAACCATTTTGACCAAT	1483
Qy	1484	GGACATCCCCCTTTCTGTATCATATCTTCAAGGAAGTTGACTTCCATCAAAAGCTTAAACGA	1543
Db	1484	GGACATCCCCCTTTCTGTATCATATCTTCAAGGAAGTTGACTTCCATCAAAAGCTTAAACGA	1543
Qy	1544	CTTGATATGTATCATCTTTCGATTAAGAGTGTATCAACGCTGTCTTCAAGAGCAGACAGGCG	1603
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Qy	1604	CCGTGAGAGAAAGCTTGCTGTATATCATGTGTATATGAAAGCAATCTGTGATTTAACGA	1663
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Qy	1664	AGAAAGATGCTCTGAAATCATATCAACTTATGTATCAAGGACCGCAATCAGAGAAATTTAAATTG	1723
Db	1664	AGAAAGATGCTCTGAAATCATATCAAGGACCGCAATCAGAGAAATTTAAATTTG	1723
Qy	1724	GGAGCTTTTAAGCGAGCAACAGGTGTTCCATCACTTCCAAAGAAACAACGATTTTGACAT	1783
Db	1724	GGAACTTTTCAAAACGAGCATCAATGTTTCCATCTCCGCGAGAAAGAAACATGCTTTTGACAT	1783
Qy	1784	AAGCAGATTTGGCATCAACGTTTACAGATTCAGATACCGAGATGGCTTACAGCTTTGCCAACGTTGA	1843

Db	1784	CGCCAGACCTTTCATTACGCGCTACAAATCCGAGACGGCTACACGCTTCCACGTTGA	1843
Qy	1844	AACAAAGAGTTTGTATGATGAGAACCGTCATTGAACTGTGCTTTGTAAACAACCTTCAA	1903
Db	1844	AACGAAGAGTTTGTATGATGAGAACCGTCATTGAACTGTGCTTTGTAAACAACCTTCAA	1903
Qy	1904	ATCTACATATTAACCTGAGATGCGCTTATATGAGGATATATAGGACACACAAATATATAT	1963
Db	1904	ATCTACATATTAACCTGAGATGCGCTTATATGAGGATATATAGGACACACAAATATATAT	1963
Qy	1964	GTTGTGTATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	2013
Db	1964	GATTAAGTTTGTATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	2013
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LOCUS	AR222097	2018 bp	DNA
DEFINITION	Sequence 3 from patent US 6429014.		Linear
ACCESSION	AR222097		
VERSION	AR222097.1		GI:23239471
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2018)		
AUTHORS	Steele, C. L., Bohlmann, J. and Croteau, R. B.		
TITLE	Monoterpene synthases from grand fir (<i>Abies grandis</i>)		
JOURNAL	Patent: US 6429014-A 3 06-AUG-2002;		
FEATURES	Location/Qualifiers		
source	1..2018		
ORIGIN	/organism="unknown"		
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Query Match	64.9%; Score 1306.8; DB 6; Length 2018;		
Best Local Similarity	31.0%; Pred. No. 0;		
Matches 1595; Conservative	0; Mismatches 342; Indels 33; Gaps 5;		
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Qy	128	TGAAATCTGCAGGCGCGGGAATCCGTCGCGCATTCATAAACAATGTTTACAAAGCT	187
Db	113	AGGAATGATGAGGGAAGGAATTTATACATCTTCCATGAGCATGAGCTCTACACCGT	172
Qy	188	CGCATCTACTGATTTCTGTACAGAGACGCGTGGCACTATATTTCCAACTGTGGAGCA	247
Db	173	TGTAAACGATGATGTTGTACGAGACGATGGCGATTTCCATTCCAACCTCTGGAGCA	232
Qy	248	TGATTTCAATCAGTCTCGATCTCAAGGCGCTTATGAGACCTGATTAACGGGAACGTC	307
Db	233	TGATTTCAATCAGTCTCGATCTCAAGGCGCTTATGAGAGAAATCTGATCTGAGCGTC	289
Qy	308	TGACAGACTTATATGAGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGAGAGATG	367
Db	290	TGAAATACTATATGAGGGAAGTAAAG---ACATGTTCAATTCGATGTCATTAGAAAGATG	346
Qy	368	AG-----GCAATGATCTCTTCAACGACTTTTCTGCTGATGACGTTGA	412
Db	347	AGATTTAATGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	406
Qy	413	ACGTTTGGGAATGACAGGCACTTCAAAAAAGATATTAATAACGGCACTCGATTAATGTTAA	472
Db	407	ACGTTTGGGAATGACAGGCACTTCAAAAAAGATATTAATAACGGCACTCGATTAATGTTAA	466
Qy	473	CAGTTATTTGGAACGAAAAAGGATGATGAGGAGGAGAGATGTTGATCTGACCTCAA	532
Db	467	CAGTTATTTGGAACGAAAAAGGATGATGAGGAGGAGAGATGTTGATCTGATCTGAA	526
Qy	533	CTCAACCGCTTGGGCGCTTGCACACTTCCGACTACAGATACCTGTCCTTCAATGT	592

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Db      527 CTCAACGCGCTGGGGCTTCGAAACCTCTACGACTACAGCATACCGGGGTCTTCGAGATGT 586
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Qy      713 GAAAGTTATGATGAAAGCTGAAACATTTCTTACAAATATTTTAAAGAGAGCCCTGCAAAA 772
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Qy      833 CACCAATTTGCGCAGCTTGAAGAGCAATTTACATGAGACGCTTTGAGACAGCACTAA 892
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Qy      1064 CTGCAATTCGCTTGAAGCTTCAACATTTCTGATTCAGACTCGGCTTTTACCAAGATCTCA 1123
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Db      1304 GGGCTCAAGGCGGAGACAGCTCACTATGCAAGACAGGCTTGGAGGGGCTTTTGAATTC 1363
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Qy      1484 GGAGATCCCTCTTCTGATCACTCTCAAGAGAGATGTAAGATGTAAGATGTAAGATGTAAGAT 1543
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Qy      1784 AAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1843
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DEFINITION Sequence 19 from patent US 6468772.
ACCESSION  AR240696
VERSION     AR240696.1  GI:27285845
KEYWORDS
SOURCE      Unknown.
            Unclonified.
REFERENCE   1 (bases 1 to 2018)
AUTHORS    Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLE      Methods of making modified polypeptides
JOURNAL    Patent: US 6468772-A 19 22-Oct-2002;
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ORIGIN

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Query Match      64.9%; Score 1306.8; DB 6; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
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Qy      68 CAGGTCGCTGAGTCTTCTCATGAGATTAAGGCTCTCGTGAAGCAATCCCACTCT 127
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Qy      188 CGCATCTAATGATTTCTGACAGAGACGCGTGGCACTATATTCCAACTGTGGAGCA 247
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Qy      248 TGAATTCATACAGCTCGATCTCAAGCGCTTATGAGAGACCTGATTAACGGGAGACGTG 307
Db      233 TGAATTCATACAGCTCTTACCAAGCGCTTATGAGAGAAATCTGATCTGAGAGCGTGC 289
Qy      308 TGAAGAGATTAATGAGAGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 367
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DEFINITION Sequence 19 from patent US 6495354.
ACCESSION AR266971
VERSION AR266971.1 GI:29696426
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLES Synthesizes
JOURNAL Patent: US 6495354-A 19 17-DEC-2002;
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Qy 128 TGAATTCGAGGCGGGAATACGTCGCGCATTCATAAACAATGTTGACAAGCGT 187
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 DEFINITION Sequence 19 from patent US 6559297.
 ACCESSION AR316320
 VERSION AR316320.1 GI:31711055
 KEYWORDS
 SOURCE
 ORGANISM
 Unclasseified.
 REFERENCE 1 (bases 1 to 2018)
 AUTHORS Chappelil,J., Manna,K.R., Noel,J.P. and Starks,C.M.
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 Best Local Similarity 81.0%; Pred. No. 0;
 Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

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LOCUS AR338463 2018 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 19 from patent US 6569656.
ACCESSION AR338463
VERSION AR338463.1 GI:33725240
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2018)
AUTHORS Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLE Syntheses

JOURNAL Patent: US 659656-A 19 27-MAY-2003;
FEATURES Location/Qualifiers

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Query Match 64.9%; Score 1306.8; DB 6; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
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ACCESSION AR429869
VERSION AR429869.1 GI:40190267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLE Synthesizes
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Best Local Similarity 81.0%; Pred. No. 0; Mismatches 342; Indels 33; Gaps 5;
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Db		1304	GGCTCAAGGGCCGAAATACGCTCACTATATGCTCGGGAACTTGGAGGGCTTATATTTGATTC	1363
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Db		1364	GTATATGACAAACCAAGTGGATTCGCCACCTGGTTACTCGCTCTCTTTGATGAGTACTA	1423
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Db		1484	GGACATCCCCCTTTTCTGTATCATCTTCCTCAAGAAAGTTGACTTCCCATNAAGCTTAAAGCA	1543
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VERSION	AY237645			
KEYWORDS	AY237645.1 GI:34582666			
SOURCE	Picea sitchensis (Sitka spruce)			
ORGANISM	Picea sitchensis (Sitka spruce)			
REFERENCE	Eukaryote; Vascular plantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.			
AUTHORS	Byun McKay,S.A., Hunter,W.L., Godard,K.A., Wang,S.X., Martin,D.M., Bohlmann,J. and Plant,A.L.			
TITLE	Insect Attack and Wounding Induce Traumatic Resin Duct Development and Gene Expression of (-)-Pinene Synthase in Sitka Spruce			
JOURNAL	Plant Physiol. 133 (1), 368-378 (2003)			
PubMed	12970502			

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RESULT 12
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 ACCESSION AF543527
 VERSION AF543527.1 GI:28894481
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 2082)
 AUTHORS
 Phillips,M.A., Wildung,M.R., Williams,D.C., Hyatt,D.C. and
 Croteau,R.
 TITLE
 cDNA isolation, functional expression, and characterization of
 (-)-alpha-pinene synthase and (-)-alpha-pinene synthase from
 loblolly pine (Pinus taeda): Stereoccontrol in pinene biosynthesis
 Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
 MEDLINE 22510022
 PUBMED 12623076

REFERENCE
 2 (bases 1 to 2082)
 AUTHORS
 Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B.
 TITLE
 Direct Submission
 Submitted (09-SEP-2002) Institute of Biological Chemistry,
 Washington State University, PO Box 646340, Pullman, WA 99164-6340,
 USA

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ORIGIN

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 Best Local Similarity 80.2%; Pred. No. 0;
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RESULT 13
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 LOCUS AF543529
 DEFINITION Pinus taeda alpha-terpineol synthase mRNA, complete cds.
 ACCESSION AF543529.1
 VERSION AF543529.1
 KEYWORDS
 SOURCE
 ORGANISM
 Pinus taeda (loblolly pine)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 2162)
 PHILIPPS, M.A., Wildung, M.R., Williams, D.C., Hyatt, D.C. and
 Croteau, R.
 TITLE
 cDNA isolation, functional expression, and characterization of

(+)-alpha-pinenene synthase and (-)-alpha-pinenene synthase from
loblolly pine (*Pinus taeda*): Stereocontrol in pinene biosynthesis
Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
JOURNAL MEDLINE 22510022
PUBMED 12623076
2 (bases 1 to 2162)
REFERENCE Phillips, M.A., Wildung, M.R., Williams, D.C. and Croteau, R.B.
AUTHORS Direct Submission
TITLE Submitted (09-SEP-2002) Institute of Biological Chemistry,
JOURNAL Washington State University, PO Box 646340, Pullman, WA 99164-6340,
USA

FEATURES

source

CDS

Location/Qualifiers
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ORIGIN

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RESULT 14
AF461460
LOCUS AF461460 2186 bp mRNA linear PLN 27-MAR-2003
DEFINITION Picea abies (+)-3-carene synthase (JF67) mRNA, complete cds.
ACCESSION AF461460
VERSION AF461460.1 GI:29293033
KEYWORDS
SOURCE Picea abies (Norway spruce)
ORGANISM Picea abies
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE
AUTHORS Faeldt, J., Martin, D., Miller, B., Rawat, S. and Bohlmann, J.
TITLE Truncation of the resin defense in Norway spruce (Picea abies): methyl
jasmonate-induced terpene synthase gene expression, and cDNA
cloning and functional characterization of (+)-3-carene synthase
JOURNAL Plant Mol. Biol. 51 (1), 119-133 (2003)
MEDLINE 22490501
PUBMED 12602896
REFERENCE 2 (bases 1 to 2186)
AUTHORS Faeldt, J. and Bohlmann, J.
TITLE Direct Submision
JOURNAL Submitted (20-DEC-2001) Biotechnology Laboratory, University of
British Columbia, 237-6174 University Blvd, Vancouver, BC V6T1Z4,
Canada

FEATURES
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1927. 2186
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Best local similarity 76.1%; Pred. No. 1.1e-293; Indels 30; Gaps 5;
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Db TTTCAGGTGCTGCTCAGTTCCTCATGAGATTAAAGCTCTCCGTAACATCCAA 145
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Search completed: July 26, 2004, 12:26:24
 Job time : 7598 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:53 ; Search time 762 Seconds
(without alignments)
11222.602 Million cell updates/sec

Title: US-10-025-145A-64

Perfect score: 2013

Sequence: 1 ttctgacgtcctcttcac.....aaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY NUC

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2013	100.0	2013	4	AAAF73411 Grand fir
2	1306.8	64.9	2018	2	AAAX08644 Pinene syl
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4	1306.8	64.9	2018	4	AAAX08644 Pinene syl
5	1092.4	54.3	1890	4	AAAF73372 Grand fir
6	1072.4	53.3	2186	4	AAAF73412 Grand fir
7	1071.6	53.2	2196	2	AAAX08643 Myricene s
8	1071.6	53.2	2196	3	AAAX08643 Myricene s
9	1071.6	53.2	2196	4	AAAF73371 Grand fir
10	1071.6	53.2	2205	2	AAAX08663 Grand fir
11	1071.6	53.2	2205	4	AAAF73391 Grand fir
12	929.4	46.2	2429	4	AAAF73413 Grand fir
13	925.4	46.0	2089	2	AAAX08645 Limonene
14	925.4	46.0	2089	3	AAAX08645 Limonene
15	925.4	46.0	2089	4	AAAF73373 Grand fir
16	807.4	40.1	1513	3	AAAF69551 Pinus rad
17	805.8	40.0	1634	3	AAAF69644 Pinus rad
18	623.6	31.0	1173	3	AAAF69643 Pinus rad
19	471	23.4	696	4	AAAF73414 Grand fir
20	448.6	22.3	1885	2	AAAX87534 Delta-sel
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ALIGNMENTS

RESULT 1
AAAF73411 standard; cDNA; 2013 BP.

AC AAFA73411;

DT 30-APR-2001 (first entry)

DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 64.

KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

KW terpinolene synthase; insect resistance; nutrition; ss.

XX Abies grandie.

XX WO200107565-A2.

XX 01-FEB-2001.

XX 24-JUL-2000; 2000MO-US020264.

XX 26-JUL-1999; 99US-00360545.

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.

XX Steele CL, Bohlmann J, Croteau RB, Phillips MA;

XX WPI; 2001-182782/18.

XX P-PSDB; AAB69390.

XX New nucleic acid encoding monoterpene synthases, for increasing terpene

XX synthesis in plants, e.g. for increasing resistance to pests or for

XX treatment of cancer.

XX Claim 8; Page 147-149; 175pp; English.

XX The present invention provides the protein and coding sequences of

XX monoterpene synthases from the grand fir. These include (-)-camphene

XX synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-

XX limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase

XX and pinene synthase. The sequences can be used to produce transgenic

XX plants expressing high levels of the enzymes, resulting in levels which

XX are useful in protecting against and treating cancers, and to confer

XX insect resistance on plants

Sequence 2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1141 ACGACATGTCAGAGTCTTGGGCACTAGTACAGAGCTGGAACCTTTCACAGCGCAATTA 1200
DB 1141 ACGACATGTCAGAGTCTTGGGCACTAGTACAGAGCTGGAACCTTTCACAGCGCAATTA 1200
QY 1201 AGAGATGGGATTCGTCGCGGATGGAATGCCCTCCAGATATATGAAAGAGTATACATGA 1260
DB 1201 AGAGATGGGATTCGTCGCGGATGGAATGCCCTCCAGATATATGAAAGAGTATACATGA 1260
QY 1261 TGGTTTATCAACCCGTAATGAAATGGCTCGAGTGGCAGAGAAAGCTCAAGCCGAGACA 1320
DB 1261 TGGTTTATCAACCCGTAATGAAATGGCTCGAGTGGCAGAGAAAGCTCAAGCCGAGACA 1320
QY 1321 CGCTCAACTATGCAAGACAGGCTTGGAGCGCTGTTTGAATCGTATATGAGAGACAA 1380
DB 1321 CGCTCAACTATGCAAGACAGGCTTGGAGCGCTGTTTGAATCGTATATGAGAGACAA 1380
QY 1381 AGTGAATCGGCACTGTTATCTGCGCAAGTTTGAAGATCTTGAAGACGGAAAGTTA 1440
DB 1381 AGTGAATCGGCACTGTTATCTGCGCAAGTTTGAAGATCTTGAAGACGGAAAGTTA 1440
QY 1441 GCTCTGTCATCGGCCATGCGGCACTGCAACCCATTCGACGTTGGACATCCCTTCTCG 1500
DB 1441 GCTCTGTCATCGGCCATGCGGCACTGCAACCCATTCGACGTTGGACATCCCTTCTCG 1500
QY 1501 ATCAATCTCTCAAGAAAGTTGACTTCCCATGCAAGCTCAATGACTTGTATATGATATCC 1560
DB 1501 ATCAATCTCTCAAGAAAGTTGACTTCCCATGCAAGCTCAATGACTTGTATATGATATCC 1560
QY 1561 TTTGATTAAGAGGTGATACACGGTGTACAAAGGACAGAGGCGCGTGGAGAAAGCTT 1620
DB 1561 TTTGATTAAGAGGTGATACACGGTGTGTACAAAGGACAGAGGCGCGTGGAGAAAGCTT 1620
QY 1621 CGTCTATATCACTGTTATATGAAAGCAATCTCGGATTAACGGAAGAAATGCTTGAATC 1680
DB 1621 CGTCTATATCACTGTTATATGAAAGCAATCTCGGATTAACGGAAGAAATGCTTGAATC 1680
QY 1681 ATATCAACTTCAATATCAAGGAGCGCAATCAAGAAATTAATTTGGAGCTTCTAAAGCCAG 1740
DB 1681 ATATCAACTTCAATATCAAGGAGCGCAATCAAGAAATTAATTTGGAGCTTCTAAAGCCAG 1740
QY 1741 ACAACAGTGTCCCATCACTTCCAAAGAAACACGCAATTTGACATGAGCAGATTTGGCATC 1800
DB 1741 ACAACAGTGTCCCATCACTTCCAAAGAAACACGCAATTTGACATGAGCAGATTTGGCATC 1800
QY 1801 ACGGTTACAGATACCGAGATGCTACAGCTTTGCGCAAGCTTTGAAACAAAGAGTTGGTGA 1860
DB 1801 ACGGTTACAGATACCGAGATGCTACAGCTTTGCGCAAGCTTTGAAACAAAGAGTTGGTGA 1860
QY 1861 TGAAGAACCGTCATTTGAACCTGTGCTTTGTGAACAACCTTCAAAATTCATATTAACCTG 1920
DB 1861 TGAAGAACCGTCATTTGAACCTGTGCTTTGTGAACAACCTTCAAAATTCATATTAACCTG 1920
QY 1921 AGGATGCCCTATGGGTGTATATAGGACACAAATAATATGTTGTGTAGTAAGC 1980
DB 1921 AGGATGCCCTATGGGTGTATATAGGACACAAATAATATGTTGTGTAGTAAGC 1980
QY 1981 TGTATATTATGAAAAAATGAAAAAATGAAAAA 2013
DB 1981 TGTATATTATGAAAAAATGAAAAAATGAAAAA 2013
RESULT 2
AA08644
ID AA08644 standard; cDNA; 2018 BP.

XX AAX08644;
XX 27-SEP-1999 (first entry)
XX
XX
DE Pinene synthase gene.
XX Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
XX defense; plant seed; oil; meal; ss.
XX
XX Abies grandis.
XX
XX Key Location/Qualifiers
XX CDS 6..1892
XX FT /*tag= a
XX FT /product= "Pinene synthase"
XX
XX WC902030-A1.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US014528.
XX PF
XX 11-JUL-1997; 97US-0052249P.
XX PR
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
XX Bohlmann J, Steele CL, Croteau RB;
XX
XX WPI: 1999-120396/10.
XX DR P-PSDB; AAM85701.
XX
XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
XX fir (Abies grandis), used to provide plants with modified production of
XX monoterpenes, e.g. myrcene, limonene or pinene.
XX
XX Claim 10; Page 74-77; 121pp; English.
XX
XX Nucleotide sequences encoding myrcene synthase, limonene synthase and
XX pinene synthase from Grand fir may be incorporated into any organism
XX (e.g. intact plant, animal, microbe), or derived cell culture that
XX produces geranyl diphosphate for the production of the aforementioned
XX enzymes or their products. The sequences when expressed in transfected
XX cells may also be used for the production or modification of flavour and
XX aroma properties, improvement of defense capability, and the alteration
XX of other ecological interactions mediated by myrcene, limonene, pinene,
XX or their derivatives. In particular they can be used for the production
XX of plant seeds for the extraction of oil or meal
XX
SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;
Query Match 64.9%; Score 1306.8; DB 2; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;
QY 68 CAGGTGCTGCTTCAGTTCTTCTCATGAGATTAAAGGCTTCGGTAGAACAATCCCACTCT 127
DB 53 CAATTCGTTGATGCTTCTACCACTGAGCTTAAGGCTTCCTCTGMAAACAATTCAGCTCT 112
QY 128 TGAATCTGACGCGGGAATCGGTGGCGATTCCATAAAGTGTGTTGACAAAGCT 187
DB 113 AGAATGATGAGGAGGGAATATATCACTCTTCCTACAGCATGAGCTTACCAAGCT 172
QY 188 CGCATCTACTGATTCTGTACAGAGACGGGTGGCAACTATTCATTCGAACCTGTGGAGCA 247
DB 173 TGTAAACGATGATGATGTAACAAGACGATGGCGATTTCATTCGAACCTGTGGAGCA 232
QY 248 TGAATTCATAGTCTGATCTCAAGCGCTTATGAGACACCTGATTCGCGGAACGTC 307
DB 233 TGAATGATAGTCTCTTACCAACGGCTTATGAGGAAAAATGTAACCTGAGCGTC 289
QY 308 TGACAGCTTATTTGGGAAATGAAGATATATGTTCAATTCAGTGCCTGAGAGATGG 367

DB 290 TGAGAACTGATCGGGGAATGAAG---ACATGTTCAATTGATGTCATTAGAAGATG 346
QY 368 AG-----GCAATGATCTCTTCAACGACTTTTGCTGCTGATGACCTTGA 412
DB 347 AGAGTTAATGAGTCCGCTCAATGATCTCATTCACAGCTTTGATGTCAGAGCTTGA 406
QY 413 ACGTTGGGAATGACACGCGATTTCAAAAAAGATATAAAACGCACTGATTAATGTTAA 472
DB 407 ACGTTGGGATTCATGACATTTCAAGATGAATATAAAATGCGCTTGATTAATGTTTA 466
QY 473 CAGTTAATGGAACGAAAAAGCATTTGATGAGGAGAGATGTTGATCTGACCTCA 532
DB 467 CAGTTAATGGGCGAAAAATGGCATTCGATGGGAGGAGAGATGTTGATCTGATCTGAA 526
QY 533 CTCAACGCTTGGGCGCTTGAACCTTCGACCTACAGGATACACTGTGCTTCAGATGT 592
DB 527 CTCAACGCTTGGGCGCTTGAACCTTCGACCTACAGGATACACTGTGCTTCAGATGT 586
QY 593 TTTGAACGTTTTTAAAGCAAAATGCGCAATTTTCCCTGCACTGCAATATTCAGATGA 652
DB 587 TTTCAAGCTTTGAAAGGCAAAATGCGCAATTTTCCCTGCACTGCAATATTCAGATGA 646
QY 653 GCGAGAGATTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTGCTGCTTCCGCGCA 712
DB 647 TGAAGAGATCGAGCGCTTCTCAATTTATTCAGGCGCTCCCTGCTGCTTCCGCGCA 706
QY 713 GAAAGTATGAGTGAAGCTGAACATTTCTTCAAAATATTTAAAGAGAGCCCTGCAAAA 772
DB 707 GAAATATATGATGAGGCTGAATCTTCTTCAACAAATATTTAAAGAGAGCCCTGCAAAA 766
QY 773 GATTCGCGCATCGATGATCTTCACTGATAGATACGCGGACGTTGCAATATGTTGGCA 832
DB 767 GATTCGCGCATCGATGATCTTCACTGATAGATACGCGGACGTTGCAATATGTTGGCA 823
QY 833 CACCAATTTGCGCAAGCTTGAAGCAAGATTAATGACGCTTGTGACACGACACTPA 892
DB 824 CACATATTTGCGCGATTTGAAGCAAGATTAATGACGCTTGTGACACGACACTGA 883
QY 893 AATTAAGAACCC-----CGCCGAGAACTTTTGAACCTTGTGCAAAATTTGAATTCAA 943
DB 884 GAAACAGCAAGTCAATGATGAAGACCAAAACCTTTGMACTCCGCAAAATTTGAGTTCAA 943
QY 944 TATATTTCACTCTTCAAGAGAGAGATTAAACATGTTTCCGAGTGTGAAAGACTC 1003
DB 944 CATCTTCAATCTTCAAAAGAGAGATTAAAGATGTTGTCAGATGTTGAAGAAATC 1003
QY 1004 GGGTTCTCTGATGATGACCTTCTGTGACATGTCAGCTGATGAAATGTAAGCTTTGCTTC 1063
DB 1004 GGGTTCTCTGATGATGACCTTCTGTGACATGTCAGCTGATGAAATGTAAGCTTTGCTTC 1063
QY 1064 CTGATTCGCTTCAAGCTTCAACATTTGATGATGACACTCGGCTTTGCAAGACGTCGCA 1123
DB 1124 TCTTATACCGGTTCTTGAAGCATGATGACAGCTGTTGGGCAAGTGAAGAGCTGGAAT 1183
QY 1184 CTTCACAGCGAATTAAGATGAGATCGCTTCGCGATGAGATGCTTCAGAAATATAT 1243
DB 1184 CTTCACAGCGAATTAAGATGAGATCGCTTCGCGATGAGATGCTTCAGAAATATAT 1243
QY 1244 GAAAGAGATGATCATGATGTTTATCACACCGTTAAATGAAATGCTGAGATGGCAGAGAA 1303
DB 1244 GAAAGAGATGATCATGATGTTTATCACACCGTTAAATGAAATGCTGAGATGGCAGAGAA 1303
QY 1304 GGGTCAAGGCGCAAGACGCTCAACTATGCAAGACAGGCTTTGGAGGCGTGTATGATTC 1363
DB 1304 GGGTCAAGGCGCAAGATGACCTCAATATGCTGGGAAGCTTTGGAGGCGTGTATGATTC 1363
QY 1364 GTATATGAGAGAACAAAGTGAATGCGCACTGTTATCTGCCAGCTTTGAGAGATCTT 1423
DB 1364 GTATATGAGAGAACAAAGTGAATGCGCACTGTTATCTGCCAGCTTTGAGAGATCTT 1423

Qy	1424	GGAGAAGCGGAAAGTTACTCTGCTGCATACGCGCAACGAGCACTGCAAGCCATTCTGAGGTT	1483
Db	1424	CGAGATGCGAAAGTTAGCTGTGGTCATCGCATATCCGCAATTGCACACCCATTCTGCACAT	1483
Qy	1484	GGACATCCCTCTTCCGTGATCAATCTCTCAAGGAAGTTACTTCCATCGAAGCTCAATGA	15443
Db	1484	GGACATCCCTCTTCCGTGATCAATCTCTCAAGGAAGTTACTTCCATCGAAGCTTAAAGCA	15443
Qy	1544	CTTGATATGATCATCTCTTCGATTTAAGAGGTGATACAGGTGCTTCAAGCGACAGAGGC	1603
Db	1544	CTTGCGATGTCGCATCTTTCGATTAAGAGGTGATACGGGTGCTTCAAGCGCGACAGGGC	1603
Qy	1604	CGGTGGAAGAAGCTGCTGATATCAATGTTATATGAAAGCAATCCGGAATTAAAGGA	1663
Db	1604	TCTGTGAAGAAGAAGTTCTCTCTATATCAATGTTATATGAAAGCAATCTCGAGATACGA	1663
Qy	1664	AGAAGATCCTCTGATCATATCAATCTTATGATCAGGAGCGCAATCAGAGATTTAAATTG	1722
Db	1664	GGAAGATGCTCTCGATCATATCAATCGCATGATCAGTACGTTACATCAAGAGATTTAAATTG	1722
Qy	1724	GAGCTTCTTAAAGCGACAAACAGTGTCCCATCACTTCCAAAGAAACAGCATTTGACAT	1783
Db	1724	GGAATCTTCTCAACCGACATCAATCAATGTTCCCATCTCGCGAAGAAACATGCTTTGACAT	1783
Qy	1784	AAGCAGATTTGGCATCAAGGTTAAGATACCGAATGCGATACACTTTGCGCAAGTTGA	1843
Db	1784	CGCCAGACCTTTCATTAACGGTTACAAATACCGAAGCGCTACACGTTGGCCAAAGTTGA	1843
Qy	1844	AACAAGAGTTTGGTGGATGAGAACCGCATTTGAACCTGTGCTTGTGTAACAACACTTCAA	1903
Db	1844	AACGAAAGTTTGGTGCACGAGAACCCCTCCTTGAATCTGTGCTTGTGACAAACACTCAA	1903
Qy	1904	ATCTTCAATATTAATCTGAGGATGCCCTTATGGGTGATATATGGGCGCACAAATATTAATAT	1963
Db	1904	ATCTATGCCCTATGCTATGTGCGGTTTAAATATATGTGAAGGTGCGGTTGATGATGA	1963
Qy	1964	GGTGTGTTAGTAAAGCTGTATATTATGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT	2013
Db	1964	GGATTAAGTTTGTATTAATTTAATTAAGTTTATTAATTTAATTTAATTTAATTTAATTTAATTTA	2013
RESULT 3			
AAA38922			
ID	AAA38922	standard; DNA; 2018 BP.	
AC	AAA38922;		
XX			
DT	25-AUG-2000	(first entry)	
DE			
XX		Grand fir pine synthase DNA sequence SEQ ID NO:19.	
XX			
KW		Synthase; protein co-ordinate date; active site; modification; terpenoid;	
KW		3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;	
KW		isoprenoid; breeding programme; fragrance; flavour; pheromone;	
KW		defensive agent; pigment; anticlimate; antitumor; steroid hormone;	
KW		signal transduction pathway; bile acid; affinity purification;	
KW		phoreceptor; enzymatic synthesis; nutrient supplement;	
KW		immunological reagent; ds.	
XX			
OS		Abies grandis.	
XX			
PN	MO200017327-A2.		
XX			
FD	30-MAR-2000.		
XX			
PF	17-SEP-1999;	99WO-US021419.	
XX			
PR	18-SEP-1998;	98US-0100993P.	
PR	22-APR-1999;	98US-0130628P.	
PR	23-AUG-1999;	99US-0150262P.	
XX			
PA	(KENT) UNIV KENTUCKY RES DEPT.		

PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Starke CM;
XX
XX WPI; 2000-292839/25.
DR P-PSDB; AAY90837.
XX
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
XX Disclosure; Page 363-366; 450pp; English.
XS

Query Match	Best Local Similarity	81.0%;	Score 1306.8;	DB 3;	Length 2018;
Matches 1595;	Conservative	0;	Mismatches 342;	Indels 33;	Gaps 5
CC	The present invention describes an isolated terpene synthase (I)				
CC	comprising a region with at least 20% identity to region 265-515 of a 548				
CC	amino acid (aa) sequence (Ia), given in AA190831. (I) contains nine alpha				
CC	-carbon atoms (alphaC) that have an interatomic distance, between each				
CC	other, within tabulated ranges, have a centre point (within a sphere of				
CC	radius 2.3 Angstrom) within tabulated ranges, and have an ordered				
CC	arrangement of R groups (defining as side chains), excluding specific				
CC	tabulated arrangements (tables given in the specification). (I) and				
CC	related enzymes, are used to produce a wide range of terpenoids (e.g.				
CC	cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,				
CC	flavours, pheromones, defensive agents, pigments, antitumour agents,				
CC	components of signal transduction pathways, precursors of steroid				
CC	hormones and bile acids, as photoreceptors and as co-factor side chains.				
CC	Some synthases with little or no catalytic activity (and nucleic acids				
CC	encoding them) are used as controls in the analysis of products formed by				
CC	enzymatic synthesis, as nutrient supplements, for affinity purification				
CC	of isoprenoids, or to develop immunological reagents or nucleic acids for				
CC	monitoring expression of terpene synthase or inheritance of the gene in				
CC	plant breeding programs. The new synthases may produce novel terpene				
CC	products. AA18910 to AA18938 and AA190831 to AA190859 represent				
CC	sequences used in the exemplification of the present invention				
XX					
SO	Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;				
QY	68 CAGGTCCGCTCAGTCTCTTCATGATTAAGCGTCCTCGTGAACAATCCAACT	127			
DB	53 CAAATCGTGTACAGTTCTTACCACAGACTTAAGGCTCTCTTGAAACAATTCACGCTT	112			
QY	128 TGGATCTGCAGCGCGGGGAATCCGTCGCGCATTCCTCAATAACATGTTTGACAAGCGT	187			
DB	113 AGGAATAGTAGTAGGGAAGGAATGATCATCTCTTCATCAGCATGAGACTTACACCGT	172			
QY	188 CGCATCTAAGTATTTCTGTACAGAGACCGGTGGGCACTATCATTTCCAACTGTGGGACGA	247			
DB	173 TGTAAACGATATGATGTATCAACAAACGATGGGCGATTTCCATTCCAACTCTGGACGA	232			
QY	248 TGAATTCATACAGTCTCGATCTCAACGCCCTTATGAGACACCTGATTAACCGGGAACGTGC	307			
DB	233 TGAATGTATACAGTCT---TTACCAACGCGCTTATGAGGAAAAATGTACCTGGACGTGC	289			
QY	308 TGACAGACTTATTTGGGGAAGTAAGATATATATGTTCAATTTCAAGTCGCTGGAAAGTGG	367			
DB	290 TGAATAAATCGATCGGGGAAGTAAAG---AAATGTTCAATTCGATGTATTAGAAAGTGG	346			
QY	368 AG-----GCATGATCTTCCTTCACAGCACTTTTGCGTGCAGTAAAGCTTGA	412			
DB	347 AGAGTTATGAGTCGCGCTCAATGATCTATTCACAGCGCTTGGATTTGCGACAGCTTGA	406			
QY	413 ACGTTTGGGATTCGACAGGCAATTTCAAAAAAGATATAAAAACGCGACTCGATTATGTTAA	472			
DB	407 ACGTTTGGGATTCATGACATTTCAAAAGATGAGATATAAACCGGCGCTGATTATGTTTA	466			
QY	473 CAGTTATTTGGAACGAAAAAGCATTTGGATGTGGGAGGAGAGTGTGTGACATGACCTGAA	532			
DB	467 CAGTTATTTGGGCGCAAAATGGCATCTCGATTCGGGAGGAGAGTGTGTGTTATCGATCTGAA	526			

QY 533 CTCAACGCGCTTGGGCGCTTGCAGCTCTCCGACTACAGGATACACTGCTGCTTCAGATGT 592
 DB 527 CTCAACGCGCTTGGGCGCTTGCAGCTCTCCGACTACAGGATACCGGAGTCTTCAGATGT 586
 QY 593 TTTGACGCTTTTAAAGCAAAATTTGGCAATTTTCTCTCACTGCGCAATATTCAGATAGA 652
 DB 587 TTTCAAGCTTTCAAAAGCCAAAATGGGCAATTTTCTGCTCTGAAAATATTCAGACAGA 646
 QY 653 GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGAGCGCTCTCGTGGCTTTCCCGGCA 712
 DB 647 TGAAGAGATCAGAGCGCTTGAATTTATTCGGGCGCTCCCTCATGCTTTCCAGGGGA 706
 QY 713 GAAAGTATGATGAGCTGAAGCACTCTCTACAAATTTTAAAGAGCGCTGCAAAA 772
 DB 707 GAAATATATGATGAGCTGAAGCACTCTCTACAAATTTTAAAGAGCGCTGCAAAA 766
 QY 773 GATTCCGCGATCAGATATCTTTCATGAGTACGAGACGTTCTGAAATATGTTGGCA 832
 DB 767 GATTCCGCGTCCAGT---CTTGGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCA 823
 QY 833 CACCAATTTGCGACGCTTGAAGCAAGAAATTCATGACGCTTTTGAACAGCACACTGA 892
 DB 824 CACATATTTGCGCGATGGAAGCAAGAAATTCATCCAGCTTTTGAACAGCACACTGA 883
 QY 893 AAATTAAGAACG-----CGCGAAGAACTTTTGAACCTTGAAGAAATTTGAATTCGA 943
 DB 884 GAAACAGAAATGATATGTAAGAGCAAAAATTTTGAACCTTGAAGAAATTTGAATTCGA 943
 QY 944 TATATTTCACTCTCTTCAAGAGAGAGATTAATAATCATGTTTCCGAGTGGAAAGACTC 1003
 DB 944 CATCTTTCAATCTCTTCAAAAAGAGGAGATTGAAGATCTGCTGAGATGTTGAAGAAATC 1003
 QY 1004 GGGTTTCTCTGAGATGACCTTCTGTGCAATCTGTCAGCTGGAATATCACTGTTGGCTTC 1063
 DB 1004 GGGTTTCTCTGAGATGACCTTCTGTGCAATCTGTCAGCTGGAATATCACTGTTGGCTTC 1063
 QY 1064 CTGATTTGCGTTCAGAGCTCAACATTTGAGTTCAGACTCGGCTTTTACCAAGATGCTCA 1123
 DB 1064 CTGATTTGCGTTCAGAGCTCAACATTTGAGTTCAGACTCGGCTTTTACCAAGATGCTCA 1123
 QY 1124 TCTTATCAGGCTTCTTGAAGCATGTCAGAGCTCTTCCGCAACAGTACAGAGCTGGAATC 1183
 DB 1124 TCTTATCAGGCTTCTTGAAGCATGTCAGAGCTCTTCCGCAACAGTACAGAGCTGGAATC 1183
 QY 1184 CTTTCAACGCGCAATTAAGATGAGATCGCTCGCGCATGGAATGCTTCCAGAAATATAT 1243
 DB 1184 CTTTCAACGCGCAATTAAGATGAGATCGCTCGCTCGATGATGCTTCCAGAAATATAT 1243
 QY 1244 GAAAGAGTGTATCATGATGTTTATCAACCGTAAATGAATGCTGAGTGGCAGAGAA 1303
 DB 1244 GAAAGAGTGTATCATGATGTTTATCAACCGTAAATGAATGCTGAGTGGCAGAGAA 1303
 QY 1304 GGGCTCAAGGCGGAGACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGTTGATTC 1363
 DB 1304 GGGCTCAAGGCGGAGATGAGCTCAACTATGCTCGGGAACCTTGGAGGCGTGTATGATTC 1363
 QY 1364 GTATATGAGAGCAAGATGAGATCGCACTGCTGTTATCTGCCACGTTTGAAGAGTACTT 1423
 DB 1364 GTATATGAGAGCAAGATGAGATCGCACTGCTGTTATCTGCCACGTTTGAAGAGTACTT 1423
 QY 1424 GGAGAAAGGGAAAGTATGCTGCTCATGCGCACTGCGCACTGCAAGCAACCATTTGACAT 1483
 DB 1424 CGAAGATGGGAAAGTATGCTGCTCATGCGCACTGCGCACTGCAAGCAACCATTTGACAT 1483
 QY 1484 GGACATCCCTTTCTCTGATCATCTCTCAAGAAAGTTGACTTCCCATCAAAAGCTTAAAGA 1543
 DB 1484 GGACATCCCTTTCTCTGATCATCTCTCAAGAAAGTTGACTTCCCATCAAAAGCTTAAAGA 1543
 QY 1544 CTTGATATGATCATCTCTGATTAAGAGTGTATCAGAGTGTCTCAAGGAGCAAGAGGCG 1603
 DB 1544 CTTGATATGATCATCTCTGATTAAGAGTGTATCAGAGTGTCTCAAGGAGCAAGAGGCG 1603
 QY 1604 CCGTGAAGAAAGCTTGTCTATATCATGTTATGAAGCAATCTGATTAACGGA 1663

DB 1604 TCGTGAAGAAAGCTTCTCTATATCATGTTATATGAAGCAATCTTGAAGTATCAGA 1663
 QY 1664 AGAAGATGCTGTATCATATCAACTTCATGATGATGAGGAGCAATCAGAGAAATTAATTG 1723
 DB 1664 GGAAGATGCTGTATCATATCAAGGAGTATGATGATGATGATGATGATGATGATGATGATG 1723
 QY 1724 GGAAGTCTTAAAGCAGCAACAGTGTTCATCATCTTCCAAAGAAACAGCATTTGACAT 1783
 DB 1724 GGAAGTCTTAAAGCAGCAACAGTGTTCATCATCTTCCAAAGAAACAGCATTTGACAT 1783
 QY 1784 AAGCAGATTTGGCATCAGCTGCTTACAGATCCGAGATGCTTACAGCTTGGCAAGTGA 1843
 DB 1784 CGCCAGAGCTTTCATTTACGCTTACAGATCCGAGATGCTTACAGCTTGGCAAGTGA 1843
 QY 1844 AACAAAGATTTGGTGTATGAGAACCGTCAATGAACTGTGCTTTTGAACAACACTTGA 1903
 DB 1844 AACAAAGATTTGGTGTATGAGAACCGTCAATGAACTGTGCTTTTGAACAACACTTGA 1903
 QY 1904 ATCTATGCTTATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1963
 DB 1904 ATCTATGCTTATTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1963
 QY 1964 GGTGCTGTTAGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2013
 DB 1964 GGTGCTGTTAGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2013
 QY 1964 GGTGCTGTTAGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2013
 DB 1964 GGTGCTGTTAGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2013

RESULT 4
 AAF73372
 ID AAF73372 standard; CDNA; 2018 BP.
 XX
 AC AAF73372;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Grand fir (-)-pinene synthase coding sequence SEQ ID NO: 3.
 XX
 KM Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
 KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
 KM terpinolene synthase; insect resistance; nutrition; ss.
 OS
 XX Abies grandis.
 PN WO200107565-A2.
 XX
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-US020264.
 XX
 PR 26-JUL-1999; 99US-00360545.
 XX
 PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
 PI Steele CL, Bohlmann J, Croreu RB, Phillips MA;
 DR WPI: 2001-182782/18.
 DR P-PSDB; AAB69371.
 XX
 PT New nucleic acid encoding monoterpene synthases, for increasing terpene
 PT synthesis in plants, e.g. for increasing resistance to pests or for
 PT treatment of cancer.
 XX
 PS Claim 38; Page 108-110; 175pp; English.
 CC
 CC The present invention provides the protein and coding sequences of
 CC monoterpene synthases from the grand fir. These include (-)-camphene
 CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
 CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
 CC and pinene synthase. The sequences can be used to produce transgenic
 CC plants expressing high levels of the enzymes, resulting in levels which
 CC are useful in protecting against and treating cancers, and to confer
 CC insect resistance on plants

XX Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;

Query Match 64.9%; Score 1306.8; DB 4; Length 2018;

Best Local Similarity 81.0%; Pred. No. 0;

Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

```
QY 68 CAGGTCGCTGCTGCTCTCTCATGAGATTAAAGGCTCTCCGTAGAAACAATCCCACTCT 127
DB 53 CAATCTGTTGATCAGTTCTACCCCATGAGCTTAAGGCTCTCTCTGAAACAATTCAGCTCT 112
QY 128 TGAATCTGACGCGCGGGAATCCGTGCGCATTTCCATAAACAATGTTTGAACAAGCT 187
DB 113 AGAATAGATGAGGAGGAATCTATCACTCTTCCATCAGATGAGCTCTACCAACGCT 172
QY 188 CGCATCTACTGATCTCTGACAGAGACCGGTGGCACTATCTTCCAACTCTGTGGAGCA 247
DB 173 TGTAAACGATGATGATGATGACAGACGATGGGCGATTTCCATTTCCAACTCTGGAGCA 232
QY 248 TGATTTTATACAGTCTCTGATCTCAACGCTTATGAGACACCTGATTAACGCGGAACGTC 307
DB 233 TGATGCTATACAGTCTCT--TTACCAACGCGCTTATGAGAAAATCTACCTGGAGCGTC 289
QY 308 TGACAGACTTATTTGGGAGATGAAAGATATATGTTCAATTTCAAGTCTGGAAGATGG 367
DB 290 TGAGAACTGATCGGGAGATGAAAG--ACATGTTCAATTCGATGCTATTGAAAGATGG 346
QY 368 AG-----GCAATGATCTCTTCCAACTGATTTGCTGCTGCTGATGAGCTTGA 412
DB 347 AGAGTTAATGATGCTCGCTCAATGATCTCATTCACGCTTTGATGCTGACAGCTTGA 406
QY 413 ACCTTTGGGAATGACAGAGCAATTTCAAAAAGATAAACGCACTCGATTAATGTTAA 472
DB 407 ACCTTTGGGAATGACAGAGCAATTTCAAAAAGATAAACGCACTCGATTAATGTTAA 466
QY 473 CAGTTATTTGGAACGAAAAAGCATTTGATGAGAGGAGTGTGATGACTGCA 532
DB 467 CAGTTATTTGGGAGCAATTTGATGAGAGGAGTGTGATGACTGCA 526
QY 533 CTCAACGCGCTTGGGCGCTTCAACCTCCGACTCAACGATTAACCTGCTTCAAGATG 592
DB 527 CTCAACGCGCTTGGGCGCTTCAACCTCCGACTCAACGATTAACCTGCTTCAAGATG 586
QY 593 TTTGAACGTTTAAAGCAAAAATGGGCAATTTTCTCACTGCACTGCAATATTCAGATGA 652
DB 587 TTTGAACGTTTAAAGCAAAAATGGGCAATTTTCTCACTGCACTGCAATATTCAGATGA 646
QY 653 GGGAGAGTTTGAAGCGCTTCTCAATTTATTCAGGCGCTCTCGCTGCTTCCGCGCA 712
DB 647 TGAAGAGATCAGAGCGCTTCTGAATTTATTCGCGCGCTCTCTCAATGCTTTCAGAGGGA 706
QY 713 GAAAGTTATGATGAAAGCTGAACCTCTCAAAAATTTTAAAGAAAGCCCTGCANAA 772
DB 707 GAAATTTATGATGAAAGCTGAACCTCTCAAAAATTTTAAAGAAAGCCCTGCANAA 766
QY 773 GATTCGCGCATCAGTATCTTCACTAGAGATACGGACGCTTCTGAAATATGTTGGCA 832
DB 767 GATTCGCGCATCAGTATCTTCACTAGAGATACGGACGCTTCTGAAATATGTTGGCA 823
QY 833 CACCAATTTTGGCAGCTTGGAGAGCAAGATTTACATGAGACGCTTGGACACACCTAA 892
DB 824 CACCAATTTTGGCAGCTTGGAGAGCAAGATTTACATGAGACGCTTGGACACACCTAA 883
QY 893 AAATTAAGAGC-----CGCGAGAACTTTTAAAGCTTGCAGAAATTTGAATTGAA 943
DB 884 GAAACGAGATGATGATGAAAGAGCAAAAACCTTTTAAAGCTTGCAGAAATTTGAATTGAA 943
QY 944 TATATTTCACTCTTCAAGAGAGAGATTAACATGTTTCCGATGCTGAAAGACTC 1003
DB 944 CATCTTTCAATCTTTCAAAAAGAGGAGTTGAAAGCTGTGGTCAAGATGCTGAAAGACTC 1003
QY 1004 GGGTTCTCTGAGATGACCTTCTGTGACATGCTGACGTTGAATCTACGCTTTGGCTTC 1063
```

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DB 1004 GGGTTTCTGAGATGACCTTCTGCGCAGATCGTACAGTGAATATCACTTTGGCTTC 1063
QY 1064 CTGATTCGCTTGAGGCTCAACATTTGATTCAGACTCGGCTTTTCAAGATGCTCA 1123
DB 1064 CTGATTCGCTTGAGGCTCAACATTTGATTCAGACTCGGCTTTTCAAGATGCTCA 1123
QY 1124 TCTTATCAGGCTTCTTGAACGATGTAAGAGTCCGTTCGGCAACATGACAGCTGGAAT 1183
DB 1124 TCTTATCAGGCTTCTTGAACGATGTAAGAGTCCGTTCGGCAACATGACAGCTGGAAT 1183
QY 1184 CTTTACAGCCGCAATTTAAGATGAGATCCGTCCGCGATGGAATGCCCTTCCAGAAATAT 1243
DB 1184 CTTTACAGCCGCAATTTAAGATGAGATCCGTCCGCGATGGAATGCCCTTCCAGAAATAT 1243
QY 1244 GAAAGAGTGTACATGATGTTTATCAACCGTAAATGAAATGAGCTGAGTGGCAGAGAA 1303
DB 1244 GAAAGAGTGTACATGATGTTTATCAACCGTAAATGAAATGAGCTGAGTGGCAGAGAA 1303
QY 1304 GGCTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTC 1363
DB 1304 GGCTCAAGGCGGAGATACGCTCAACTATGCTCGGGAAGCTTGGAGGCGTGTGATTC 1363
QY 1364 GTATATGAGAGACCAAGTGGATCGGCACTGTTATCTGCCACGTTTGGAGAGTACT 1423
DB 1364 GTATATGAGAGACCAAGTGGATCGGCACTGTTATCTGCCACGTTTGGAGAGTACT 1423
QY 1424 GGAGACGGGAAAGTTTATGCTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGACGTT 1483
DB 1424 GGAGATGGGAAAGTTTATGCTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGACGTT 1483
QY 1484 GGACATCCCTCTTCTGATCACTCTCAAGAAAGTTGACTTCCATGAAAGCTCAATGA 1543
DB 1484 GGACATCCCTCTTCTGATCACTCTCAAGAAAGTTGACTTCCATGAAAGCTCAATGA 1543
QY 1544 CTTGATATGATCACTCTTCAATTAAGAGTGAATCAACGCGTCAACAGGAGCAAGGCG 1603
DB 1544 CTTGATATGATCACTCTTCAATTAAGAGTGAATCAACGCGTCAACAGGAGCAAGGCG 1603
QY 1604 CCGTGAAGAAAGACTTCTGCTATATATCATGTTATATGAAGACATCTCGATTAACGGA 1663
DB 1604 TCGTGAAGAAAGACTTCTGCTATATATCATGTTATATGAAGACATCTCGATTAACGGA 1663
QY 1664 AGAAGATGCTCTGATCATATCAACTTCATGATCAGGAGCGCAATCAGAGATTAATTG 1723
DB 1664 GGAAGATGCTCTGATCATATCAACGCGCATGATCAGTACGTAATCAAGGATTAATTG 1723
QY 1724 GGAAGATGCTCTGATCATATCAACGCGCATGATCAGTACGTAATCAAGGATTAATTG 1723
DB 1724 GGAAGATGCTCTGATCATATCAACGCGCATGATCAGTACGTAATCAAGGATTAATTG 1723
QY 1784 AAGCAGATTTGCGATCAAGGTTACAGATACCGAGATGCTTACAGCTTTGCCAAGTTGA 1843
DB 1784 AAGCAGATTTGCGATCAAGGTTACAGATACCGAGATGCTTACAGCTTTGCCAAGTTGA 1843
QY 1844 AACCAAGGTTTGGTATGAGAACCGTCAATTTGAACCTGTGCTTTTGAACAACCTTCA 1903
DB 1844 AACCAAGGTTTGGTATGAGAACCGTCAATTTGAACCTGTGCTTTTGAACAACCTTCA 1903
QY 1904 AATCAAAATTTAATCTGAGATGCGCTATGCGGTATATATGAGGCAACAAATAATATAT 1963
DB 1904 AATCAAAATTTAATCTGAGATGCGCTATGCGGTATATATGAGGCAACAAATAATATAT 1963
QY 1964 GGTGTGTAGTAAAGCTGTAAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 2013
DB 1964 GGTGTGTAGTAAAGCTGTAAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 2013
RESULT 5
AAF73421
ID AAF73421 standard; cDNA; 1890 BP.
XX
AC AAF73421;
XX
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QY 413 ACGTTGGGAATCAGACGATTTCAAAAAAGATATAAAAGCGACATCGATTATGTAA 472
DB 470 ACGTTGGGAATAGCTAGACATTTCAAGAGAGATTAACATCACTCTGATTTGTTTT 529
QY 473 CAGTTATTTGAAACAAAAAGCATTTGATGGAGGAGGTGTGTGACTGACCTTCA 532
DB 530 CCGTTATCGGAGAGAAAAAGCATTTGATGGAGAGACAGTATTTGATCTCA 589
QY 533 CTCAACGCGCTGGGGCTTCCAGCTCCGCTACAGGATACCTGTGTTCAGATGT 592
DB 590 CTCAACGCGCTGGGGCTTCCAGCTCCGCTACAGGATACCTGTGTTCAGAGGT 649
QY 593 TTGAAGCTTTTAAAGCAAAAAATGGGCAATTTTCTCCATCCCATATTTAGATGA 652
DB 650 TTTTAAAGCTTTTCAAGATCAAAATGACAGATTTGTATGCTCCGCC---GGTCAAGAGA 706
QY 653 GGGAGAGATTAGAGCGCTTCAATTTATTCAGGGCTCCCTCGCTTCCCGGCA 712
DB 707 GGGAGAGATCAGAGCGCTTCAATTTATATCGGGCTCCCTCATTCGCTTCCCTGTGTA 766
QY 713 GAAAGTTATGAGTGAAGCTGAACATTTCTACAAAATTTTAAGAGAGCGCTGCAAAA 772
DB 767 GAAAGTTATGAGTGAAGAGCTGAACATTTCTCCCAAGATATTTGAAGAGCTTACAAA 826
QY 773 GATCCCGCATCCAGTATCTTCTACTAGATACGGGACGCTTGAATATGGTTGGCA 832
DB 827 GATTCAGATCTCCGCT---CTTTCACAAAGATATAAGTTTGTATGAAATATGGCTGGCA 883
QY 833 CACCAATTTTGGCAGCTTGGAGAGAGATTAATGACGCTTTTGGACACACACTA- 891
DB 884 CACCAATTTTGGCAGATTTGGAGAGAGATTAATGACACACTTGGAGAGACACAG 943
QY 892 -----AAATAGAACCGCGCGGAAACCTTTTGAACCTTGCAAAATTTGAAATCAA 943
DB 944 TGCATGCTCAATAAATGCTGGAGAGAGCTTTTGAACCTTGCAAAATTTGAGTTCAA 1003
QY 944 TATATTTCACTCTTACAGAGAGAGATTAAACATGTTTCCGATGTGAAAGACTC 1003
DB 1004 TATATTTTAACTCTTACAGAGAGAGATTAAACATGTTTGGATGTGAAAGAGTCT 1063
QY 1004 GGGTTCCTCTGAGATGACCTTCTGTCAGATGTCACGTGATCTAGCTTTGGCTTC 1063
DB 1064 GGAATTCCTTAAATTTGACATTTGCTCGGATGTCATGTCGAAATTTCTACCTTTGGCTTC 1123
QY 1064 CTGATGCTGCTTGGAGCTCAACATTTCTGATTCAGACTCGGCTTTTACAGAGTCTCA 1123
DB 1124 TTGTATTTGCAATTAACCAAAACATTTCTGATTCAGACTAGGCTTTCGCAAAATGTCTCA 1183
QY 1124 TCTTATCAGCGTTCCTTGAAGATGTAAGACGTCTTGGCAAGTGAAGAGCTGAACT 1183
DB 1184 TCTTATCAGCGTTCCTTGAAGATGTAAGACGTCTTGGCAAGTGAAGAGCTGAACT 1243
QY 1184 CTTTCAACGCGCAATTAAGAGATGGATCGCTCGCGATGGAATGCTTCCAGAAATATAT 1243
DB 1244 CTTTCAACGCGCAATTAAGAGATGGATCGCTCGCGATGGAATGCTTCCAGAAATATAT 1303
QY 1244 GAAAGAGTGTACATGATGTTTATCAACCGTAAATGAATGGCTGAGTGGCAGAGAA 1303
DB 1304 GAAATGTGTGTACATGCTGTGTTTGAACCTGTAAATGAATGACAGAGAGCGAGAGAA 1363
QY 1304 GAGCTCAAGCGCGAGACAGCTCAACTATGACAGAGCGCTTGGAGGCGGTGTTTGTATTC 1363
DB 1364 GACTCAAGCGAGAGAACTCTCAACTATGTTGAAAGCGCTTGGAGGCGGTGTTTGTATTC 1423
QY 1364 GTATATGAGAGAGCAAAATGATGCGCACTGTGTTATTTGCCACGTTTGAAGATATCT 1423
DB 1424 ATATATGAGAGAGCAAAATGATGCTTAAATGTATGCTGCAATGTTTGAAGAGTACCA 1483
QY 1424 GAGAGAGGAGAAAGTTAGCTGCTGATCGGCAATGCGACATGCAACCATTTGACGTT 1483
DB 1484 TGAGAAATGGAGAAATGAGCTCTGATATCGGCTAGCAACATTTGCAACCATCTTCACTTT 1543
QY 1484 GAGACATCCCTTTCTGTATCAATCTTCAAGAGAGTTGACTTCCCATGAAAGCTCAATGA 1543

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DB 1544 GAATGATGCTTCTCTGATTATCACTTGAAGGGAATGATTTTCCATCCAGTTCAATGA 1603
QY 1544 CTGTATATGATATCACTCTTGTGATTAAGAGTGTATACAGGCTATCAAGGAGACAGGGC 1603
DB 1604 TTTGGCATCTGCTCTTCTGCGCTACAGAGTACACAGCTGTACAAAGCGCGATAGGGA 1663
QY 1604 CCGTGAAGAAAGCTTCTGTATATCATGATGATATGATGAAGACAAATCTCGATTTAAGCGA 1663
DB 1664 TCGTGTGGAAGAGCTTCTGTATATCATGTTATATGAAGACAACTCTGATCAACCGA 1723
QY 1664 AGAAGATGCTGTGAATCATATCAACTTCATGATGACGAGAGCGCAATCAAGAAATTAATTG 1723
DB 1724 AGAAGATGCTGTGAATCATATCAACTTCATGATGACGAGAGCGCAATCAAGAAATTAATTG 1783
QY 1724 GAGACTTCTTAAAGCAGACAAACAGTGTCCCATCACTTCCAGAAACAGCATTTGACAT 1783
DB 1784 GGAACCTTCTTAAAGTCAACAGCAATATTCATGCTGCGCCAAAGAAACGTCTTTGACAT 1843
QY 1784 AAGCAGAGTTTGGCATCAGCGTTACAGATACCGAGATGCTACAGCTTTTGGCAAGTTGA 1843
DB 1844 AACAAAGCTCTCCACCATCTCTACATATATCGAGATGCTTTAGTGTGCAACAAAGGA 1903
QY 1844 AACAAAGAGTTTGGTGTATGAGAAACCGTCAATTTGAACCTTGTGTAAACAACTTCAA 1903
DB 1904 AACAAAGAGTTTGGTGTATGAGAAACCGTCAATTTGAACCTTGTGTAAACAACTTCAA 1963
QY 1904 ATCTACATATTAATCTGAGAGATGCGCTATGAGTGTATATAGGAGACA 1950
DB 1964 TCCTATATTAATTAAGCTCAATATGCTAAATTTATGCTTATGACATA 2010

RESULT 8
AAA38927
ID AAA38927 standard; DNA; 2196 BP.
XX
AC AAA38927;
XX
DT 25-AUG-2000 (first entry)
XX
DB Grand fir myrcene synthase DNA sequence SEQ ID NO:29.
XX
XX Synthese; protein co-ordinate data; active site; modification; terpenoid;
XX 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
XX isoprenoid; breeding programme; fragrance; flavour; pheromone;
XX defensive agent; pigment; antitumor; steroid hormone;
XX signal transduction pathway; bile acid; affinity purification;
XX photoreceptor; enzymatic synthesis; nutrient supplement;
XX immunological reagent; ds.
XX
OS Abies grandis.
XX
XX WO200017327-A2.
XX
PD 30-MAR-2000.
XX
XX 17-SEP-1999; 99WO-US021419.
XX
XX 18-SEP-1998; 98US-0100993P.
XX 22-APR-1999; 99US-010628P.
XX 23-AUG-1999; 99US-0150262P.
XX
PA (KENT ) UNIV KENTUCKY RES DEPT.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Chappell J, Manna KR, Noel JP, Starks CW;
XX
XX WPI; 2000-292839/25.
XX
XX P-PSDB; AAY90842.
XX
XX Novel terpene synthase enzymes, useful for producing terpene
XX hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
XX enzymes by specific amino acid alterations.

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XX Disclousure: Page 387-390; 450pp; English.

XX The present invention describes an isolated terpene synthase (I)
XX comprising a region with at least 20% identity to region 265-535 of a 548
XX amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
XX -carbon atoms (alphaC) that have interatomic distances, between each of
XX other, within tabulated ranges, have a centre point (within a sphere of
XX radius 2.3 Angstrom) within tabulated ranges, and have an ordered
XX arrangement of R groups (defining as side chains), excluding specific
XX tabulated arrangements (tables given in the specification). (I), and
XX related enzymes, are used to produce a wide range of terpenoids (e.g.
XX cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
XX flavours, pheromones, defensive agents, pigments, anticancer agents,
XX components of signal transduction pathways, precursors of steroid
XX hormones and bile acids, as photoreceptors and as co-factor side chains.
XX Some synthases with little or no catalytic activity (and nucleic acids
XX encoding them) are used as controls in the analysis of products formed by
XX enzymatic synthesis; as nutrient supplements; for affinity purification
XX of isoprenoids; or to develop immunological reagents or nucleic acids for
XX monitoring expression of terpene synthase or inheritance of the gene in
XX plant breeding programs. The new synthases may produce novel terpene
XX products. AAY90831 to AAY90838 and AAY90831 to AAY90859 represent
XX sequences used in the exemplification of the present invention

XX Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Query Match 53.2%; Score 1071.6; DB 3; Length 2196;

Best Local Similarity 75.0%; Pred. No. 3.1e-293;

Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTGCTGCTCACTTCTTCTCATGAGTTAAGCTCTCCGTAGAACATCCACTCT 127
DB 116 CAAAGCTGTTGATCAATTCATGAAACATAGGCTCCCTATAGAACATCCAAATCT 175
QY 128 TGGATTCGACGGCGGGGAAATCGTGGCGATTCATTAACATGTTTGAACAGGCT 187
DB 176 TGAATGCGTGAAGCGAGGAAATCTGTCAAGCTTCATGACATCAAGTTGGCCACGC 235
QY 188 CGCATCTACTGATCTGTACAGAGACGCGTGGGCACTATCTCAACCTGTGGAGCA 247
DB 236 TGACCTGATGATGTGTATCAAGAGCATAGTGATCAATTCATTCATTCGTGGAGCA 295
QY 248 TGATTTCTACAGTCTGTGATCTCAACGCTTATGAGACCTGATTTACCGGGAACGTCG 307
DB 296 TGATTTCTACAGTCT 352
QY 308 TGACGATCTATGAGGAGTAAAGATATATGTTCAATTCATGCGTGGAGAGATGG 367
DB 353 TGAGGATTAATGTGAGGATTAAGATTA--TTCAATTCATGTAACCTGGATGATGG 409
QY 368 AGG-----CAATGATCTCTCTCAACGACTTTTGTCTGTGATGAGCTTGA 412
DB 410 AAGATTAATGAGTCTTAAATGATCTCATGCAAGCCTTTGGATGATGATGAGCTTGA 469
QY 413 ACCTTTGGGAATCGACAGGCAATTTCAAAAAGATTAATAAGGCACTGATTAATTTAA 472
DB 470 ACCTTTGGGAATCGACAGGCAATTTCAAAAAGATTAATAAGGCACTGATTAATTTAA 529
QY 473 CAGTTATTTGAGAGGAAAGGATGATGAGGAGGAGGAGTGTGATGAGCTTCA 532
DB 530 CCGTTACTGGAGAGAAAGGCAATTTGATGAGGAGGAGGAGTGTGATGAGCTTCA 589
QY 533 CTCAACGCTTGGGCTTGGAACTCTCGACTACAGGATACACTGTCTTCCAGATGT 592
DB 590 CTCAACGCTTGGGCTTGGAACTCTCGACTACAGGATACACTGTCTTCCAGATGT 649
QY 593 TTTGAACCTTTTAAAGCAAAAAGGCAATTTTCTCCACTGCAATATTCAGATGA 652
DB 650 TTTAAACCTTTTAAAGCAAAAAGGCAATTTTCTCCACTGCAATATTCAGATGA 706
QY 653 GGAAGAGATTTAGAGGCTTCAATTTTATTCAGGCGCTCCCTGCTGCTTCCCGGCA 712

DB 707 GGGTGAATCAGAAAGCGTTCTTAATCTTATATCGGCGCTCCCTCATTCCTCCGTGTA 766
QY 713 GAAAGTATGATTAAGCTGAAACATTTCTTACAAAATATTTAAGAGAACCTTCCAAA 772
DB 767 GAAAGTATGATTAAGCTGAAACATTTCTTACAAAATATTTAAGAGAACCTTCCAAA 826
QY 773 GATTCGGGATTCAGTATACCTTCACTAGATACGGGACGTTCCGAAATATGTTGGCA 832
DB 827 GATTCAGTCTCCGCT---CTTTCACAGAAATTAAGTTGTATGAGAAATGCTGGCA 883
QY 833 CACCAATTTGGCAGCTTGAAGAGCAATTAACATGAGAGCTTTTGAACAGACACTA- 891
DB 884 CACCAATTTGGCAGCTTGAAGAGCAATTAACATGAGAGCTTTTGAAGAGACAGCAG 943
QY 892 -----AAATTAAGAGCGCCCGAGAACTTTAAGACTTGAATTTGAATTCAA 943
DB 944 TGATGCTCAATTAATAATGCTGGAGAAACCTTTAAGACTTGAATTTGAATTCAA 1003
QY 944 TATATTCACCTCTTACAGAGAGAGAGTAAACATGTTTCCGATGGTGAAGAGCTC 1003
DB 1004 TATATTTAATCTCTTACAGAGAGAGAGTAAACATGTTTGAAGATGAGAGAGCTC 1063
QY 1004 GGGTCTCTGAGATGACCTTCTGTGACATGTCAGCTGGAATTAAGCTTTGGCTTC 1063
DB 1064 GGAATTTGCTTAATTTGACATTTGCTGGGATCTGATGATGAGATTTCTACCTTTGGCTC 1123
QY 1064 CTGATTCGCTTGAAGCTTCAACATTTGATTCAGACTCGGCTTTCAAGATGCTCA 1123
DB 1124 TTGTATTCCTTGAAGCTTCAACATTTGATTCAGACTCGGCTTTCAAGATGCTCA 1183
QY 1124 TCTTATACAGCTTCTTGAAGCTTCAACATTTGATTCAGACTCGGCTTTCAAGATGCTCA 1183
DB 1184 TCTTATACAGCTTCTTGAAGCTTCAACATTTGATTCAGACTCGGCTTTCAAGATGCTCA 1243
QY 1184 CTTCACAGCAATTAAGATGAGATGAGTCCGCTCCGATGAGATGCTTCCAGATATAT 1243
DB 1244 CTTCACATCTGCAATTAAGATGAGATGAGTCCGCTCCGATGAGATGCTTCCAGATATAT 1303
QY 1244 GAAAGAGTGTACATGATGTTTATACACCGTAAATGATGCTGAGTGGAGAGAA 1303
DB 1304 GAAATGTGTGTACATGATGTTTATACACCGTAAATGATGCTGAGTGGAGAGAA 1363
QY 1304 GGGTCAAGCGGAGACAGCTCACTATGAGCAAGGCTTGGAGGCGTGTGATTC 1363
DB 1364 GACTTAAGGAGAAACATCTCACTATGTTGAGAAAGCTTGGAGGCGTGTGATTC 1423
QY 1364 GTATATGAGAGAGCAATGAGATGAGTCCGCTCCGATGAGATGCTTCCAGATATAT 1423
DB 1424 ATATATGAGAGAGCAATGAGATGAGTCCGCTCCGATGAGATGCTTCCAGATATAT 1483
QY 1424 GAGAGAGGGAAGTTAGCTTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGAGCTT 1483
DB 1484 TGAGATGAGGAAGAGCTCTGCAATATCGGATGAGCAATTTGCAACCCATTTGAGCTT 1543
QY 1484 GAGATGCGCTTCTGATCAATCTCAAGAGAGTGAATTTCCATGAGAGCTCAATGA 1543
DB 1544 GAAAGCATGCGCTTCTGATCAATCTCAAGAGAGTGAATTTCCATGAGAGCTCAATGA 1603
QY 1544 CTGTATATGATCAATCTTCTGATTAAGAGTGAATCAAGGCTTCAAGAGAGGCG 1603
DB 1604 TTTGGCATGCGCTTCTTCTGCTGATGAGAGTGAATCAAGGCTTCAAGAGAGGCG 1663
QY 1604 CCGTGGAGAGAGCTTCTGCTGATTAATGAGTGAATCAAGGCTTCAAGAGAGGCG 1663
DB 1664 TCGTGGAGAGAGCTTCTGCTGATTAATGAGTGAATCAAGGCTTCAAGAGAGGCG 1723
QY 1664 AGAAGATGCTGATCAATCTTCAATGATGAGAGAGGAGGAGGAGGAGATTAATTTG 1723
DB 1724 AGAAGATGCTGATCAATCTTCAATGATGAGAGAGGAGGAGGAGGAGATTAATTTG 1783
QY 1724 GGAAGCTTCAAGGAGAGCAAGTGTTCATGATCACTTCAAGAGAGGAGATTTGACAT 1783
DB 1784 GGAAGCTTCAAGGAGAGCAAGTGTTCATGATGATGATGATGATGATGATGATGAT 1843

QY 1784 AAGCAGATTGGCATCGGTTACAGATCCGAGATGGCTTGGCAAAGTTGA 1843
DB 1844 AACAGAGCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGGCAACAGGA 1903
QY 1844 AACAAAGATTGGTGTATGAGAACCGTCATTGAACCTGTGCTTTGTAACAACACTTCA 1903
DB 1904 AACAAAAAATTTGGTATGAGAAACCTCTGAAATCTATGCTTTTAACTATAACATA 1963
QY 1904 ATCTACATATTTATCTAGATGCGCTTATGGTGTATATAGGACCA 1950
DB 1964 TCCATTAATTAAGCTCATTAATGCTAAATTAATTTGGCTTATGACATA 2010

RESULT 9
AAF73371
ID AAF73371 standard; cDNA; 2196 BP.
XX AAF73371;
AC
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir myrcene synthase coding sequence SEQ ID NO: 1.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
XX MO200107565-A2.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000MO-US020264.
XX
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIM) UNIV WASHINGTON STATE RES FOUND.
XX
XX Steele CL, Bohlmann J, Croteau RB, Phillips MA;
PI WPI; 2001-182782/18.
DR P-PSDB; AAB69370.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
FT treatment of cancer.
XX
XX
XX Claim 28; Page 103-106; 175bp; English.
XX
XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
XX Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Query Match 53.2%; Score 1071.6; DB 4; Length 2196;
Best Local Similarity 75.0%; Pred. No. 3.1e-293;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGGTGCTGCTCAGTCTCTTCATGATTAAGGCTCTCGTAGAACAAATCCAACTCT 127
DB 116 CAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 175
QY 128 TGGAAATCGCAGCGCGGGAATTCGTGGCGATTCCTTAAACATGTTTGAACAAGGT 187
DB 176 TGGAAATCGTGGCGGGAATTCGTGGCGATTCCTTAAACATGATGATGATGATGATGAT 235

QY 188 CGCATCTACTGATTTCTGTACAGAGACCGGTGGCAACTATCATTTCCAACTGTGGACGA 247
DB 236 TGCACGTGATGATGTGTATCAAAACGCGATGATGATGATGATGATGATGATGATGATGAT 295
QY 248 TGATTTCAATACGCTCTGATCTCAACGCTTATGAGACACTGTATTAACGGGAACGTGC 307
DB 296 TGATTTCAATACGCTCTGATCTCTCAACGCTTATGAGACACTGTATTAACGGGAACGTGC 352
QY 308 TGAAGACCTATTTGGGGAAGTAAGATATATATGTTCAATTTCAAGTCCGTAAGATGG 367
DB 353 TGAAGACCTATTTGGGGAAGTAAGATATATATGTTCAATTTCAAGTCCGTAAGATGG 409
QY 368 AGG-----CAATGATCTCTTCAACGACTTTTGGCTGTGATGATGATGATGATGATGAT 412
DB 410 AAGATTAATAGATTCCTTTAATGATCTCATGCAACGCTTTGGATGATGATGATGATGATGAT 469
QY 413 ACGTTTGGGAATGACACGCGATTTCAAAAAGATTAACGCGACTCGATTAATGTTTAA 472
DB 470 ACGTTTGGGATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
QY 473 CAGTTATTTGAACGAAAAAGCATTTGATGAGGAGGAGGATGATGATGATGATGATGATGATGAT 532
DB 530 CCGTTACTGGGAGGAAAAAGCATTTGATGAGGAGGAGGATGATGATGATGATGATGATGATGAT 589
QY 533 CTCAACGCGCTTGGGCTTCGAACTCTCCGACTACAGGATACACTGTGTCTTCAAGATGT 592
DB 590 CTCAACGCGCTTGGGCTTCGAACTCTCCGACTACAGGATACACTGTGTCTTCAAGATGT 649
QY 593 TTTGAACGTTTAAAGCAAAAATGGCAATTTTCTCCACTGCGCAATATTCAGATGA 652
DB 650 TTTAAAGCTTTTCAAGATCAAAAATGACAGTTTGTATGCTCCGCC--GGTCAAGACGA 706
QY 653 GGGAGATTAAGAGCGGCTTCATTTATTCAGGGGCGCTCCGCTGCTTCCCGGCGA 712
DB 707 GGGTGAATCAAGAGCGTCTTCACTTATGCGGCTTCCCTCATGCTTCCCTCGGGA 766
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTTCAAAAATTTTAAAGAAAGCCTGCAGAAA 772
DB 767 GAAAGTTATGATGAAGAGTGAATCTTCCCAAGAAATTTGAAAGAAAGCCTGCAGAAA 826
QY 773 GATTCGGCATCCGATATCTTCACTAGATACGGAAGCTTCTGGAATATGTTGGCA 832
DB 827 GATTCGAGCTCTCCCT--CTTCAAGAAATTAAGTTTGTATGAAATTTGCTGGCA 883
QY 833 CACCAATTTGCGAGCTTGAAGCAAGAAATTAATGAGACGCTTTGGACAGCACATA- 891
DB 884 CACCAATTTGCGAGCTTGAAGCAAGAAATTAATGAGACACACTTGAAGAAAGACACAG 943
QY 892 -----AAATTAAGAAAGCGCGCGGAAAACTTTTGAACCTTGAACATTTGAATGCA 943
DB 944 TGCAATGCTCAATTAATAATGCTGGGAAGAAAGCTTTTGAACCTTGAACATTTGAATGCA 1003
QY 944 TATATTTACCTCTTCAACAGAGAGATTAACATATTTTCCGATGATGATGATGATGATGATGAT 1003
DB 1004 TATATTTAATCTCTTCAACAGAGAGATTAACATATTTTCCGATGATGATGATGATGATGATGAT 1063
QY 1004 GGGTTTCTCTGAGATGACCTCTGTCGACATGTCAGTGAATTAATGATGATGATGATGATGATGAT 1063
DB 1064 GGAATTTGCTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
QY 1064 CTGATGCTGCTGAGCTCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
DB 1124 TTTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
QY 1124 TCTTATACGCTTCTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
DB 1184 TCTTATACGCTTCTTGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
QY 1184 CTTCACAGCGCAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
DB 1244 CTTCACATCTGCAATTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303

QY 1244 GAAGAGCTGACATGCTTATCAACCGTAATGAATGCTGAGTGGAGAGAA 1303
 DB 1304 GAAATGCTGACATGCTGCTTGAATGAATGAATGACAGAGAGCGAGAA 1363
 QY 1304 GGCTCAAGCGCGAGACAGCTCACTATGCAAGACAGGCTTGGAGCGTGTATTC 1363
 DB 1364 GACTCAAGGAGAAACCTCTCACTATGCTGAAAGGCTTGGAGCGTGTATTC 1423
 QY 1364 GTATATGAGAGCAAGAGTATGCACTGCTTATGCTTCCAGCTTGGAGTACTT 1423
 DB 1424 ATATATGAGAGCAAGAGTATGCTTATGCTTATGCTTCCAGTGTATGAGTACCA 1483
 QY 1424 GGAGAGCGGAGAAAGTATGCTTCACTGCAAGCGCACTGCAAGCGCTTCAAGCTT 1483
 DB 1484 TGAGAGTGGAGAAAGTATGCTTCACTGCAAGCGCACTGCAAGCGCTTCAAGCTT 1543
 QY 1484 GGAGATCCCTTCTGATCATCTTCAAGAGAGTATGCTTCCAGTCAAGCTCAATGA 1543
 DB 1544 GAATGCAATGCTTCTGATCATCTTCAAGAGAGTATGCTTCCAGTCAAGCTCAATGA 1603
 QY 1544 CTGATATGATCATCTTCTGATCAAGAGTATGCAAGCGCTTCAAGAGAGAGGCG 1603
 DB 1604 TTGTCATGCTTCTTCTGCTTCAAGAGTATGCAAGCGCTTCAAGAGAGAGGCG 1663
 QY 1604 CCGTGGAGAGAGCTTCTGATCATCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAG 1663
 DB 1664 TCGTGGAGAGAGCTTCTGATCATCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAG 1723
 QY 1664 AGAGATGCTTCTGATCATCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATG 1723
 DB 1724 AGAGATGCTTCTGATCATCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATG 1783
 QY 1724 GGAGCTTCTGATCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1783
 DB 1784 GGAATCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1843
 QY 1784 AAGAGATGCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1843
 DB 1844 AAGAGATGCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1903
 QY 1844 AAGAGATGCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1903
 DB 1904 AAGAGATGCTTCAAGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1963
 QY 1904 ATCTCAATATTAATGAGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 1950
 DB 1964 TCCATATATATGAGTATGCAAGCGCTTCAAGAGAGTATGCAAGAGTATG 2010
 RESULT 10
 AAX08663
 ID AAX08663 standard; cDNA; 2205 BP.
 XX
 AC AAX08663;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Grand fir monoterpene synthase clone AG3.48.
 XX
 KW Myrcene synthase; limonene synthase; pinene synthase; flavour;
 KW monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
 KW probe; 88.
 XX
 OS Abies grandis.
 XX
 FT Key Location/Qualifiers
 FT CDS 57..1940
 FT FT /*tag= a
 FT FT /product= "Monoterpene synthase"
 PN MO9902030-A1.
 PD 21-JAN-1999.

XX 10-JUL-1998; 98MO-US14528.
 XX 11-JUL-1997; 97US-0052249P.
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX Bohlmann J, Steele CL, Croteau RB;
 XX WP1; 1999-120396/10.
 DR P-PSDB; AAW85710.
 XX
 PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
 PT fir (Abies grandis), used to provide plants with modified production of
 PT monoterpenes, e.g. myrcene, limonene or pinene.
 XX
 PS Example 3; Page 104-107; 121pp; English.
 CC Nucleotide sequences encoding myrcene synthase, limonene synthase and
 CC pinene synthase from Grand fir may be incorporated into any organism
 CC (e.g. intact plant, animal, microbe), or derived cell culture that
 CC produces geranyl diphosphate for the production of the aforementioned
 CC enzymes or their products. The sequences when expressed in transfected
 CC cells may also be used for the production or modification of flavour and
 CC aroma properties, improvement of defense capability, and the alteration
 CC of other ecological interactions mediated by myrcene, limonene, pinene,
 CC or their derivatives. In particular they can be used for the production
 CC of plant seeds for the extraction of oil or meal
 XX
 SQ Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;
 Query Match 53.2%; Score 1071.6; DB 2; Length 2205;
 Best Local Similarity 75.0%; Pred. No. 3.1e-293;
 Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;
 QY 68 CAGGTCGCTGCTGATCATGATTAAGGCTTCCGTAAGCAATCCCACTCT 127
 DB 104 CAGTCTGATTAAGTCAATTCATGAAATTAAGCTTCCATATGAATCCCAATCT 163
 QY 128 TGAATCTGAGGCGCGGAAATCCGTCGATTCATTAACATGCTTGAACAGCT 187
 DB 164 TGAATGCGTGAAGGAGAAATCGTCAAGCTTCCATGACATGATTTGGCCACCGC 223
 QY 188 CGCATCTACTGATCTGATCAAGAGCGGTGGCAATCATATTCACACCTGTGGAGCA 247
 DB 224 TGCACCTGATATGCTGATCAAGAGCGATAGGATCAATTCATTAATCTGGAGCA 283
 QY 248 TGATTTCAATGAGCTCTGATCTCAAGCGCTTATGAGACCTGATTAACCGGAACTGC 307
 DB 284 TGATTTCAATGAGCTCTGATCTCAAGCGCTTATGAGACCTGATTAACCGGAACTGC 340
 QY 308 TGACAGCTTATGAGGAGAGTAAAGATATATGTTCAATTTCAAGTCTGAGAGATG 367
 DB 341 TGACAGCTTATGAGGAGAGTAAAGATATATGTTCAATTTCAAGTCTGAGAGATG 397
 QY 368 AGG-----CAATGATCTCTTCAAGAGCTTTGCTGCTGATGAGAGTGA 412
 DB 398 AAGATTAATGAGTCTTATTAATGATCTATCAAGCGCTTGGATGAGTGAAGGTTGA 457
 QY 413 ACGTTTGGGATCAAGAGGATTTCAAAAAAGATTAAGAGCGGACTGATTAATGTTAA 472
 DB 458 ACGTTTGGGATCAAGAGGATTTCAAAAAAGATTAAGAGCGGACTGATTAATGTTAA 517
 QY 473 CAGTTATTTGAAAGAAAAAGCATTTGATGAGAGGAGAGTGTGATGATGACTCA 532
 DB 518 CCGTTACTGGAGAGAAAAAGCATTTGATGAGAGGAGAGTGTGATGATGACTCA 577
 QY 533 CTCAACGCGCTTGGGAGCTTGAACCTCCGACTACAGGATACATGCTTCAAGATGT 592
 DB 578 CTCAACGCGCTTGGGAGCTTGAACCTCCGACTACAGGATACATGCTTCAAGATGT 637
 QY 593 TTGAGCGTTTAAAGCAAAAAAGGCAATTTTCTCTCACTGCAATATTCAGATGA 652

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Db      TTTAAAAGCTTTCAAGTCAAAAATGACAGATTGTATGCTCCCC--GGTCAGACAGA 694
Qy      GGGAGAGATTAGAGCGCTCTCAATTATTGAGGGCCCTCGCGCTTCCCGAGCA 712
Db      GGGGAGATGAGAAAGCGTTCTTAATTATGCGGCTTCCCTCATGCTCCCTGGGA 754
Qy      GAAAGTATGATGAGAGCTGAAACATTTCTTACAAAATATTTAAGAGAGCCCTGCAAA 772
Db      GAAAGTATGAGAAAGAGTGAATCTTCTCAAGAGATTTGAAGAGAGCTTACAAA 814
Qy      GATTCGGGATCCAGTATCTTCACTAGAGATACGGGACGTTCCGAAATGTTGGGCA 832
Db      GATTCAGATCCCTCTCTTCAAGAGATTAAGTTGTTATGAGATATGCTGGCA 871
Qy      CACCAATTTGCGAGCTTGAAGAGAGATTAACATGAGCGTTTGGAGCGACACTA- 891
Db      CACCAATTTGCGAGATTTGAGAGAGAGATTAACATGAGCGTTTGGAGAGACACG 931
Qy      -----AAAATAGAACGCCGCCGAGAAACTTTTGAACCTTGCAAAATTTGAATTCAA 943
Db      TGCATGGCTCAATAAATATGCTGGGAGAGAGCTTTTGAACCTTGCAAAATTTGAGTTCAA 991
Qy      TATATTTCACTCTTTCAGAGAGAGAGTTAAAACATGTTTCCGATGCTGAAAAGACTC 1003
Db      TATATTTCACTCTTTCAGAGAGAGAGTTAAAACATGTTTGAAGATGCTGAAAAGACTC 1051
Qy      GGGTTCCTGAGAGACCTTCTGTCGACATGTCAGCTGGAATTAAGCTTTGGGCTTC 1063
Db      GGAATTTGCTTAATTAATGACATTTGCTCGGATGTCAGTGAATTTCAACCTTTGGCTTC 1111
Qy      CTGCATTCGCTTCGAGCTCAACATTTCTGATTCAGACTCGGCTTTTACCAAGATGCTCA 1123
Db      TTGATTTGCCATTTGACCCAAAACATTTCTGATTCAGACTTACGCTTCGCAAAATGTCGA 1171
Qy      TCTTATACAGGTTCTTGAAGCATGTCAGACTCTTCCGCAAGTGAAGAGCTGGAACCT 1183
Db      TCTTGTCAACAGTTTTCGAGATTTTTCGACACTTTTGGAAAGATTCGAGCTTGAACCT 1231
Qy      CTTCAAGCGGCAATTAAGAGATGGAGATCGGTCGCGAGATGGAATGCTTCAGAAATATAT 1243
Db      CTTCAACATCTGCAATTAAGAGATGGAGATTTTCAGAGATTAAGAACCTTCCAGATATAT 1291
Qy      GAAAAGAGTGTACATGATGTTTATACACCGTAAATGAAATGGCTGAGTGGCAGAGAA 1303
Db      GAAATGTGTATACATGTCGTGTTTGAATCTGAAATGAACTGACAGAGAGGCGAGAA 1351
Qy      GGGCTAAGGCGCGAAGACAGCTCAACTATGACAAAGACAGGCTTGGAGGCGTGTGATTC 1363
Db      GACTCAAGGAGAAACACTCTCAACTATGTTGCAAAAGGCTTGGAGGCGTGTATTTGATTC 1411
Qy      GTATATGAGAGAGAAAGATGATCGGACTGTTATCTGCCCAAGTTTGAAGAGTACTT 1423
Db      ATATATGAGAGAGAGAAATGATCTCTATGCTTATGCTTATGCTTGAAGAGTACCA 1471
Qy      GGAGAACGGGAAAGTTAGCTTCTGCTCATGCGCCATGCGCACTGCAACCCATTTGACGTT 1483
Db      TGAGAAATGGAGAAAGTGAAGCTCTGCACTATCGGTAGCAACATTTGCCATCTCACTTT 1531
Qy      GGAATCCCTCTTCTGATCACTCTTCAAGAAAGTGAAGTTCCTCATGGAAGCTCAATGA 1543
Db      GAAATGCAATGCGCTTCTGATCACTCTTGAAGGAAATGATTTTCCATCAGGTTCAATGA 1591
Qy      CTTGATATGATATCACTTCTGATTAAGAGTGTATACAGGTCGTCAGAGCAGACAGGCG 1603
Db      TTTGGCATCGTCTCTTCTTCCGCTACGAGGTGACACAGCTGCTACAGAGCGGATGGGA 1651
Qy      CCGTGAAGAGAGAGCTTCTGATATATCACTGTTATATGAAAGCAATCTGATTAACGGA 1663
Db      TCGTGAAGAGAGAGCTTCTGATATATCACTGTTATATGAAAGCAATCTGATTAACGGA 1711
Qy      AGAAGATGCTGTGAATCATATCAACTTATGATCAGGAGCGCAATCAGAGATTAATTTG 1723
Db      AGAAGATGCTGTGAATCATATCAATGCGATGTCATATGCAATTAATCAAAAGATTAATTTG 1771

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Qy      1724 GAGACTTCTAAAGCCAGACAAAGTGTCCCATCATCTTCCAAAGAAACGCAATTGACAT 1783
Db      1772 GGAATCTTAAAGATCCAAAGCAATATTTCCATATCTGCGCAAGAAACATGCTTTGACAT 1831
Qy      1784 AAGCAGATTGGGATCACGGTTACAGATACCGAGATGCTACAGCTTTGCCAAGCTTGA 1843
Db      1832 AACAGAGCTCTCCACATCTCTACATATATCGAGATGCGTTTATGTCGCAACAGGA 1891
Qy      1844 AACAGAGCTTGGATGAGAGAACCGTCAATTAACCTGTCCTTGTATACAAACCTTCAA 1903
Db      1892 AACAAAAAATGGATATGAGAAACATCTCTGAATCTATGCTTTTATTAATTAACATA 1951
Qy      1904 ATCTACATATTTAACTGAGATGCGCTTATGAGTGTATATAGGAGCA 1950
Db      1952 TCATATATTAAGCTCATATATGCTAAATTAATTTGCGCTTATGACATA 1998

RESULT 11
AAF73391
ID AAF73391 standard; cDNA; 2205 BP.
XX
AC AAF73391;
XX
DT 30-Apr-2001 (first entry)
XX
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 31.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN W0200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000MO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX
DR WPI: 2001-182782/18.
XX
DR P-PSDB; AAB69380.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Example 3; Page 135-137; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;

Query Match 53.2%; Score 1071.6; DB 4; Length 2205;
Best Local Similarity 75.0%; Pred. No. 3.1e-23;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

Qy      68 CAGGTGCTGCTCAGTCTTCTCATGAGATTAAGGCTCTCGTGAACATCCCAACT 127
Db      104 CAGGTGCTGATCAGTTCAATTCAATGAACATAGGCTCTCCATTAAGAACATCCCAACT 163

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QY 128 TGAATCTGACGCGCGGGAATCCGTGCGCATTCCTAAACATGTGTGACAGAGT 187
 Db 164 TGAATGCTGTGCGGGAATCTGTCAAGCTTCATGAGCATCACTGTGGCCACGCG 223
 QY 188 CGCATCTACTGATTTCTGTACAGAGCGCGTGGGCACTATCATTCCTCAACTGTGGGAGA 247
 Db 224 TGCACCTGATGATGTGTACAAAGAGCATAGTGATCACTTCCATATCTGGAGACGA 283
 QY 248 TGATTTACATCAGTCTGTGATCTCAACCGCTTATGAGACACTGATTTACCGGGAACGTC 307
 Db 284 TGATTTACATCAGTCTCTCTCAAGCATTTATGGGGAACCGCTTACAGGAACGTCG 340
 QY 308 TGACAGACTTATTTGGGGAAGTAAAGATATATGTTCAATTCAGTCCCTGGAAGATG 367
 Db 341 TGAAGATATTAATTTGGAGTAAAGATATA--TTCAATTCAGTCTGGAAGATG 397
 QY 368 AGG-----CAATGATCTGCTCAACGACTTTTGTGTGTGATGAGTGA 412
 Db 398 AAGATTAATGATCTCTTAATGATCTCATGACGCTTTGGATGTGATAGCTTGA 457
 QY 413 ACGTTGGGAATCGACAGCATTTCAAAAAAGATTAATAACGCGCATCGATTTATTTAA 472
 Db 458 ACGTTGGGAGTAGGTGACATTTCAAGACGATTAACATGAGCTGTGATTTATGTTT 517
 QY 473 CAGTTATTTGAAAGCAAAAGCATTTGATTTGGGAGGAGAGTGTGATGACTGACCTCA 532
 Db 518 CCGTTACTGGGAGGAAAACGCGATTTGATTTGGGAGACAGATATTTTACTGATCTCA 577
 QY 533 CTCAACGCGCTTGGGCGCTTCAACCTGCGACCTACAGGATTAACCTGTCTGATGAT 592
 Db 578 CTCAACGCGCTTGGGCGCTTCAACCTGCGACCTACAGGATTAACCTGTCTGATGAT 637
 QY 593 TTTGAACGTTTTTAAAGCAAAATGGGCAATTTCTCACTGCGCAATTTCAATGATA 652
 Db 638 TTTAAAGCTTTTCAAGATCAAAATGACAGATTTGATGCTCCCC--GGTACAGACGA 694
 QY 653 GGGAGAGTTAGAGCGCTTCTCAATTTATTCAGGGCGCTCCCTGCGCTTTCCCGGGA 712
 Db 695 GGGAGAGTTAGAGCGCTTCTCAATTTATTCAGGGCGCTCCCTGCGCTTTCCCGGGA 754
 QY 713 GAAAGTATGATGAGTGAAGCTGAACATTTCTTACAAATATTTTAAAGAGAGCGCTGCAAA 772
 Db 755 GAAAGTATGATGAGTGAAGCTGAACATTTCTTCAAGATATTTTAAAGAGAGCTTACAAA 814
 QY 773 GATTCGCGCATCCAGTATATCTTCACTAGAGATACGGGAGCTTCTGAATATGTTGCA 832
 Db 815 GATTCAGTCTCCGCT--CTTCAAGAGATTAAGTTGTATGGAATATGGCTGCA 871
 QY 833 CACCAATTTGCGCAGCTTGAAGCAAGATTTACATGACGCTTTTGAACAGACACTA- 891
 Db 872 CACCAATTTGCGCAGCTTGAAGCAAGATTTACATGACGCTTTTGAAGAGACAG 931
 QY 892 -----AAATATAGAACGCGCGGAGAACTTTTAAAGCTTGAAGATTTGAA 943
 Db 932 TGCATGCTCAATTAATAATGCTGGAGAGAGCTTTTAAAGCTTGAAGATTTGAGTTCA 991
 QY 944 TATATTTCACTCTTCAAGAGAGAGATTAACATGTTTCCGAGTGTGAAAGACTC 1003
 Db 992 TATATTTCACTCTTCAAGAGAGAGATTAACATGTTTCCGAGTGTGAAAGACTC 1051
 QY 1004 GGGTTCTCTGAGATGACCTTCTGTGACATGCTGACAGTGAATCTACGCTTTGGCTTC 1063
 Db 1052 GGGTTCTCTGAGATGACCTTCTGTGACATGCTGACAGTGAATCTACGCTTTGGCTTC 1111
 QY 1064 CTGATGCTGCTGAGCTCAACATTTGATTTGAGATCTGCGCTTACCAAGATGCTCA 1123
 Db 1112 TTGATTTGCTGAGCTCAACATTTGATTTGAGATCTGCGCTTACCAAGATGCTCA 1171
 QY 1124 TCTTATCAGGTTCTTGAAGACATGACAGCTCTTCCGACACAGTGAAGAGCTGAACT 1183
 Db 1172 TCTTATCAGGTTCTTGAAGACATGACAGCTCTTCCGACACAGTGAAGAGCTGAACT 1231

QY 1184 CTTCAAGCGCACTTAAAGAGATGGAGTCCGTCCGCGATGGAATGCTTCCAGATATAT 1243
 Db 1232 CTTCAAGCTGCACTTAAAGATGGAATTTCAAGAGATGAACACTTCCAGATATAT 1291
 QY 1244 GAAAGAGTGTACATGATGTTTATCAACCGTAAATGAAATGGCTCGAGTGGCAGAGA 1303
 Db 1282 GAAATGTGTACATGATGCTGCTTGAAGCTGTAATGAACCTGACAGAGAGGGGAGAA 1351
 QY 1304 GGGTCAAGCGGAAACAGCTCAACTATGACAGAGAGCTTTGGAGCGCTGTTGATTC 1363
 Db 1352 GACTCAAGGGAGAAACCTCTCAACTATGTGAAAGGCTTGGAGCGCTTATTTGATTC 1411
 QY 1364 GTATATGAGGAACCAAGTGGATGCGCACTGTTATGCGCCAGCTTGGAGTACTT 1423
 Db 1412 ATATATGAGGAACCAAAATGGAATCTCAATGTATATGCAACGTTGAAGATACA 1471
 QY 1424 GAGAAACGGGAAATGATGCTGCTCACTGCGCAATGCGCACTGCAACCAATTCGACGTT 1483
 Db 1472 TGAAGATGGGAAATGAGCTCTGCAATTCGCGTGAACAATTTGAACCACTCTCACTT 1531
 QY 1484 GGAATCCCTTCTGATCACTCTCAAGAAAGTTGATTTCCCATGAAAGCTCAATGA 1543
 Db 1532 GAATGATGCTCTCTGATCACTCTGAAAGGAAATGATTTCCATCAGATTCATAGA 1591
 QY 1544 CTTGATATGATGATGATCTTGAATTAAGAGTATACAGCGCTTACAAAGGAGACAGGCG 1603
 Db 1592 TTTGGCATGCTGCTCTTCCGCTACAGAGTGAACAGCTGCTACAAAGCGGATGGGA 1651
 QY 1604 CCGTGAAGAAACCTTCTGATATCACTGTTATATGAAGAAACAATCTGATTAACGGA 1663
 Db 1652 TCGTGTGAAGAAAGCTTCTGATATCACTGTTATATGAAGAAACAATCTGATTAACGGA 1711
 QY 1664 AAGAGTCTCTGATATCACTGATATCACTGATATCAAGGAGCAATCAGAGATTAATTG 1723
 Db 1712 AAGAGTCTCTGATATCACTGATATCACTGATATCAAGGAGCAATCAGAGATTAATTG 1771
 QY 1724 GGAGCTTCAAGGAGCAAGGATTTCCATCACTTCAAGAAACGCGATTTGACAT 1783
 Db 1772 GGAGCTTCAAGGAGCAAGGATTTCCATCACTTCAAGAAACGCGATTTGACAT 1831
 QY 1784 AAGCAGATTTGATCACTGATATCACTGATATCACTGATATCAAGGAGCAATCAGAGATTTGACAT 1843
 Db 1832 AAGCAGATTTGATCACTGATATCACTGATATCACTGATATCAAGGAGCAATCAGAGATTTGACAT 1891
 QY 1844 AAGCAGATTTGATGATGAGAACCGTCACTGATGAACTGTGCTTTGTAACAACTTCA 1903
 Db 1892 AAGCAGATTTGATGATGAGAACCGTCACTGATGAACTGTGCTTTGTAACAACTTCA 1951
 QY 1904 ATCTAATATTTAATGAGATGCGCTATGGGTGATATAGGAGCA 1950
 Db 1952 TCATATATATAGCTCATTAATGCTTAATATTTGCGCTTATGACATA 1998

RESULT 12
 AAF73413
 ID AAF73413 standard; cDNA; 2429 BP.
 XX AAF73413;
 AC AAF73413;
 DT 30-APR-2001 (first entry)
 DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 68.
 KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
 KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
 RN terpinolene synthase; insect resistance; nutrition; ss.
 OS Abies grandis.
 XX Abies grandis.
 XX WO200107565-A2.
 XX PD 01-FEB-2001.
 XX

PF 24-JUL-2000; 2000WO-US020264.
XX
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
XX Steele CL, Bohlmann J, Croten RB, Phillips MA;
DR WPI: 2001-182782/18.
DR P-PSDB; AAB69392.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
XX
XX Claim 23; Page 156-159; 175pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2429 BP; 726 A; 484 C; 512 G; 707 T; 0 U; 0 Other;
Query Match 46.2%; Score 929.4; DB 4; Length 2429;
Best Local Similarity 71.1%; Pred. No. 7.7e-253;
Matches 1335; Conservative 0; Mismatches 491; Indels 51; Gaps 6;
QY 72 TCGTGGCCGATGTTCTCTCATGAGATTAAAGCTCCGCTAGAACATCCCAACTCTTGA 131
DB 89 TCGTTGATCACTTCACGCAATGTGACAGAAAGCTCTGTATCTTACACGACGTCCCACT 148
QY 132 ATCTGACGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTTGACAAGCGTCGCA 191
DB 149 CTCGAATATGGCTAGCGGCAAGAAAGCTCTGTCATCAACATGAATGACACATGTATCC 208
QY 192 TCTACTGATTT-----GTACAGACGCGGTGGGCACTATCATTTCCAA 236
DB 209 CATGTGATGATTAATGTGTGTGTGTACTGCAAAAGCGCATAGCCGATCATATCCCAAC 268
QY 237 CTGTGGGACGATGATTTTCATACAGTCTCTGATTCACAGCCCTTAATGAGACCTGATAT 296
DB 269 CTGTGGGAAAGTATTTTCATATCAATCATTTGCTCA---CTTATGAGGAGATCTTCGAC 325
QY 297 CGGGAACGTGCTGACAGACTTATTTGGGAGTAAAGATAT-----AATGTTCAAT 347
DB 326 AGTGAACGTGCTGTGACAGTGTGAGGAATGAAGATGTTCAATTCATACCAAT 385
QY 348 TTCAAGTCGTGGAAGATGAGGCAATGATCTCTTCAAGCACTTTTGTCTGTGATGAC 407
DB 386 AATGAGAAATTAATTTGTTCCAAATGATCTCTTACACGCTTTGATGTGATGAC 445
QY 408 GTTGAACGTTTGGGAATGACAGGCAATTTCAAAAAAGATTAATAACGGCACTGATAT 467
DB 446 ATTGAAGCTGTGGGATGATGACATTTTCCAAATGAGATGAAGTACCCCTGATAT 505
QY 468 GTTAAAGATTATTTGAACGAAA---AAGCATTTGATGTGGAGGAGAGTGTGTGACT 524
DB 506 GTTAAAGATTATTTGAAGAAAAGGAAGCATTTGGGTGTGACAGATTCTACTTTTCT 565
QY 525 GACCTCAACTAACCCCTTGGGCTTGAACCTCTCGCATACACGATTAACGTGTCT 584
DB 566 GATCTCAACTGACTGCTGTGGCTTCGAACCTTTGACATGCAAGATTAAGTGTCT 625
QY 585 TCAGATGTTTGAAGCTTTTAAGAATAAATGGCAATTTTCTCACTGCAATAT 644
DB 626 TCAGATGTCTGGAATACTTAAAGATCAAAAGGGGCAATTTTGTCTGCTGTGCAATCTTA 685
QY 645 CAGATAGAGGAGAGATTAGAGCGTCTTCAATTATTCAGGGGCTCCCTGTGCTCTTT 704

DB 686 ACCGAGGACAGATCACTAGAAAGTTCCTAAATTTATATGCGGCTCCGTGTGCTTT 745
QY 705 CCGCGGAGAAAGATTATGATGTAAGCTGAACAATTCCTCAAAATTTTAAGGAAGCC 764
DB 746 CCGGGGAGAAAGTTATGAAAGGCTGAAGATCTTCGGCATCTTATTTGAAGAAAGTC 805
QY 765 CTGCAAAAGATTCGGGATCCAGTATATCTTCACTAGAGATACGGGAGCTTCTGAATAT 824
DB 806 TTACAAAAGATTCAGTCTCAGT---TTTTCAGAGAGATAGAAATCGTTTGTGAATAT 862
QY 825 GGTGGACACCAATTTTCCACGCTTGAAGCAAGAAATTAATGACGTCTTTGACAG 884
DB 863 GGTTGGCACCAATTTTCCAGATTTGAAGCAAGAAATTAATGACGTCTACGGGACAG 922
QY 885 CACACTAAAAATAGAACGCG-----CCGGAACCTTTTGAACCTT 926
DB 923 GACGCTATGAAATTCAAACGAGATCCATATGTGAATACGCAAGCTTTAAACCTT 982
QY 927 GCAAAATTTGAATTCATATATTTCACTCTCTTACAAAGAGAGATTAAACATGTTTCC 986
DB 983 GCAAAATTTGAGTTTATATCTTTCATCTTTTGAACAGAAAGTTGCAATATATCTCT 1042
QY 987 CGATGTGAAAGACTCGGCTTCTCTGAGATGACCTTGTGTGCAATCGTCACTGGA 1046
DB 1043 AGATGTGAAAGATGTGTTCATCTCATCTGACTTTTACTGACACCGTCACTGGA 1102
QY 1047 TACTAGCTTTGGCTTCTGATGCTGATGAGCTGACCATTTGATTCAGACTGCGC 1106
DB 1103 TACTACCAAAATGAGATTTTGTATTTATGAGCGCAAACTCTCGCTTCAGATTGGGG 1182
QY 1107 TTTACCAAGATGTCTCATCTTATACCGCTTCTTGACACAGTATGACAGCTTTGGGACA 1166
DB 1163 TTTGTCAAAACATGTATCTTCTTACAGATTCTGATATATATGACATTTTGAACA 1222
QY 1167 GTAGACAGCTGGAATCTTTCACAGCACAATTAAGATGGGATCCGTCCGCAATGGA 1226
DB 1223 CTGACCAACTCCCACTTTTACAGCTGCTTTAAGAGATGGGATTTGTACAGAACAAAG 1282
QY 1227 TGCCCTTCAGAAATTAAGAAAGGATGATCATGATGATTTATCAACGTAATGAATG 1286
DB 1283 TGTCTTCAGAAATTAAGAAAGGATGATGATGATGATGATGATGATGATGATGATG 1342
QY 1287 GCTGAGTGGCAGAAAGGCTCAAGGCCGAGACAGCTCAACTATGCAAGACAGGCTTGG 1346
DB 1343 GCGCAAGAGGCTGAGAAAGCTCAAGGCAAGATACGCTCAACTATATTCGAAATGCTTAT 1402
QY 1347 GAGCGGTGTTTGAATGTGTATATGCAAGAAAGCAAGTGAATCCGCACTGTATCTGCC 1406
DB 1403 GAGTCTCATTTTGAATGTGTATATGCAAGAAAGCAAAATGATCTCAGTGTATCTCCA 1462
QY 1407 ACGTTTGAAGAGTACTTGAAGAACGGGAAGTTAGCTCTGCTCATTCGCCCATGCGCACTG 1466
DB 1463 ACGTTTGAAGAGTACTTGAAGAAATGGAAGATTTAGTTCCGTTTCCGACAGCACTTTA 1522
QY 1467 CAACCAATTCGACGTTGACATCCCTTCTGATCAATCTTCAAGAAAGTTGACTTC 1526
DB 1523 CAACCAATTCGACCTTGAATGATCACTTCTTATATCAATGCAAGAAATGATAT 1582
QY 1527 CCATCGAAGCTCAATGATGATATGATATCATCTTGTGATTAAGAGTGAATACCGGTCC 1586
DB 1583 CCATCTGAGTTCAATGACTTGGCTTCGCTCCCTTGGGCTACCTGTGTGACACGCGCTGC 1642
QY 1587 TACAAGGACAGACAGGCGCGTGAAGAAAGCTTCGCTATATCATGTTATATGAAGAC 1646
DB 1643 TACAAGGCGATTAAGGCTCGTGAAGAAAGCTTCACTATATGTGTATATGAAGAC 1702
QY 1647 AATCTCGAATTAACGAAGAAGATCTCTGAATCATATCAACTTCATGATACAGGACGA 1706
DB 1703 CATCTCGATCAACAGAGGAAGATGCTCTCATATCATATCAACGTCATGATGATGATGA 1762
QY 1707 ATCAGAAATTAATTTGGAGCTTCTTAAAGCAGACACAGTGTTCCTCATCTTCCAAAG 1766

Db 1763 ATCAGAGATTAAATTTGGAGCTCTCAGACGACGATAGCAAAAGTCCATCTTCCAAAG 1822
Qy 1767 AACACGCAATTTGACATAGCAGATTTGGCATCAGCGTTACAGATPACCGAGATGGCTAC 1826
Db 1823 AAACATGCTTTTGGACATACCGAGCTTCCATCAGCTTACAGATACCGAGATGGTAC 1882
Qy 1827 AGCTTGGCAACGTTGAAACAAGAGTTTGGATGAGAGAACCGTATTTGAACCTGGCT 1886
Db 1883 ACTGTGGAGATGATGAAACAAAGAAATTTGGATGAAACAGTCTTGAACCTGGCA 1942
Qy 1887 TTGTAAACAACCTTCAA 1903
Db 1943 TTGTAAAAAATATCAA 1959
RESULT 13
AA08645
ID AA08645 standard; cDNA; 2089 BP.
XX
AC AA08645;
XX
DT 27-SEP-1999 (first entry)
XX
DE Limonene synthase gene.
XX
KM Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
KM defense; plant seed; oil; meal; ss.
XX
OS Abies grandis.
XX
FH Key Location/Qualifiers
FT CDS /*tag= a
FT /*product= "Limonene synthase"
XX
PN W0902030-A1.
XX
PD 21-JAN-1999.
XX
PE 10-JUL-1998; 98WO-US014528.
XX
PR 11-JUL-1997; 97US-0052249P.
XX
PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
XX
PI Bohlmann J, Steele CL, Croteau RB;
XX
DR WPI; 1999-120396/10.
XX
PT P-PSDB; AAM85702.
XX
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (Abies grandis), used to provide plants with modified production of
PT monoterpenes, e.g. myrcene, limonene or pinene.
XX
XX Claim 11; Page 79-82; 121pp; English.
XX
CC Nucleotide sequences encoding myrcene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by myrcene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
XX Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;
Query Match 46.0%; Score 925.4; DB 2; Length 2089;
Best Local Similarity 70.6%; Pred. No. 9.8e-252;
Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

Qy 72 TCGTCCCTCAGTCTCTCTCATGAGATTAAAGGCTCCGGTAGAAACATCCCACTGTGGA 131
Db 127 TCGTGTATCATGTTCCAGCAATGTGCAGAAAGGCTCTGTATCTTACAGCACTCCACAA 186
Qy 132 ATCTGACGCGCGGGGAAATCCGCTCGCATTCATATAACATGTGTTGACAGAGCTGCA 191
Db 187 CTCGAATGCGGTAGGCGACAGAAAGCTCTGGTCAATCAATGAATTTGACACTGTATCC 246
Qy 192 TCTACTGATTTCT -----GTACAGAGACCGGTGGCACTATCATTTCCAA 236
Db 247 CATCGGTGATGATTAATGTGTGTGTGTACTGCAAAAGCCATATGCCGATCATATCCCAAC 306
Qy 237 CTGTGGGAGATGATTTGATATACGCTCTGATCTTCAAGCCCTTATGAGCACTGATTAAC 296
Db 307 CTGTGGGAGATGATTTGATATACGCTCTGATCTTCAAGCCCTTATGAGCACTGATTAAC 363
Qy 297 CGGGAACGTGCTGCAGACTTATTGGGAGTAAAGATAT -----AATGTTCAAT 347
Db 364 AGTGAACGTGCTGCAGACGCTGTGAGAGATTAAGAGATGTTCAATTAACCAAT 423
Qy 348 TTCAAGTCGCTGGAAGATGAGGCAATGATCTCTTCAACGACTTTGCTGTGATGAC 407
Db 424 AATAGAGATTAATTTGTTCCCAAAATGATCTCTTACACCGCTTGGATGTGATAGC 483
Qy 408 GTTGAACGTTTGGAAATGACAGGCAATTTCAAAAAGATTAAGACGCACTGATTAAT 467
Db 484 ATGGAACGCTGCGGATGATGATGACATTTCCAAATGATGAAGTGAAGCTTCATTAAT 543
Qy 468 GTTAAAGCTTATTTGAAACGAAA -----AAGCAATTTGATGAGGAGAGATGTTGTGACT 524
Db 544 GTTTAAAGCTTATTTGAAAGAGAAAAGAGCAATTTGGTGTGCAAGATTTCACTTTCTCT 603
Qy 525 GACCTCAACTCAACCGCTTGGGGCTTGAACCTTCGCACTACAGGATACACTGTCTCT 584
Db 604 GATCTCAACTCGACTGCTTGGCGCTTGAACCTTTCGACTGCAACGGAATGAATGTGCT 663
Qy 585 TCAGATGTTTGAACGTTTAAAGACAAATGAGGCAATTTCTCCACTGCCAATAT 644
Db 664 TCAGATGCTGTAATTAATTTCAAGATGAAGAGGCAATTTGCTGCTGCAATCCTA 723
Qy 645 CAGATGAGGAGATGATTAAGAGGCTTCTCAATTTATTCAGGGCTCCCTGCTGCTTT 704
Db 724 ACCGAGGAGACAGATCACTAGAAAGTGTCTAATTTATTCGGGCTCCCTGCTGCTTT 783
Qy 705 CCGGCGGAGAAATTTATGATGAGAAAGCTGAACATTTCTTACAAATATTTAAGAGAAC 764
Db 784 CCGGCGGAGAAATTTATGAGAAAGGCTGAATCTTCTGCGCATCTTATTTAATAAAGTC 843
Qy 765 CTGCAAAAGATTTCCGGCATCCAGTATTAATTTCACTAGAGATACGGGACGTTCTGGAATAT 824
Db 844 TTACAAAGATTTCCGGTCTCAAT ---CTTCAAGAGATGAATATGTTTGGAAATAT 900
Qy 825 GGTGGACACACCAATTTGCCACGCTTGGAGCAAGAAATTAATGACGCTTTGGACAG 884
Db 901 GGTGGACACCAATTTGCCAGATTTGGAACCAAGAAATTAATGACGCTTACAGACAG 960
Qy 885 CACACTAATAAAT -----AGAACGCCCGGAGAAACTTTAGAACTT 926
Db 961 AGCGGCTATGAACCTTAAACGAGATGCAATATTAATGAACATGAAGAACTTTTACAACTT 1020
Qy 927 GCAAAATTTGAATTAATATTTTCACTCTTACAAAGAGAGATTAATGATTTCC 986
Db 1021 GCAAAATTTGAGTTCAATATTTTCACTCTTACAAAGATTAATGATTTCC 1080
Qy 987 CGATGTTGAAGAACTCGGCTTCTCTGAGATGACCTTCTGTCGACATGTCACGTTGAA 1046
Db 1081 AGATGTTGAAGAAATGATGAGTTGCTTCACTGACTTTTACACGGCACTGTCAGTGA 1140
Qy 1047 TACTACGCTTGTGCTCTGATGAGTGTGAGAGCTCAACATTTGATTAAGACTGCGC 1106
Db 1141 TACTACGCTTGTGATCTGATGATTTGATGTTGCAAAACATTAAGCTTTAGAGATGAG 1200
Qy 1107 TTACCAAGATGTCATCTTATATCAAGGTTCTTACGACATGTACGACGCTTGGGACA 1166

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Db 1201 TTTGTCAAGTGTGTCTTGTAAAGTTCCTGATGATATATATGACATCTTTGGAAACA 1260
Qy 1167 GTAAACGAGCTGGAACTCTTCAACGCCACATTTAAAGATGGAGTCCGCCGATGGAA 1226
Db 1261 ATGAACGAACTCCAACTTTTACGATGCAATTAAGATGGATGGATTTTCAACGACAAAG 1320
Qy 1227 TGCCTTCAGAAATATGAAAGAGTGTACATGATGGTTTATCAACCGTAAATGAATG 1286
Db 1321 TGGCTTCAGAAATATGAAAGAGTGTACATGATGGTTTATCAATGATTAATGAATG 1380
Qy 1287 GCTTCAGTGGCAGAAAGCTCAAAGCCGAGACACGCTCAAATGCAAGACAGCTTGG 1346
Db 1381 GTGAAGAGGCTGAGAAAGACTCAAGCCGAGATATGCTCAATATTTCAAAAGCTTGG 1440
Qy 1347 GAGCGGTGTTTGTATGCTATATGACAGAAAGTGTATGCTGATATGCTTATGCTCC 1406
Db 1441 GAAGCCCTATTTGATCTTATGCAAGAACAAAGTGAATCTCCAGCATTTATCTCCA 1500
Qy 1407 ACGTTTGAGAGTACTTGGAGAGCGGAAAGTTAGCTGCTCATTCGCCATGCGCACTG 1466
Db 1501 ACGTTTGAGAGTACTTGGAGAGCGGAAAGTTAGCTGCTCATTCGCCATGCGCACTT 1560
Qy 1467 CAACCCATTCGAGCTGGAGATCCCTTTCTGATCATCTTCAGAGAGTGGACTTC 1526
Db 1561 CAACCCATTCGAGCTGGAGATCCCTTTCTGATCATCTTCAGAGAGTGGATTTAT 1620
Qy 1527 CCATTCGAGCTGATGATCTGATATGATATCTCTTCATTAAGAGTGTATGACGCTG 1586
Db 1621 CCATTCGAGCTGATGATGATCTGATATGATATCTCTTCATTAAGAGTGTATGAC 1680
Qy 1587 TACAAGGAGACAGAGGCGCGTGGAGAAAGACCTGCTATATATCAATGTTATGAAAGAC 1646
Db 1681 TACAAGGAGATAGGCGCGTGGAGAAAGACCTGCTATATGATGCTGTTATGAAAGAC 1740
Qy 1647 AATCTGATTAACGAGAAAGATGCTTGAATCATATCAATTCATGATGAGGAGCA 1706
Db 1741 CATCTGATTAACGAGAAAGATGCTTGAATCATATCAATTCATGATGAGGAGCA 1800
Qy 1707 ATCAGAGATTAATGAGGAGCTTGAAGCCAGACACAGTGTTCATCTCCATCTCCAG 1766
Db 1801 ATCAGAGATTAATGAGGAGCTTGAAGCCAGACACAGTGTTCATCTCCATCTCCAG 1860
Qy 1767 AAACAGCATTTGACATAGAGAGATTTGATCAGCTGATCAGATACCGAGATGCTAC 1826
Db 1861 AAACAGCTTTGACATACAGAGCTTTCATCATGCTTACAAATATCGAGATGCTAC 1920
Qy 1827 AGCTTTGCAACGTTGAAACAAAGATTTGATGAGAACCGTCAATGAACTGTGCT 1886
Db 1921 AGCTTTGCAACGTTGAAACAAAGATTTGATGAGAACCGTCAATGAACTGTGCT 1980
Qy 1887 TTGTAAACAGCTTCAATCTCAATATTAATGAGG 1923
Db 1981 TTGTAAACAGCTTCAATCTCAATATTAATGAGG 2017

```

RESULT 14
AAA38938 standard; DNA; 2089 BP.

AAA38938;
25-AUG-2000 (first entry)
Grand fir limonene synthase DNA sequence SEQ ID NO: 57.
Synthase; protein co-ordinate data; active site; modification; terpenoid;
3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
isoprenoid; breeding programme; fragrance; flavour; pheromone;
defensive agent; pigment; antitumor; steroid hormone;
signal transduction pathway; bile acid; affinity purification;
photoreceptor; enzymatic synthesis; nutrient supplement;
immunological reagent; ds.

```

XX Abies grandis.
OS WO200017327-A2.
XX 30-MAR-2000.
XX 17-SEP-1999; 99WO-US021419.
XX 18-SEP-1998; 98US-0100993P.
XX 22-APR-1999; 99US-0130628P.
XX 23-AUG-1999; 99US-0150262P.
XX (KENT) UNIV KENTUCKY RES DEPT.
XX (SALK) SALK INST BIOLOGICAL STUDIES.
XX Chappell J, Manna KR, Noel JP, Starks CM;
XX WPI; 2000-292839/25.
XX P-PSDB; AAY90859.
XX Novel terpene synthase enzymes, useful for producing terpene
XX hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
XX enzymes by specific amino acid alterations.
XX Disclosure; Page 445-448; 450pp; English.
XX The present invention describes an isolated terpene synthase (1)
XX comprising a region with at least 20% identity to region 265-535 of a 548
XX amino acid (aa) sequence (1a), given in AAY90831. (1) contains nine alpha
XX -carbon atoms (aliphatic) that have interatomic distances, between each
XX other, within tabulated ranges, have a centre point (within a sphere of
XX radius 2.3 Angstrom) within tabulated ranges, and have an ordered
XX arrangement of R groups (defining as side chains), excluding specific
XX tabulated arrangements (tables given in the specification). (1), and
XX related enzymes, are used to produce a wide range of terpenoids (e.g.
XX cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
XX flavours, pheromones, defensive agents, pigments, antitumor agents,
XX components of signal transduction pathways, precursors of steroid
XX hormones and bile acids, as photoreceptors and as co-factor side chains.
XX Some synthases with little or no catalytic activity (and nucleic acids
XX encoding them) are used as controls in the analysis of products formed by
XX enzymatic synthesis; as nutrient supplements; for affinity purification
XX of isoprenoids; or to develop immunological reagents or nucleic acids for
XX monitoring expression of terpene synthase or inheritance of the gene in
XX plant breeding programs. The new synthases may produce novel terpene
XX products. AAA38938 and AAY90831 to AAY90859 represent
XX sequences used in the exemplification of the present invention
XX
XX Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;
XX
XX Query Match 46.0%; Score 925.4; DB 3; Length 2089;
XX Best Local Similarity 70.6%; Pred. No. 9.8e-252;
XX Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;
Qy 72 TCGTGCTCAGATTCTTCTCATGAGATTAAAGCTCTCCGTAGAACATCCCACTTTGGA 131
Db 127 TCGTTGATCACTTCCAGCAATGTCAGAGGCTCTGTATCTTCAACGAGTCCCAACA 186
Qy 132 ATTCGACAGCGCGGAAATCCGTCGCGATTCATTAACATGTTTGGACAGGCTCGCA 191
Db 187 CTCAGAAATGCGTAGAGCAGACAAAGCTCTGTCATCAACAGAAATGACCACTGTATCC 246
Qy 192 TCTACTGATCTT-----GTACAGAGACGCGGCACTATCTCCAC 236
Db 247 CATGTGATGATTAATGCTGTGTGATCTGCAAGAGCATAGCCATCATCATCCAC 306
Qy 237 CTGTGGACGATGATTTTCACTCTCTGATTCACAGCCTTATGAGCACTGATATAC 296
Db 307 CTGTGGAGATGATTTTCACTCATCATATTCCTCA---CCTTATGGGAGATCTTCGATC 363
Qy 297 CGGAAAGCTGCTGACAGACTTATTTGGGAGATTAAGATAT-----AATGTTCAAT 347

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Tue Jul 27 08:32:44 2004

us-10-025-145a-64.rng

Page 21

Search completed: July 26, 2004, 10:16:48
Job time : 773 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:57 ; Search time 4682 Seconds
(without alignments)
12839.079 Million cell updates/sec

Title: US-10-025-145A-64

Perfect score: 2013

Sequence: 1 ttttgacgtgcctctatc.....aaaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmva:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gsa_hum:*
18: em_gsa_inv:*
19: em_gsa_pla:*
20: em_gsa_vrt:*
21: em_gsa_fun:*
22: em_gsa_mam:*
23: em_gsa_mus:*
24: em_gsa_pro:*
25: em_gsa_rtd:*
26: em_gsa_rhg:*
27: em_gsa_vrt1:*
28: gb_gsa1:*
29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564.2	28.0	745	14	CF477103 RTW3_5_A
2	475.2	23.6	697	13	BQ196773 NXLV105_B
3	447.2	22.2	599	13	BX680641 BX680641
4	428.2	21.3	599	12	BG526917 NXPV_057

5	427	21.2	700	14	CF474786 RTW2_7_B
6	425.8	21.2	637	14	CF476978 RTW3_5_A
7	419.2	20.8	696	14	CF401916 RTW1_15-
8	413	20.5	669	14	CF479802 RTW3_12-
9	399.6	19.9	615	14	CF663845 RTCNT1_5-
10	388.6	19.3	515	13	BQ698077 NXPV_064
11	384.4	19.1	517	13	BX677624 BX677624
12	384.2	19.1	804	14	CF666338 RTCNT1_22
13	376	18.7	481	9	AL750951
14	375	18.6	740	14	CF477562 RTW3_8-G
15	352.4	17.5	539	14	AM287756 EST0004_S
16	343.8	17.1	557	14	CF666483 RTCNT1_23
17	339.8	16.9	651	14	CF479884 RTW3_12-
18	327.4	16.3	682	14	CF663768 RTCNT1_5-
19	324.8	16.1	534	10	AM287755 EST0003_S
20	315.4	15.7	569	10	AM287754 EST0002_S
21	312.2	15.5	430	13	BQ702557 NXSV_129
22	302.4	15.0	591	14	CA305371 CA305371
23	300.4	14.9	541	14	CF672979 RTCNT1_75
24	284.2	14.1	618	9	AL750955
25	283.6	14.1	542	10	BG039521 NXSV_099
26	264	13.1	734	14	CF474640 RTW2_7-B
27	264	13.1	733	14	CF666270 RTCNT1_22
28	245.4	12.2	574	9	AM065088 ST39E04_P
29	239	11.9	597	14	CF666416 RTCNT1_23
30	215.4	10.7	365	10	AM697531 RTGSA12_P
31	211.6	10.5	725	14	CF470471 RTDS1_17-
32	197.4	9.8	634	14	CF397946 RTDS3_23-
33	197.2	9.8	725	14	CF397293 RTDS3_2-A
34	193.2	9.6	353	14	CA305444 CA305444
35	188.6	9.4	552	13	BQ696735 NXPV_044
36	187.8	9.3	529	13	BQ698322 NXPV_068
37	185	9.2	400	14	CF672970 RTCNT1_75
38	181.8	9.0	601	9	AM043070 ST28H10_P
39	181.2	9.0	530	9	AU298829 AU298829
40	180.6	9.0	537	9	AM011129 AU011129
41	176.6	8.8	629	9	AU299287 AU299287
42	176.2	8.8	487	14	292688 SCS1571/11 No
43	164	8.1	306	10	AM226490 ST82H11_P
44	162.4	8.1	730	13	BX682869 BX682869
45	156.6	7.8	530	9	AU298828 AU298828

ALIGNMENTS

RESULT 1
CF477103
LOCUS RTW3_5_A06_g1_A022 Well-watered loblolly pine roots W3 Pinus
DEFINITION taeda cDNA clone RTW3_5_A06_A022 5', mRNA sequence.
ACCESSION CF477103.1 GI:34505972
VERSION
KEYWORDS
SOURCE
ORGANISM
Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 745)
REFERENCE
Pratt, L., Cordomier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Devlin, C., Martin, T., White, T., Davis, J. and
Neale, D.
An EST database from well-watered loblolly pine (Pinus taeda) roots
Unpublished (2003)
Other ESTs: RTW3_5_A06_b1_A022
Contact: Cordomier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpat@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGAC).

Location/Qualifiers

1..745

source

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="CCLONES"

/db_xref="taxon:3352"

/clone="RTW3.5 A06 A022"

/lab_host="DH10B-r1 phage-resistant E. coli"

/clone_lib="Well-watered loblolly pine roots WM3"

/note="Vector: pSL180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 Mpa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 28.0%; Score 564.2; DB 14; Length 745;

Best Local Similarity 84.8%; Pred. No. 6e-90;

Matches 632; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

1100 ACTGCGCTTACCAAGATGCTCATCTTATGACGGTTCTTGACGACATGACAGCTTT 1159

1 ACTGCGCTTACCAAGATGCTCATCTTATGACGGTTCTTGACGACATGACAGCTTT 60

1160 CGGACAGTACGACGCTGGAAGCTTTCACGCGCAATTAAGATGGATCCGCTCCG 1219

61 CGGACAGTACGACGCTGGAAGCTTTCACGCGCAATTAAGATGGATCCGCTCCG 120

1220 GATGGAATGCTTCCAGATATATGAAAGAGTATCATGATGGTTATCACACCGTAA 1279

121 GACGAGTGGCTTCCAGATATATGAAAGAGTATCATGATGGTTATCACACCGTAA 180

1280 TGAATGCTTCCAGATATATGAAAGAGTATCATGATGGTTATCACACCGTAA 1339

181 TGAATGCTTCCAGATATATGAAAGAGTATCATGATGGTTATCACACCGTAA 240

1340 GCGTGGAGGCGCTTGTGATGTTATGACGGAAGCAAGTGGATCGCATCGTTA 1339

241 GCGTGGAGGCGCTTGTGATGTTATGACGGAAGCAAGTGGATCGCATCGTTA 300

1400 TCTGCCACGTTTGAAGAGTATGAGAAAGGAAAGTATGCTCTGCTATCGCCATG 1459

301 GGTCCCAACATTTGAGAGTATGAGAAAGGAAAGTATGCTCTGCTATCGCCATG 360

1460 CGCAGTCAACCTTCTGAGCTTGAACATCCCTTCTGATCAATCTCTCAAGAAAT 1519

361 GGCATTGCAACCTTCTGAGCTTGAACATCCCTTCTGATCAATCTCTCAAGAAAT 420

1520 TGACTTCCATCGAAGCTCATGATGATATGATCATCTTGGATTAAGAGGATAC 1579

421 TGACTTCCATCGAAGCTCATGATGATATGATCATCTTGGATTAAGAGGATAC 480

1580 ACGGTGCTACAGGACAGACAGGCGCTGAGAAAGAGCTTCTGATATCATGTTAT 1639

481 GCGGTGCTACAGGACAGACAGGCGCTGAGAAAGAGCTTCTGATATCATGTTAT 540

1640 GAAAGACATCTTGATTAACGAAAGAGTCTGATATCATCAATCTCATGATAG 1699

541 GAAAGACATCTTGATTAACGAAAGAGTCTGATATCATCAATCTCATGATAG 600

1700 GGAGGACATGAGAAATTAATGGAGCTTCTAAGCAGACAAAGATTTCCATAC 1759

601 TGATGATTAATTAAGGATTAATGGAGCTTCTAAGCAGACAAAGATTTCCATAC 660

Qy 1760 TTCGAGAAACAGCATTGTGACATGACGATTTGGCATTCACGGTTACAGATACCGAGA 1819

Db 661 TGCAGAAACATGCTTTGACATTAACAGAGCTTCCATATGCTAACAAATATCGAGA 720

Qy 1820 TGGCTACAGCTTTCGCAAGCTTGA 1844

Db 721 TGGCTACAGGCTTTCGCAAGCTTGA 745

RESULT 2

LOCUS

DEFINITION

BQ196773 697 bp mRNA linear EST 07-MAY-2003

NX1V105 B02 F NX1V (Nef Xylem Late wood Vertical) Pinus taeda cDNA

Clone NX1V105 B02 5' similar to Arabidopsis thaliana sequence

At4g16730 limonene cyclase like protein see

http://mips.gsf.de/proj/tha/db/index.html, mRNA sequence.

BQ196773

BQ196773.1 GI:20379276

EST.

Pinus taeda (loblolly pine)

Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

Sederoff, R.

Molecular Basis of Wood Formation in the Pine Megagenome

Unpublished (2000)

Contact: Sederoff, Ron

Forest Biotechnology

North Carolina State University

840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,

NC 27695, USA

Tel: 919 515 7800

Fax: 919 515 7801

Email: ron_sederoff@ncsu.edu, jerry_johnson@ncsu.edu

Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further

information.

Seq primer: T3.

Location/Qualifiers

1..697

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="Coastal plain loblolly pine from North Carolina"

/db_xref="taxon:3352"

/clone="NX1V105 B02"

/tissue_type="primary xylem"

/dev_stage="late wood"

/lab_host="XLI-BIUE"

/clone_lib="NX1V (Nef Xylem Late wood Vertical)"

/note="Vector: pT11EX; Site_1: EcoRI; The library is

from late (summer-August) wood, taken from below the crown

of a 20 year old tree. The harvested xylem tissue was on

the cusp between transitional and mature wood. NOTE:

The sequences contain a 'cDNA adapter' between the EcoRI

site and the start of the EST. The adapter sequence is

'AATTCGCGCATTAATGCGC.'

ORIGIN

Query Match 23.6%; Score 475.2; DB 13; Length 697;

Best Local Similarity 83.0%; Pred. No. 3.3e-74;

Matches 534; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

1250 AGTGTACATGATGTTATACACCGTAAATGAATGCTGAGTGGCAGAGAGCTCA 1309

22 AGTTATCATGATATTTTCAACACCTGTAATGAATGCTTACAGAGCAGACAGGCTCA 81

Qy 1310 AGCGCGAGACCGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTTGATAT 1369

Db 82 AGCGCGAGACCGCTCAACTATGCTGACAGGCTTGGAGGAGAAATATTTGATGCTATAT 141

Qy 1370 GCAGAGCAAAAGTGAATCGGCACTGTTATCTGCCACGTTTGAAGAGTCTTGAGAA 1429

Db 142 GCAGAGCAAAAGTGAATCGGCGTGTGAGTGCCTCAACATTTGAGAGTATGAGAA 201

QY 1430 CGGAAAGTTAGCTCTGCTCATGCGCCATGGGCACTGCAACCCATTCTGACGTTGACAT 1489
 DB 202 CGGAAAGTTAGCTCTGCTCATGCGCCATGGGCACTGCAACCCATTCTGACGTTGACAT 261
 QY 1490 CCCCTTCTGATCACTCCCAAGAAAGTTGACTTCCCATGGAAGCTCATGACTGAT 1549
 DB 262 CCCCTTCTGATCACTCCCAAGAAAGTTGACTTCCCATGGAAGCTCATGACTGAT 321
 QY 1550 ATGTATCATCTTGTGATTAAGAGGTGATACAGGTGCTACAGGCGACAGGCGCCGTG 1609
 DB 322 ATGTATCATCTTGTGATTAAGAGGTGATACAGGTGCTACAGGCGACAGGCGCCGTG 381
 QY 1610 AGAAGAACTTGTCTAT 1669
 DB 382 AGAAGAACTTGTCTAT 441
 QY 1670 TGCTCTGATCATATCACTCATGATCAGGGAAGCAATCAGAGATTAATTAATTTGGAGCT 1729
 DB 442 TGCTCTGATCATATCACTCATGATCAGGGAAGCAATCAGAGATTAATTAATTTGGAGCT 501
 QY 1730 TCTAAGCCAGACAAGAGTGTTCATCATCTTCCAAAGAAACAGCATTTGACATTAAGCAG 1789
 DB 502 TCTAAGCCAGACAAGAGTGTTCATCATCTTCCAAAGAAACAGCATTTGACATTAAGCAG 561
 QY 1790 AGTTGGCATACGGTTACATACATACCGAGATGGCTACAGCTTTGGCAAGTTGAACAA 1849
 DB 562 AGCTTCCATTTGTGGCTACAAATATCGAGATGGCTACAGCTTTGGCAAGTTGAACAA 621
 QY 1850 GAGTTGGTGTGAGAAACCGTCAATGAACTGTGCTTTGTAA 1892
 DB 622 NGTTTGGTANNMNAACCGTCAATGAACTGTGCTTTGTAA 664

RESULT 3
 LOCUS BX680641 599 bp mRNA linear EST 28-OCT-2003
 DEFINITION BX680641 RS Pinus pinaster cDNA clone RS46D06, mRNA sequence.
 ACCESSION BX680641
 VERSION BX680641.1 GI:38015099
 KEYWORDS EST.
 SOURCE Pinus pinaster
 ORGANISM Pinus pinaster
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 599)
 Frigerio, J. and Plomion, C.
 Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach
 Unpublished (2002)
 JOURNAL Contact: Frigerio JM
 Comment: Genetique et Amelioration 69
 INRA
 route d'Arcachon 33612 Cestas CEDEX France
 Email: Frigerio@pierroton.inra.fr
 Email: Frigerio@pierroton.inra.fr
 Seq primer: T3.
 Location/Qualifiers
 1..599
 /organism="Pinus pinaster"
 /mol_type="mRNA"
 /db_xref="taxon:71647"
 /clone="RS46D06"
 /tissue_type="root"
 /dev_stage="6 weeks old seedling"
 /lab_host="SOLR"
 /clone_lib="RS"
 /note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 Mpa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of

ORIGIN
 Query Match 23.2%; Score 447.2; DB 13; Length 599;
 Best Local Similarity 85.2%; Pred. No. 3.1e-69;
 Matches 511; Conservative 0; Mismatches 88; Indels 1; Gaps 1;
 genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambdaZAP vector arms and mass-excised to form a pluescript phagemid"

QY 1228 GCCTTCCAGAAATATATGAAAGAGTGTACATGATGTTTATACACCGTTAAATGAATG 1287
 DB 1 GCCTTCCAGAAATATATGAAAGAGTGTACATGATGTTTATACACCGTTAAATGAATG 59
 QY 1288 CTCGAGTGGCAGAAAGGCTTCAAGCCGAGCAGCTTCAACTATGCAAGAGGCTTGG 1347
 DB 60 CTCGAGTGGCAGAAAGGCTTCAAGCCGAGCAGCTTCAACTATGCAAGAGGCTTGG 119
 QY 1348 AGCGGTGTTTGAATTCGATATATGAGAGAAAGTGTATGCGCATGTTATCGCCA 1407
 DB 120 AGCATATCTTGAATTCGATATATGAGAGAAAGTGTATGCGCATGTTATCGCCA 179
 QY 1408 CGTTGAGGATCTTGGAGAACGGGAAAGTTAGCTTGTCTCATGCGCATGCGCATGC 1467
 DB 180 CGTTGAGGATCTTGGAGAACGGGAAAGTTAGCTTGTCTCATGCGCATGCGCATGC 239
 QY 1468 AACCATTTTGAATTCGATATATGAGAGAAAGTGTATGCGCATGTTATCGCCA 1527
 DB 240 AACCATTTTGAATTCGATATATGAGAGAAAGTGTATGCGCATGTTATCGCCA 299
 QY 1528 CATGAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1587
 DB 300 CATGAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 359
 QY 1588 ACAAGGACAGAGGCGCGGTGAGAGAAAGTGTCTATATCATGTTATGAAAGCA 1647
 DB 360 ATCAAGGACAGAGGCGCGGTGAGAGAAAGTGTCTATATGTTATGAAAGCA 419
 QY 1648 ATCTGTATTAACGGAAGAAAGTGTCTGATATATCAACTTATATATGAGAGCGAA 1707
 DB 420 ACCCTTGAGCAACGAGAGAAAGTGTCTTATATATCAACTTATATGAGAGCGAA 479
 QY 1708 TCAGAGATTAATTTGGAGGCTTCTAAGCCAGACAGAGTTCCTCATCTTCAAGA 1767
 DB 480 TTAAGATTAATTTGGAGGCTTCTAAGCCAGACAGAGTTCCTCATCTTCAAGA 539
 QY 1768 AACAGGATTTGACATAGCAGAGTTTGGCATCGGTTACAGATCCGAGATGCTTACA 1827
 DB 540 AAATTACTTTGACATAGCAGAGTTTGGCATCGGTTACAGATCCGAGATGCTTACA 599

RESULT 4
 LOCUS BG526917 599 bp mRNA linear EST 07-MAY-2003
 DEFINITION NXPV_057 D04 F NXPV (Nef Xylem Planting wood Vertical) Pinus taeda cDNA clone NXPV_057 D04 5' similar to Arabidopsis thaliana sequence At4g16730 lipoxygenase cycloase like protein see <http://mips.gsf.de/prot/tnal/db/index.html>, mRNA sequence.
 ACCESSION BG526917
 VERSION BG526917.1 GI:13536796
 KEYWORDS EST.
 SOURCE Pinus taeda (loblolly pine)
 ORGANISM Pinus taeda
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 599)
 Sederoff, R.
 Molecular Basis of Wood Formation in the Pine Megagenome
 Unpublished (2000)
 JOURNAL Contact: Sederoff, Ron
 Comment: Forest Biotechnology
 North Carolina State University
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA

Tel: 919 515 7800
 Fax: 919 515 7801
 Email: ron.sedger@ncsu.edu, jerri.johnson@ncsu.edu
 Please see <http://web.ahc.umn.edu/biodata/rsfpine/> for further information.
 Seq primer: T3.

FEATURES

source

Location/Qualifiers
 1..599
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXPV_057.D04"
 /issue_type="Xylem"
 /cell_type="plantings (secondary)"
 /dev_stage="Transitional"
 /lab_host="XLI-Blue"
 /clone_id="NXPV (Nef Xylem plantings wood Vertical)"
 /note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: XhoI; The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATCGGACGAG'."

ORIGIN

Query Match 21.3%; Score 428.2; DB 12; Length 599;

Best Local Similarity 80.9%; Pred. No. 7e-66;

Matches 484; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

1216 CCGCGATGAGATGCTCTTCCAGAAATATATGAAAGAGTATCATGATGTTTATACACCG 1275
 1 CGGGGACAGAGTGGCTTCCAGAAATATATGAAAGAGTATCATGATGTTTATACAACTG 60
 1276 TAAATGAAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACACGCTCAATATGCAA 1335
 61 TAAATGAAATGCTTCAGAGGCGAGACAGAGGCTCAAGGCCGAGACACGCTCAATATGCTC 120
 1336 GACAGGCTTGGAGAGCGCTGTTTGAATTCGATATGACAGAAAGATGATCGCACTG 1395
 121 GACAGGCTTGGAGAGATATATGATGCGTATATGACAGAAAGATGATCGCACTG 180
 1396 GTTATGCTCCACGCTTGAAGAGTACTTGAAGAGGAAAGTTAGTCTGCTCATCGCC 1455
 181 GTGAGGTGCCAACTTGAAGAGTACTTGAAGAGGAAAGTTAGTCTGCTCATCGCG 240
 1456 CATGGGCACTGCAACCCATTTGACAGTTCATCCCTTCTGATCATCTCTCAAGG 1515
 241 TATGGGCACTGCAACCCATTTGACAGTTCATCCCTTCTGATCATCTCTCAAGG 300
 1516 AAGTTGACTTCCATCGAAGCTCAATGACTTGAATATGATCATCTCTGATTAAGAGGTG 1575
 301 AAGTTGACTTCCATCGAAGCTCAATGACTTGAATATGATCATCTCTGATTAAGAGGGG 360
 1576 ATACAGGTGTTACAGGCAACAGGGGCCGTTGAGAAAGAGCTTCCGCTATATCATCTT 1635
 361 ATACAGGTGTTACAGGCAACAGGGGCCGTTGAGAAAGAGCTTCCGCTATATCTTGT 420
 1636 ATATGAAAGCAATCTGATTTAAACGAGAAAGATGCTCTGAATCATATCAATCTTCAGA 1695
 421 ATATGAAAGCAATCTTNNAAACAGAGAAAGATGCTCTCAATCATATCAACGGCAGTA 480
 1696 TCAGGGAGCAATGAGATTTAAATTTGGAGCTTCTAAAGCGAGACAAGTGTTCCTCA 1755
 481 TCAGTGAATGTTATTAANNNTTAAATTTGGAGCTTCTCAAAACAAACAGAGCTTCCCA 540
 1756 TCACCTTCCAAAGAACGCAATTTGACATTAACAGAGTTTGGCATCAAGCTTACAGATA 1813
 541 TATCTGCCAANNNCATGCTTTTGAATTAACNNNNNNNTCCNNNTGTGTGCTTACAAATA 598

RESULT 5

CF474786 700 bp mRNA linear EST 05-SEP-2003
 RTMW2_7.B11.g1.A021 Well-watered loblolly pine roots Wm2 Pinus

LOCUS

taeda cDNA clone RTMW2_7.B11.A021 5', mRNA sequence.

DEFINITION

CF474786

ACCESSION

CF474786

VERSION

CF474786.1

KEYWORDS

EST.

SOURCE

ORGANISM

Pinus taeda (loblolly pine)

Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

1 (bases 1 to 700)

Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,

Gebremedhin, M., Dervins, C., Martin, T., White, T., Davis, J. and

Neale, D.

An EST database from well-watered loblolly pine (Pinus taeda) roots

Unpublished (2003)

Other ESTs: RTMW2_7.B11.B1.A021

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mpratt@uga.edu

RNA prepared and library constructed by M. Walter Lorenz, School of

Forestry, University of Georgia, plant material prepared at the

University of Florida; sequencing done in the Laboratory for

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-primed sequences are presented as their reverse complement

and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGAC).

Location/Qualifiers

1..700

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="CLONES"

/db_xref="taxon:3352"

/clone="RTMW2_7.B11.A021"

/lab_host="DH10B-T1 phage-resistant E. coli"

/clone_id="Well-watered loblolly pine roots Wm2"

/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The

library was prepared from polyA+ RNA from loblolly pine

(Pinus taeda) roots watered to pot capacity every other

day. Pre-dawn water potential remained -0.3 MPa +/- 0.1.

Roots were harvested for RNA isolation. Double-stranded

cDNA was cloned unidirectionally into pSL1180. Inserts

excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 21.2%; Score 427; DB 14; Length 700;

Best Local Similarity 75.7%; Pred. No. 1.1e-65;

Matches 529; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

1034 TCGTCAGTGGAAATCAAGCTTTGGCTTCGATTCGCGTTCGAGCTCAACATTCGCG 1093
 1 TCGTCAGTGGAAATCAAGCTTTGGCTTCGATTCGCGTTCGAGCTCAACATTCGCG 60
 1094 ATTGAGACTGGGCTTTACCAAGATGCTCATCTTATCAAGGATCTTTGACGATGTACGA 1153
 61 GTTTCGACTAGGATTTGGTAAATTAATGATATGATCAGGATTTCTGACGATATCTACGA 120
 1154 CGTCTTGGGCACTAGACGAGCTGGAATCTTCAACGCAATTAAGAGATGGATCC 1213
 121 CACCTTGGGAAACAATGAGAGGCTCGAACTTTTAAACGCAAGCGTTTAAAGATGGATCC 180
 1214 GTCCGAGATGAAGGCTTCAGAAATATATGAAGAGGTGATGATGATTTATACAC 1273
 181 GTCTTGATGAGTGTCTTCCAGATTAATGAAAGAGTGTATGATGCGGTTTACGACAA 240

QY	1274	CGTAAATGAATTGGCTCGAGTGGAGAAAGGCTCAAGGCCGAGACAGCTCAACTTATGC	1333
Db	241	CATCAACGAATATGCGACGAGAGGCGCAGAAATTCAGAGCTGGAGATACGTCAGCTATGC	300
QY	1334	AAGACAGGCTTGGAGGCGTGTTTTGATTCGTATATGCAAGAGCAAAAGTGAATCGCCAC	1393
Db	301	TCGAAATATCTTGGAGGCTTTTATTTGGTGCTTATATACAAAMACCAAGTGAATTTCCAG	360
QY	1394	TGCTTATCTGCGCCAGTTTATGGAGTACTTGGAAACGGAAAGTTTGGCTCTGCTACG	1453
Db	361	TGTTATCTTCCACGTTTCAGCGAGTACTTGAAGAAATGGAAAGTCAAGCTTCGGCTCTCG	420
QY	1454	CCCATGCGCACTGCAACCCATTCTGACGTTGGAGATCCCTTCTTCGTATCATCTCTCAA	1513
Db	421	CATACACACGCTGAAACCATGCTGACTTTGGGGTTCTCTTTCGGCTCGAAATCTGCA	480
QY	1514	GGAAGTTGACTTCCCATCTGAAAGCTCAATGACTTGTATGTATCTCTTGATTAAGAG	1573
Db	481	GGAATATGACTTTCATCTGAAATTCATGATTTTATATGTGCCATCTCTTCACATGAAAG	540
QY	1574	TGATACACGCGTCTACAAAGCAGACAGAGGCCCTGAGCAAGAAACCTTCGTATATCATG	1633
Db	541	TGACATCTCAATGCTACAAAGCTGACAGGGCGCTGAGAAAGAAAGCTTCGGCCGATCTGC	600
QY	1634	TTATATGAAAGACAATCTCTGATTTAACGGAAGAAAGATGCTCTGATCATATATCAACTTCAT	1693
Db	601	TTATATGAAAGAACCATCTCTGGAATTAACAGAGAAAGATGCTCTCATCATCAATGCTAT	660
QY	1694	GATCAGGAGCGCATACAGAAATTAATTTGGAGCTTCT	1732
Db	661	GGTCGATPACTTAAACAGAGAACTGAATTTGGAGTACT	699

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/strain="CLONES"
/db_xref="taxon:3352"
/clone="RTW3_5_A06_A022"
/_db_host="DH10B-T1 phage-resistant E. coli"
/_clone_idb="Well-watered loblolly pine roots W3"
/_note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from polyA+ RNA from loblolly pine
(prinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 Mpa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL1180. Inserts
existed with EcoRI (5' end) and XhoI (3' end)."

```

Email: impratti@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and 16. Three-prime sequences are presented and have been trimmed to exclude polyA. Seq primer: M13-21 (TGTAAACGACGGCCAGT)
POLYA=Yes

FEATURES

source

location/Qualifiers

1..637

/organism="Pinus taeda"

/mol_type="mRNA"

RESULT 7					
CF401916					
LOCUS	CF401916	696 bp	mRNA	linear	EST-29-AUG-2003
DEFINITION	RTWML15_B05.g1_A015 well-watered loblolly pine roots wml Pinus				
ACCESSION	taeda cDNA clone RTWML15_B05_A015 5', mRNA sequence.				
VERSION	CF401916				
KEYWORDS	CF401916.1 GI:34360333				
SOURCE	EST.				
ORGANISM	Pinus taeda (loblolly pine)				
	Pinus taeda				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.				
REFERENCE	1 (bases 1 to 696)				
AUTHORS	Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,				

TITLE
JOURNAL
COMMENT

Gebremedhin, M., Derwinis, C., Martin, T., White, T., Davis, J. and Neale, D.
An EST database from well-watered loblolly pine (*Pinus taeda*) roots
Unpublished (2003)
Contact: Cordomier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source

Location/Qualifiers
1..696
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTMW1_15_B05_A015"
/lab_host="DH108-T1 phage-resistant E. coli"
/clove_lib="Well-watered loblolly pine roots WM1"
/notes="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI. The library was prepared from polyA+ RNA from loblolly pine (*Pinus taeda*) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 20.8%; Score 419.2; DB 14; Length 696;
Best Local Similarity 75.1%; Pred. No. 2.6e-64;
Matches 523; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

1065 TGCATTGCGTTCGAGCTCAACATCTTGATTCAGACTCGGCTTTTACAGATGTCAT 1124
1 TGCATTTCCAATGATCTTAAACATTTTGCCTTCGACTAGATTTGGTAAATTAAGCAT 60
1125 CTATTCACGGTCTTTCGACATGATGAGAGCTTCGCGACAGTAGACGAGCTGAACTC 1184
61 ATGATTCACGATTCGACGATATCTACGACACCTTCGGAACATGAGAGAGCTGAACTC 120
1185 TTCAACGCGAATTAAGAGATGGATCCGTCGCGATGAGATGCTTCCAGAAATATATG 1244
121 TTAAACGCGAGCTTTAAGAGATGGATCCGTCGATGAGATGCTTCCAGATTAATATG 180
1245 AAAGAGATGATGATGATGATTTATCAACGTAATGAAATGCGTCGAGTGGCAGAGAG 1304
181 AAAGAGATGATGATGATGATTTACGACAACTCAACGAAATGAGCAGAGAGCGCAGAAA 240
1305 GCTCAAGGCGCAGACGCTCACTATGCAAGACAGAGGCTTGGAGGCGTATTGATTCG 1364
241 ATTCAAGGCTGGATACAGTACGATAGCTGGAATATTTGGAGGCTTTTATTTGGTCT 300
1365 TATATGACAGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1424
301 TATATACAGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
1425 GAGAAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1484
361 GAGAAAGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
1485 GACATCCCTTTCTGATTCATCTCAAGAGATGATGATGATGATGATGATGATGATGATG 1544
421 GGGTTTCTCTTCGCGCTCGAATCTCGAGGAAATGATCTTCCATGCAAAATTCATGAT 480

QY 1545 TTGATATGATATCTCTTGGATTAAAGAGTGATACAGGCTGTACAGGACAGAGGCGC 1604
DB 481 TTGATATGATGATATCTCTTGGATTAAAGAGTGATACAGGCTGTACAGGACAGGCGC 540
QY 1605 CGTGGAGAAAGAGCTTCTGATATATCACTTTATATGAAAGACATCTGATTAAGCGAA 1664
DB 541 CGTGGAGAAAGAGCTTCTGATATATCACTTTATATGAAAGACATCTGATTAAGCGAA 600
QY 1665 GAAGATCTCTGATATATCACTTTATATGAAAGAGAGGAGCGCAATCAGAAATTAATGG 1724
DB 601 GAAGATCTCTGATATATCACTTTATATGAAAGAGAGGAGCGCAATCAGAAATTAATGG 660
QY 1725 GAGCTTCTAAAGCAGCAACAGTGTTCATCACT 1760
DB 661 GAGTACTTAAAGCAGCAACAGTGTTCATCACT 696

RESULT 8

CF479802/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF479802 669 bp mRNA linear EST 08-SEP-2003
RTMW3_12_D02_b1_A022 Well-watered loblolly pine roots WM3 Pinus taeda cDNA clone RTMW3_12_D02_A022 3', mRNA sequence.
CF479802 GI:34508671
EST.
Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 669)
Gebremedhin, M., Derwinis, C., Martin, T., White, T., Davis, J., Cannon, R., Owen, A. and Neale, D.
EST database from well-watered loblolly pine (*Pinus taeda*) roots
Unpublished (2003)
Other ESTs: RTMW3_12_D02_g1_A022
Contact: Cordomier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAAACGACGCGCAGT)
POLYA=No.

FEATURES

source

Location/Qualifiers
1..669
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTMW3_12_D02_A022"
/lab_host="DH108-T1 phage-resistant E. coli"
/clove_lib="Well-watered loblolly pine roots WM3"
/notes="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI. The library was prepared from polyA+ RNA from loblolly pine (*Pinus taeda*) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 20.5%; Score 413; DB 14; Length 669;
Best Local Similarity 76.1%; Pred. No. 3.3e-63;
Matches 509; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 994 GGAAGAAGCTGGGTTCTCTGAGATGACCTTCTGTCGATCGTCAAGTGAAGTACTACG 1053
 DB 669 GGAAGAATATGATGATCCCTGAAATTAACATTTCTACGGCATGTCAGTGGAAATCTAC 610
 QY 1054 CTTTGCTGCTCCGATGATGCGTTCGAGCTCAACATTTGATTCAGATCGGCTTTACCA 1113
 DB 609 CTTTATGACAGCTTGATGCAATATGATCTTAACATTTGCGTTTCGATGAGATTTGGTA 550
 QY 1114 AGATGCTCATCTTATACAGGCTTTGACGACATGATGACGCTTTGGCAGATGACG 1173
 DB 549 AAATAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
 QY 1174 AGCTGGAATCTTCAACGCGAATTAAGATGAGATGCGGCGGATGGAATGCTTC 1233
 DB 489 AGCTCAATCTTTAAACCGACGCTTTAAAGATGAGATGCGGCTTCAAGATGATCTTC 430
 QY 1234 CAGATATATGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1293
 DB 429 CAGATATATGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 370
 QY 1294 TGCGAGAGAGCTTCAAGGCGGAGACAGCTTCAACTATGACAGACAGCTTTGGAGGCT 1353
 DB 369 AGCGGCAAAATTCAGAGCTGGGATGATGATGATGATGATGATGATGATGATGATGAT 310
 QY 1354 GTTTGATGCTTATGAG 1413
 DB 309 TTATTTGCTTAT 250
 QY 1414 AGAGATCTTGAAG 1473
 DB 249 ACAGATCTTGAAG 190
 QY 1474 TTCTGAGCTTGACATCT 1533
 DB 189 TGCTGATCTTGGGCTTCT 130
 QY 1534 AGCTCATGATCTTAT 1593
 DB 129 AATTCATGATCTTAT 70
 QY 1594 CAGACAGGCGCGCTGAG 1653
 DB 69 CTGACAGGCGCGCTGAG 10
 QY 1654 GATTACCG 1662
 DB 9 GAATTAACG 1
 RESULT 9
 CF663845
 LOCUS
 DEFINITION
 RTCTNT_5_B08_A029 Root control Pinus taeda cDNA clone
 RTCTNT_5_B08_A029 5', mRNA sequence.
 CF663845
 ACCESSION
 CF663845.1 GI:37561088
 VERSION
 EST.
 SOURCE
 Pinus taeda (loblolly pine)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (base 1 to 616)
 Pratic.L., Cordonnier-Pratic.M.-M., Lorenz.W.W., Zimmermann.C. and
 Dean.J.F.D.
 An EST database from untreated loblolly pine (Pinus taeda) roots
 Unpublished (2003)
 Other ESTs: RTCTNT_5_B08_A029
 Contact: Cordonnier-Pratic.M.M.
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860

Fax: 706 583 0210
 Email: mmpatric@uga.edu
 RNA prepared and library constructed by W. Walter Lorenz (School of
 Forest Resources, University of Georgia); plant material prepared
 by Craig Zimmermann (School of Forest Resources, University of
 Georgia) using rooted cuttings provided by the Forest Biology
 Research Cooperative (FBRC) and the CCIONES project at the
 University of Florida; sequencing done in the laboratory for
 Genomics and Bioinformatics, University of Georgia. Sequence ends
 have been trimmed to exclude vector and regions below phred quality
 16. Three-prime sequences are presented as their reverse complement
 and have been trimmed to exclude polyA.
 Seq primer: JENREV (CAGGAAACAGCTATGAC).
 FEATURES
 source
 location/qualifiers
 1..616
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="3 CCIONES"
 /db_xref="taxon:3352"
 /clone="RTCTNT_5_B08_A029"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_id="Root control"
 /note="Organ: root; Vector: pSL180; Site 1: EcoRI;
 Site 2: XhoI; The library was prepared from polyA+ RNA
 from the roots of 1-year-old loblolly pine (Pinus taeda)
 cuttings that were rooted and then planted in washed sand.
 Just before harvesting roots for RNA isolation, the rooted
 cuttings were maintained for 27 days (April 2003) under
 ambient conditions in a local greenhouse. They were kept
 on a weekly regimen of 0.5x nutrient-complete Hoagland's
 solution and supplemented with additional water sufficient
 to maintain a 15% soil moisture content. Double-stranded
 cDNA was cloned unidirectionally into pSL180. Inserts can
 be excised with EcoRI (5' end) and XhoI (3' end)."
 ORIGIN
 Query Match
 Best Local Similarity 78.7%; Pred. No. 7.8e-61;
 Matches 477; Conservative 0; Mismatches 123; Indels 0; Gaps 0;
 QY 890 TAAATTAAGAGCGCGCGAGAACTTTTGAACCTTGCAAAATTTGAAATTCATATAT 949
 DB 11 TAAAGCAGCAGACCAAGACCGAAGCTTTTGAACCTTGCAAAATTTGAAATTCATATCT 70
 QY 950 TCACCTCTTAAAGAGAGAGAGATTTAAACATGTTTCCGATGAGTGAAGAGCTGGGCTT 1009
 DB 71 TCACCTCTTAAAGAGAGAGATTTAAACATGTTTCCGATGAGTGAAGAGCTGGGCTT 130
 QY 1010 TCCTGAGATGACCTTCTGTCGATCGTCAAGTGAATTAAGCTTTGGCTTCGAT 1069
 DB 131 CTCCTCACTGACATTCCTGCGCATTCGTCAGTGAATTTCTACATTTGGCTTCGAT 190
 QY 1070 TGCGTTGAGCGCTTCAACATTTGATTCAGCTCGGCTTTTCAAGATGCTCATCTTAT 1129
 DB 191 TGCCACGAGCGCCCAAAACATTCAGCATTCAGATGAGCTTTCCAAAAGCTGTATCTTGG 250
 QY 1130 CACGCTTTTAAAGCAGATGACAGCTTTTGGCAGACAGTGAAGAGCTGGAACCTTTAC 1189
 DB 251 AATAGTTCTGAGCAGCATATATGACATTTTGGAAACATGAGAGAGCTCGAATCTTAC 310
 QY 1190 AGCGCAATTAAGAGATGAGATCGTCCGAGATGGAATGCTTCAGATATATGAAGG 1249
 DB 311 AGCGCAATTAAGAGATGAGATCGTCCGAGATGGAATGCTTCAGATATATGAAGG 370
 QY 1250 AGTGTACATGATGTTTATACACACCGTAATGAAGATGCTCGAGTGCAGAGAGCTCA 1309
 DB 371 CATATATATGATGTTTATGATGATGCTTGAATCAATGCTGAGAGGCGGAGAGAGCTCA 430
 QY 1310 AGCGCGAGACAGGCTCAACTATGAGACAGCTTTGGAGGCGGCTTTGATGATAT 1369
 DB 431 AGCGCGAGACAGGCTCAACTATGAGACAGCTTTGGAGGCGGCTTTGATGATGAT 490
 QY 1370 GCAGGAGCAATGTGATGCGCACTGTATCTGCCACGTTTGAAGAGATCTTGAGAA 1429

Db 491 GGAAGAGCAAGGATGTCACGGGTTATATACCAAGTTGAGGATATTGGAGAA 550
 Qy 1430 CGGGAAGTTAGCTCTGCTATCGCCATGCGCACTGCAACCCATTCTGAGCTTGACAT 1489
 Db 551 CGGGAAGTGAAGTTTGGATTCAGCAGCAGCACTGCAACCCATTCTGAGCTTGATAT 610
 Qy 1490 CCCCTT 1495
 Db 611 TCCCTT 616

RESULT 10
 LOCUS B0698077
 DEFINITION B0698077 516 bp mRNA linear EST 07-MAY-2003
 NXPV_064_C05_F_NXPV (Nef Xylem Planings wood Vertical) Pinus taeda
 cDNA clone NXPV_064_C05 5' similar to Arabidopsis thaliana sequence
 Atg161680 hypothetical protein see
 http://mips.gsf.de/proj/thai/db/index.html, mRNA sequence.
 B0698077
 B0698077.1 GI:21823393

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Pinus taeda (loblolly pine)
 Pinus taeda
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 516)

REFERENCE
 Sederoff, R.
 Molecular Basis of Wood Formation in the Pine Megagenome
 Unpublished (2000)
 Contact: Sederoff, Ron
 Forest Biotechnology
 North Carolina State University
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
 NC 27695, USA
 Tel: 919 515 7800
 Fax: 919 515 7801
 Email: ron.sederoff@ncsu.edu, jerry.johnson@ncsu.edu
 Please see http://web.ahc.umn.edu/biodata/rsfline/ for further
 information.

FEATURES
 source
 Seq primer: T3.
 Location/Qualifiers
 1..516

/organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXPV_064_C05"
 /issue_type="Xylem"
 /cell_type="Planings (secondary)"
 /dev_stage="Transitional"
 /lab_host="XLI-Blue"
 /clone_lib="NXPV (Nef Xylem Planings wood Vertical)"
 /note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:
 XhoI; The library is from early (spring) secondary wood,
 taken from a ten year old tree in the transitional phase.
 The tree is a kind gift of the Westvaco Corporation.
 Secondary xylem was harvested from the tree by peeling
 back the bark and primary xylem and then removing the
 underlying tissue with a block plane. NOTE: The sequences
 contain a 'cDNA adapter' between the EcoRI site and the
 start of the EST. The adapter sequence is
 'AATTCGACGAG'."

ORIGIN

Query Match 19.3%; Score 388.6; DB 13; Length 516;
 Best Local Similarity 84.7%; Pred. No. 7.3e-59;
 Matches 436; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 1353 TGTGTGATGCTATGACAGCAAGGATCGCAGCTGATATCGCCACGTTT 1412
 Db 2 TATATTGATGCTATGACAGCAAGGATCGCAGCTGATATCGCCACATTT 61

Qy 1413 GAGGAGTACTTGAGAAACGGAAAGTTAGCTTGTCTATCGCCAGCCGACCTGCAACCC 1472
 Db 62 GAGGAGTACTTGAGAAACGGAAAGTTAGCTTGTCTATCGCCAGCTGCAACCC 121
 Qy 1473 ATTCTGACGTTGACATCCCTTTTCTGATCAATCTCTCAAGAAAGTTGACTTCCCATCG 1532
 Db 122 ATTTTGAACGACGACATCCCTTTTCTGACACGCTCTCAAGAAAGTTGACATTCATCG 181
 Qy 1533 AAGCTCAATGACTTGATATGATATCATCTTGAATTAAGAGGTGATACAGGCTGTACAAG 1592
 Db 182 CAGCTCAATGACTTGATATGATATCATCTTGAATTAAGAGGTGATACAGGCTGTACAAG 241
 Qy 1593 GCAGACAGGCGCGGTGAGAAAGCTTGTCTATATCATGTTATATGAAAGCAATCTT 1652
 Db 242 CGGACAGAGGCGCGGTGAGAAAGCTTGTCTATATCTTGTATATGAAAGCAATCTT 301
 Qy 1553 GGATTAACGGAAGAAAGTGTCTGAAATCATATCAATCTTCAAGTACAGGAGCGCAATGCA 1712
 Db 302 GGAACAAACAGAGAAAGTGTCTGAAATCATATCTCAAGCAATGATCAATGATGATTA 361
 Qy 1713 GAATTAATGGAGAGCTTCTAAAGCCAGACACAGTGTCCCATCTTCCAAAGAAACAC 1772
 Db 362 GATTAATGGAGAGCTTCTCAACCAACAGCAGCTTCCCATATCTGCCAABAAAACAT 421
 Qy 1773 GCATTTGACATTAACAGAGTTTGACATCAGGTTACAGATACCGAGATGCTACAGCTTT 1832
 Db 422 GCTTTGACATTAACAGAGCTTTCATTTGAGGTCACAAATATGAGATGCTACAGCTTT 481
 Qy 1833 GCCAAGCTTGAACAAAGACTTTGTGATGAGAAC 1867
 Db 482 GCCAAGCTTGAACAAAGACTTTGTGAGAGAAC 516

RESULT 11
 LOCUS B677624 517 bp mRNA linear EST 28-OCT-2003
 DEFINITION B677624 RN Pinus pinaster cDNA clone RN42B08, mRNA sequence.
 ACCESSION B677624
 VERSION B677624.1 GI:38011576
 KEYWORDS
 SOURCE
 ORGANISM
 Pinus pinaster
 Pinus pinaster
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 517)
 Frigerio, J. and Plimion, C.
 Identification of water-deficit responsive genes in Maritime pine
 (Pinus pinaster Ait.) using an EST approach
 Unpublished (2002)
 Contact: Frigerio JM
 Genetique et Amelioration 69
 INRA

route d'Arcachon 33612 Cestas CEDEX France
 Email: Frigerio@pierrot.inra.fr
 Email: Frigerio@pierrot.inra.fr
 Seq primer: T3.
 Location/Qualifiers
 1..517

/organism="Pinus pinaster"
 /mol_type="mRNA"
 /db_xref="taxon:71647"
 /clone="RN42B08"
 /issue_type="root"
 /dev_stage="6 weeks old seedling"
 /lab_host="SOLR"
 /clone_lib="RN"

/note="Vector: Uni-ZAP XR, ecotype: Landes; The library
 was made from the roots of 6 weeks old seedlings grown in
 hydroponic conditions. A mixture of genotypes were used.
 Oligo-dT primed cDNA was directionally cloned into the
 EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form
 a Bluescript phagemid"

ORIGIN

Db 658 AGAAGAGATAGAGATGTCCTCAATTAATTCGGGCAATCTCTCATGTGCTTCTCGG 717
Qy 710 CGAAGAAATTAATGATGAAGTGAACATTTCTTCAACAAAATTTAAGAGAGCCCTGCA 769
Db 718 CGAAAAATTAATGAGCGCGCTGAATCTTCTTCAATGATTAATTAAGATGCTTACA 777
Qy 770 AAAGATCCGGCATCCAGTAT 790
Db 778 AAAGATCCGGCTTCCGCTCT 798

RESULT 13
LOCUS AL750951 481 bp mRNA linear EST 20-JUN-2002
DEFINITION AL750951 RS Pinus pinaster cDNA clone RS02D01 similar to PINENE
SYNTHASE, mRNA sequence.
ACCESSION AL750951
VERSION AL750951.1 GI:21492198
KEYWORDS EST.
SOURCE pinus pinaster
ORGANISM pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 481)
Frigerio, J. and Plomion, C.
Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
JOURNAL Unpublished (2002)
COMMENT Contact: Frigerio JM
Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pietroton.inra.fr
Seq primer: T3.
Location/Qualifiers
1. .481
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS02D01"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_id="R8"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A three weeks drought stress
treatment was applied by lowering the osmotic potential of
the nutrient solution to -0.45 Mpa using 170 g/l of
polyethylene glycol as an osmoticum. A mixture of
genotypes were used. Oligo-dT primed cDNA was
directionally cloned into the EcoRI-XhoI lambda-ZAP vector
arms and mass-excised to form a pinuscript phagemid"

ORIGIN
Query Match 18.7%; Score 376; DB 9; Length 481;
Best Local Similarity 86.5%; Pred. No. 1.3e-56;
Matches 415; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1038 CACGTGGAATTAACGCTTGGCTTCTGATTCGCTTGAAGCTCAATTCGTGATTC 1097
Db 2 CACGTGAGATTAACATTTGCTTCTGATTCGCTTGAAGCTCAATTCGTGATTC 61
Qy 1098 AGATCTGGCTTACCAAGATGTCATTTATCAAGGTTCTTGAACGATGTAGAGCTC 1157
Db 62 AGACTCGGCTTTGGAAGCGTGTCAATTAATTCATCTTCTCGAAGATATAGCACTC 121
Qy 1158 TTGGGACAGTAGAGCAAGCTTCAAGCTTCAAGCAATTAAGAGATGGATCCGCTC 1217
Db 122 TTGGAAACAGTTGATGAGCTCAAACTGTTCAAGCCGCAATTAAGATGGATCCGCTC 181
Qy 1218 GCGATGGAATGCCCTTCAGAAATATATGAAGAGATGTACATGATGTTTATCACACCGTA 1277

Db 182 GCCACAGATTCCTTCACATATATATAAGAAATTAATGATGTTTACACACCGTA 241
Qy 1278 AATGAATGCTCGAGTGGAGAGAGCTCAAGGCCGAGACCGCTCACTATGACAGA 1337
Db 242 AATGAATGCTCGAGTGGAGAGAGCTCAAGGCCGAGACCTCACTATGATGCTGCA 301
Qy 1338 CAGGCTTGGAGAGCGTGTGTTGATTCGTATATGACAGAACAAAGTGATCGCCACTGT 1397
Db 302 CAGGCTTGGAGAGATTAATCTTGATTCGTATATGAAACAAAGTGATGACAGCGGT 361
Qy 1398 TATTCGCCACGTTTGAAGAGTACTTGAGAACGGGAAAGTTAGCTTGCTCATCGCCA 1457
Db 362 TATTCGCCACGTTTGAAGAGTACTTGAGAACGGGAAAGTTAGCTTGAGGATCGGCTG 421
Qy 1458 TGGGCACTGCAACCATTCGAGTTGAGATCCCTTCTGATGATCATCTCAAGAA 1517
Db 422 TGGGCTTGCACCACTGACATGAGATGCCATCCCTTCTCTCTCAATCTCAAGAA 481

RESULT 14
LOCUS CF477562/ 740 bp mRNA linear EST 08-SEP-2003
DEFINITION RTW03_8_G10_G1_A022 well-watered loblolly pine roots WM3 Pinus
taeda cDNA clone RTW03_8_G10_A022 5', mRNA sequence.
ACCESSION CF477562
VERSION CF477562.1 GI:34506431
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 740)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Devrins, C., Martin, T., White, T., Davis, J. and
Neale, D.
An EST database from well-watered loblolly pine (Pinus taeda) roots
Unpublished (2003)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmprratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGAC).
Location/Qualifiers
1. .740
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CLONES"
/db_xref="taxon:3352"
/clone="RTW03_8_G10_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from polyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 Mpa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL1180. Inserts
excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN
Query Match 18.6%; Score 375; DB 14; Length 740;
Best Local Similarity 76.1%; Pred. No. 1.6e-56;

Matches	462;	Conservative	0;	Mismatches	145;	Indels	0;	Gaps	0;
QY	1307	TCGAAGCCGAGACAGCTCAATATGACAGAGCTTGGAGGCGTGTGATTCGTA	1366						
Db	740	TCGAAGCTGGGATACAGTCACTATGCTGAAAAATCTTGGAGGCTTATATGGGCTTA	681						
QY	1367	TATCAGAGAACCAAGTGGATCGCACAGTGTATCTGCCACGTTGGAGAGTCTTGG	1426						
Db	680	TATACAGAGAACCAAGTGGATTCGAGTGTATCTTCCACGTTGACGAGTACCTTGA	621						
QY	1427	GAACGGGAAAGTATAGCTCTGCTCATCGCCCATGCGCACTGCACATCCATTCGACCTTGA	1486						
Db	620	GAATGGAGAGTACAGCTTCGGCTCTCGCATACACGCTCGAACCCATGCTGACTTGG	561						
QY	1487	CATCCCTCTTCTGATCATCATCTTCAAGAAAGTGTACCTTCCCATGCAAGCTCATGACTT	1546						
Db	560	GTTCCTCTTCTCGCTCGATCTGCAAGAAATGACTTCCATGCAATTCATGATTT	501						
QY	1547	GATATGATCATCTCTTCATTAAGAGTGTATACAGGCTGACAGGAGGAGGAGGAGG	1606						
Db	500	GATATGCTCATCTCTTCATTAAGAGTGTATACAGGCTGACAGGAGGAGGAGG	441						
QY	1607	TGGAAGAAAGCTTCTATATATCATGTTATATGAAGCAATCTTGATTAACGAGGA	1666						
Db	440	TGGAAGAAAGCTTCTGAGGCTGATCTGTTATATGAAGCAATCTTGATTAACGAGGA	381						
QY	1667	AGATGCTCTGATCATATCACTTCATGATGAGGAGGAGGAGGAGGAGGAGGAGG	1726						
Db	380	AGATGCTCTGATCATATCACTTCATGATGAGGAGGAGGAGGAGGAGGAGGAGG	321						
QY	1727	GCTTCTAAGCCACACACAGTGTCCCATCTTCCAGAAACGCAATTTGACATAG	1786						
Db	320	GTTACTTATAGACCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	261						
QY	1787	CAGAGTTGGATCAGCTTACAGATACGAGATGCTTACAGCTTGGCAAGTGAAC	1846						
Db	260	CAGAGTTGGATCAGCTTACAGATACGAGATGCTTACAGCTTGGCAAGTGAAC	201						
QY	1847	AAAGAGTTGGTGTATGAGAACCGTTCATTGAACCTTGCTTTGTAACAACCTTCAATC	1906						
Db	200	AAAGAGTTGGTGTATGAGAACCGTTCATTGAACCTTGCTTTGTAACAACCTTCAATC	141						
QY	1907	TACATA 1913							
Db	140	TACATA 134							

RESULT 15

AM287756

LOCUS AM287756 539 bp mRNA linear EST 07-JAN-2000
 DEFINITION EST0004 Sitka spruce drill-wounded bark Picea sitchensis cDNA clone
 25-1-3 5' similar to mono-terpene synthase, mRNA sequence.

ACCESSION

AM287756

VERSION

AM287756.1

KEYWORDS

EST.

SOURCE

ORGANISM

Picea sitchensis (Sitka spruce)

Picea sitchensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1 (bases 1 to 539)

Wang, S.X., Hunter, W. and Plant, A.L.

Isolation of terpene synthase gene-specific probes from Sitka

spruce and induction of gene expression by simulated white pine

weevil damage

Unpublished (2000)

Contact: Wang SX

Department of Biological Sciences

Simon Fraser University

8888 University Drive, Burnaby, BC V5A1S6, Canada

Tel: 604 584 8870

Fax: 604 584 8873

Email: sxwang@sfufoot.com

Clone sequence of a RT-PCR product from the mRNA of drill-wounded

Bark tissue
 PCR primers
 FORWARD: M13-F10
 BACKWARD: M13-R18
 Insert Length: 539 Sld Error: 0.00
 Seq primer: M13/Reverse and M13 Forward.
 High quality sequence stop: 539.
 Location/Qualifiers
 1..539
 /organism="Picea sitchensis"
 /mol_type="mRNA"
 /db_xref="taxon:3332"
 /clone="25-1-3"
 /csize_type="bark"
 /clone_id="Sitka spruce drill-wounded bark"
 /note="mRNA isolated from drill-wounded bark tissues;
 RT-PCR product"

Query Match 17.5%; Score 352.4; DB 10; Length 539;
 Best Local Similarity 79.1%; Pred. No. 1.8e-52;
 Matches 419; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY	1135	TTCTTGACGACATGACAGCTCTTGGGACAGTAGACGAGCTGGAATCTTTCACAGGA	1194						
Db	1	TGCTCGAGACCTGTACGACATTCGGACACATGACGAGAAATGAACTCTTCACAGAG	60						
QY	1195	CAATTAAGATGAGATCGCTCGCGATGAGATGCTTCAGAAATATGAAAGAGTGT	1254						
Db	61	CAGTCAGAGATGAGATCGCTCGCGATGAGATGCTTCAGAAATATGAAAGAGTGT	120						
QY	1255	ACATGATGTTTACACACGCTTAATGAAATGCTTCGATGAGGACGAGAAAGCTCAAGCC	1314						
Db	121	ACATGATGTTTACACACGCTTAATGAAATGCTTCGATGAGGACGAGAAAGCTCAAGCC	180						
QY	1315	GAGACAGCTCAATGACAGACAGGCTTGGAGAGCGTGTGATTCGTATATGACAG	1374						
Db	181	GAGACAGCTCAATGACAGACAGGCTTGGAGAGCGTGTGATTCGTATATGACAG	240						
QY	1375	AAGCAAGTGGATGCGCATGTTATCTGCGACGTTGAGAGTACTTGGAGAACGGGA	1434						
Db	241	AAGCAAGTGGATGCGCATGTTATCTGCGACGTTGAGAGTACTTGGAGAACGGGA	300						
QY	1435	AAGTATGCTTGTATCGCCATGCGACATGCAACCATCTGACATTCCTCCCT	1494						
Db	301	AAGTATGCTTGTATCGCCATGCGACATGCAACCATCTGACATTCCTCCCT	360						
QY	1495	TTCTGATCAGATCTTCAAGAGATGACTTCCATCGAAGCTCAATGATGATGTA	1554						
Db	361	TTCTGATCAGATCTTCAAGAGATGACTTCCATCGAAGCTCAATGATGATGTA	420						
QY	1555	TCATCTTGTGATTAAGAGTGTATACAGGCTTCAAGGACAGACAGGCGCCGTGAGAG	1614						
Db	421	CTTCTCTTGTGATTAAGAGTGTATACAGGCTTCAAGGACAGACAGGCGCCGTGAGAG	480						
QY	1615	AAGCTTGTCTATATCATGTTATATGAAGCAATCTCGATTTAACGGA	1664						
Db	481	AAGCTTGTCTATATCATGTTATATGAAGCAATCTCGATTTAACGGA	530						

Search completed: July 26, 2004, 13:44:34
 Job time : 4687 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 09:01:22 ; Search time 19 Seconds
(without alignments)
1679.203 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251

Sequence: 1 MALSTIPLVSRGCLSSSHR.....FANVETSLVWRTYIEPVPL 618

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patente AA: *
2: /cgn2_6/ptodata/2/1aa/5A-COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/5B-COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6A-COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/6B-COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/6CTUS-COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3251	100.0	618	US-09-360-545-65	Sequence 65, Appl
2	2453	75.5	628	US-09-360-545-4	Sequence 4, Appl
3	2453	75.5	628	US-09-398-395A-20	Sequence 20, Appl
4	2453	75.5	628	US-09-887-586A-20	Sequence 20, Appl
5	2453	75.5	628	US-09-895-752-20	Sequence 20, Appl
6	2453	75.5	628	US-09-903-012B-20	Sequence 20, Appl
7	2453	75.5	628	US-09-900-797-20	Sequence 20, Appl
8	2264	69.6	630	US-09-360-545-67	Sequence 67, Appl
9	2200.5	67.7	627	US-09-360-545-2	Sequence 2, Appl
10	2200.5	67.7	627	US-09-398-395A-30	Sequence 30, Appl
11	2200.5	67.7	627	US-09-887-586A-30	Sequence 30, Appl
12	2200.5	67.7	627	US-09-895-752-30	Sequence 30, Appl
13	2200.5	67.7	627	US-09-903-012B-30	Sequence 30, Appl
14	2200.5	67.7	627	US-09-900-797-30	Sequence 30, Appl
15	2197.5	67.6	627	US-09-360-545-32	Sequence 32, Appl
16	2137	65.7	630	US-09-360-545-78	Sequence 78, Appl
17	2084.5	64.1	637	US-09-360-545-69	Sequence 69, Appl
18	2031.5	62.5	637	US-09-360-545-6	Sequence 6, Appl
19	2031.5	62.5	637	US-09-398-395A-58	Sequence 58, Appl
20	2031.5	62.5	637	US-09-887-586A-58	Sequence 58, Appl
21	2031.5	62.5	637	US-09-895-752-58	Sequence 58, Appl
22	2031.5	62.5	637	US-09-903-012B-58	Sequence 58, Appl
23	2031.5	62.5	637	US-09-900-797-58	Sequence 58, Appl
24	1295.5	39.8	580	US-09-234-393-48	Sequence 48, Appl
25	1295.5	39.8	580	US-09-865-171-48	Sequence 48, Appl
26	1295.5	39.8	581	US-09-234-393-20	Sequence 20, Appl
27	1295.5	39.8	581	US-09-234-393-46	Sequence 46, Appl

28	1295.5	39.8	581	US-09-865-171-20	Sequence 20, Appl
29	1295.5	39.8	581	US-09-865-171-46	Sequence 46, Appl
30	1295.5	39.8	581	US-09-398-395A-48	Sequence 48, Appl
31	1295.5	39.8	581	US-09-887-586A-48	Sequence 48, Appl
32	1295.5	39.8	581	US-09-895-752-48	Sequence 48, Appl
33	1295.5	39.8	581	US-09-903-012B-48	Sequence 48, Appl
34	1295.5	39.8	581	US-09-900-797-48	Sequence 48, Appl
35	1291.5	39.7	581	US-09-234-393-44	Sequence 44, Appl
36	1291.5	39.7	581	US-09-865-171-44	Sequence 44, Appl
37	1250.5	38.5	577	US-09-360-545-18	Sequence 18, Appl
38	1240.5	38.2	862	US-09-315-861-2	Sequence 2, Appl
39	1240.5	38.2	862	US-09-398-395A-44	Sequence 44, Appl
40	1240.5	38.2	862	US-09-887-586A-44	Sequence 44, Appl
41	1240.5	38.2	862	US-09-895-752-44	Sequence 44, Appl
42	1240.5	38.2	862	US-09-903-012B-44	Sequence 44, Appl
43	1240.5	38.2	862	US-09-900-797-44	Sequence 44, Appl
44	1240.5	38.2	862	US-09-234-393-24	Sequence 24, Appl
45	1231	37.9	593	US-09-234-393-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1					
US-09-360-545-65					
Sequence 65, Application US/09360545					
Patent No. 6429014					
GENERAL INFORMATION:					
APPLICANT: Crocneau, Rodney B					
APPLICANT: Bohlmann, Jörg					
APPLICANT: Steele, Christopher L					
APPLICANT: Phillips, Michael A					
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)					
FILE REFERENCE: waur1385					
CURRENT FILING DATE: 1999-07-26					
EARLIER APPLICATION NUMBER: 60/052,249					
EARLIER FILING DATE: 1997-11-07					
EARLIER APPLICATION NUMBER: PCT/US98/14528					
EARLIER FILING DATE: 1998-07-10					
NUMBER OF SEQ ID NOS: 107					
SOFTWARE: Patentin Ver. 2.0					
SEQ ID NO 65					
LENGTH: 618					
TYPE: PRT					
ORGANISM: Abies grandis					
US-09-360-545-65					
Query Match					
Best Local Similarity 100.0%; Score 3251; DB 4; Length 618;					
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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QY	61	VGNHNSIMLMDDDFQSLSTPYGAPDVRERADRLIGVKDITMPFKSLDEGNDLQRL			120
DB	61	VGNHNSIMLMDDDFQSLSTPYGAPDVRERADRLIGVKDITMPFKSLDEGNDLQRL			120
QY	121	LVDDVERLGDHFKKEIKTALDVNSYMNKGI	CGGRESVVTJLNSLTALGRLRLHGY		180
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DB	181	TVSSDVINVFQKQGFSSSTANIQIEGIRGVNL	FRASLVAFPGEKVMDEAFETSTYLL		240
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DB	241	REALQKTPASSLSLEIRDVLEVGMHTNLPRLERANVMDVGGQHTKNNAAEKLLTAKL			300
QY	301	EFNIFHSIQERELRGVSRWMDSGSPENTFCRRHREVEYVALASCIAREPHSGFRLGFTK			360

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Db 361 MSHIITLDMYDVGTVDELFTATIKRWDPSAMECLPEYMGVYMMVHTVTEMARV 420
Qy 421 AEKAGSDTLNVAQAEACFDSYMOEAKWIATGYLPTFEEYLENGKVSASHPCALOPI 480
Db 421 AEKAGSDTLNVAQAEACFDSYMOEAKWIATGYLPTFEEYLENGKVSASHPCALOPI 480
Qy 481 LTTDIPPPDHILKEVDPSPKINDLICIILRLGDTRCYKADRANGEEASSISCYMKONGP 540
Db 481 LTTDIPPPDHILKEVDPSPKINDLICIILRLGDTRCYKADRANGEEASSISCYMKONGP 540
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Db 541 LTERDALNHINFMRDALRELNMELKPDNSVPTTSKHAADISRVMHGYRBDGYSFA 600
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Db 601 NVETKSLVMRTVIBPVL 618
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RESULT 2
US-09-360-545-4
; Sequence 4, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wgrt13885
; CURRENT APPLICATION NUMBER: US/09/360, 545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052, 249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-360-545-4
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Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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Qy 113 --NDLQRLLLVNDVERLGIIDRHFKKEIKTALDVYNSYMNKKGICGGRSVVTDLNSTAL 170
Db 119 PLNDLIQRLMIVDSLERLGIHRHFKDEIKSALDVYYSWGENGIGCGRESVVTDLNSTAL 178
Qy 171 GLRTLRLHGYTVSSDVLVNFKDKNGQFSSSTANIQIEBEGIRGVNLFPASLVAFGEKMD 230
Db 179 GLRTLRLHGYTVSSDVLFKAFKQNGQFSSCENIOTDEIRGVNLFPASLVAFGEKMD 238
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Db 358 EPOHSGFRLGFTKMSHIIYVLDDMYDVGTVDELFTATIKRWDPSAMECLPEYMGVY 417
Qy 408 MMYHTVTEMARVAEKOQSDTLNVAQAEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
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Db 478 VSCGRISALOPIITLTDIPPPDHILKEVDPSPKINDLICALRLRGDTRCYKADRANGEE 537
Qy 528 ASSISCYMKONGPGLTTEEDALNHINFMRDALRELNMELKPDNSVPTTSKHAADISRVM 587
Db 538 ASSISCYMKONGPGESEBDALDHINAMISDVIKGNMELKPDINVPISAKHAPDIARAF 597
Qy 588 HHGYRBDGYSFANVETKSLVMRTVIBPVL 618
Db 598 HHGYRBDGYSFANVETKSLVTRTLESVPL 628
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RESULT 3
US-09-398-395A-20
; Sequence 20, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398, 395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100, 993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130, 628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150, 262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-398-395A-20
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Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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Qy 408 MMVHTNEMARVAKOGRDTLYARQWACFDSYQOBAKWTATGCLPFEYELENGK 467
Db 418 IAVDTNEMAREBEAOGRTLYARQWACFDSYQOBAKWTATGCLPFEYELENGK 477
Qy 468 VSSARPCALOPILTLDPFPDHLKEVDPSKNDLICIILRLRGDTRCYKADARAGEE 527
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Qy 588 HHGRYRDGYSFANVETKSLVMRTVIEBPVL 618
Db 598 HHGRYRDGYSFANVETKSLVMRTVIEBPVL 628
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RESULT 4
US-09-887-586A-20

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; Sequence 20, Application US/09887586A
; Patent No. 649354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P.
; APPLICANT: No. 6493541, Joseph P.
; APPLICANT: Starkes, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTBASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
; US-09-887-586A-20
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Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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Qy 113 --NDLLQRLLVDDVERLIGIRHFKKEIKTALDVNSYWNKKGICGGRSVVTDLNSAL 170
Db 119 PLNPLIQGLMVLVDSEIRGIRHFKKEIKTALDVNSYWNKKGICGGRSVVTDLNSAL 178
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Qy 291 ---AEKLELAKLEAFENIFSHLOERELKHSRWKDSGSEMTFCRHRHVEYALASCIAP 347
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Qy 348 EPOHSGRGLGTGKSHLITVLDMDYVGTDELELFTATIKRNDPSAMECLPEYMKGV 407
Db 358 EPOHSGRGLGTGKSHLITVLDMDYVGTDELELFTATIKRNDPSAMECLPEYMKGV 417
Qy 408 MMVHTNEMARVAKOGRDTLYARQWACFDSYQOBAKWTATGCLPFEYELENGK 467
Db 418 IAVDTNEMAREBEAOGRTLYARQWACFDSYQOBAKWTATGCLPFEYELENGK 477
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Db 538 ASSISCYKONPGVSEBDALDHINAMISDVIKGLWELLKPDINVPISAKKGAFDIARAF 597
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Db 598 HHGRYRDGYSFANVETKSLVMRTVIEBPVL 628
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RESULT 5
US-09-895-752-20

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; Sequence 20, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P.
; APPLICANT: No. 6559297, Joseph P.
; APPLICANT: Starkes, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTBASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
; US-09-895-752-20
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Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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Db 1 MALVSTAPLASKSCLHSLISSTHEIKALSRITIPALGMSRGRKSTTPISMSSTTVVTD 60
Qy 56 SVORRVGNYSNLWDDDFIOGLISTPYGAPDYRRARDLIGEVDIMNFKSLDGC--- 112
Db 61 GVRRRMGDFHNLWDDDFIOGL-PTAYEEKSYLERAELIGEVRK-MENSMLEDEGELMS 118
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Db 179 GLATRLHGTVSSDVLVNFKDKNGQSSSTANIOIBEGIRGVNLPRASLVAFGEKYM 238
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Db 239 EAETFSKYREALOKIPASSISLSLEIRDVLEYGMHNLPRLEARNYMDVFGQHTKXNA 297
Qy 291 ---AEKLELAKLEFNIFHSLQERELKGVSRWMDSSPEMTFCRHHVHEYTLASCIAP 347
Db 298 YVSKSKLELAKLEFNIFHSLQERELKGVSRWMDSSPEMTFCRHHVHEYTLASCIAP 357
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Qy 408 MMVYHTVNMARVAEKAQGRDITLVNARQAWACFDSYMOEAKWTATGYLPTFEEYLENGK 467
Db 418 IAYVDITNEMAREBEAEOGRDITLVNARQAWACFDSYMOEAKWTATGYLPTFEEYLENGK 477
Qy 468 VSSAHPICALQPIITLIDIPFPDHLKEVDPPSKLNDLICITLRLRGDTRCYKADARAGEE 527
Db 478 VSCGHRISALQPIITLIDIPFPDHLKEVDPPSKLNDLICITLRLRGDTRCYKADARAGEE 537
Qy 528 ASSISCYMKONPGITBEDALNHINFMIRDAIRELWELKPDNSVPTTSKHAADISRWW 587
Db 538 ASSISCYMKONPGITBEDALNHINFMIRDAIRELWELKPDNSVPTTSKHAADISRWW 597
Qy 588 HHGYRYRDGYSFANVETKSLVMRTVIEBPVL 618
Db 598 HHGYRYRDGYSFANVETKSLVMRTVIEBPVL 628
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RESULT 6
US-09-903-012B-20
; Sequence 20, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRN
; ORGANISM: Abies grandis
US-09-903-012B-20
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Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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Db 119 PLNDLIQRLMIVDSLEBLGJHRHFKDEIKSALDYYVSYMGENGICGCRESVTDLNSTAL 178
Qy 171 GLATRLHGTVSSDVLVNFKDKNGQSSSTANIOIBEGIRGVNLPRASLVAFGEKYM 230
Db 179 GLATRLHGTVSSDVLVNFKDKNGQSSSTANIOIBEGIRGVNLPRASLVAFGEKYM 238
Qy 231 EAETFSKYREALOKIPASSISLSLEIRDVLEYGMHNLPRLEARNYMDVFGQHTKXNA 290
Db 239 EAETFSKYREALOKIPASSISLSLEIRDVLEYGMHNLPRLEARNYMDVFGQHTKXNA 297
Qy 291 ---AEKLELAKLEFNIFHSLQERELKGVSRWMDSSPEMTFCRHHVHEYTLASCIAP 347
Db 298 YVSKSKLELAKLEFNIFHSLQERELKGVSRWMDSSPEMTFCRHHVHEYTLASCIAP 357
Qy 348 EPOHSGFRIGPFTKMSHILITVLDMDYDVFCTVDELELFTATIKRWDPSAMGCLPEYMGVY 407
Db 358 EPOHSGFRIGPFTKMSHILITVLDMDYDVFCTVDELELFTATIKRWDPSAMGCLPEYMGVY 417
Qy 408 MMVYHTVNMARVAEKAQGRDITLVNARQAWACFDSYMOEAKWTATGYLPTFEEYLENGK 467
Db 418 IAYVDITNEMAREBEAEOGRDITLVNARQAWACFDSYMOEAKWTATGYLPTFEEYLENGK 477
Qy 468 VSSAHPICALQPIITLIDIPFPDHLKEVDPPSKLNDLICITLRLRGDTRCYKADARAGEE 527
Db 478 VSCGHRISALQPIITLIDIPFPDHLKEVDPPSKLNDLICITLRLRGDTRCYKADARAGEE 537
Qy 528 ASSISCYMKONPGITBEDALNHINFMIRDAIRELWELKPDNSVPTTSKHAADISRWW 587
Db 538 ASSISCYMKONPGITBEDALNHINFMIRDAIRELWELKPDNSVPTTSKHAADISRWW 597
Qy 588 HHGYRYRDGYSFANVETKSLVMRTVIEBPVL 618
Db 598 HHGYRYRDGYSFANVETKSLVMRTVIEBPVL 628
```

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RESULT 7
US-09-900-797-20
; Sequence 20, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/0398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRN
; ORGANISM: Abies grandis
US-09-900-797-20
```

Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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Qy 1 MALISITPIVRSCL-----SSSHEIKALRRTIPTLIGCRGKSVASHINMCLTSTVASTD 55
Db 1 MALVSTAPLASKSGCLHKSLSISTHKLKLSRTIPALGMSRKGKSTPISISMSTTVVTD 60
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QY 56 SVORRVGNHNSNMDDDFIQLSLSTPGADPYREBRADRLIGVYDIMEFKSLDGC--- 112
 DB 61 GVRNRMGHNSNMDDDFIQLSL-STPYGEPSYERAEKLLGEVYE-MFNSMPSDGSMS 118
 QY 113 --NDLORLLVDDVERLIDRHFKEIKTALDYVNSYVNEKIGCGRESVTTDLNSTAL 170
 DB 119 PLNDLORLLVDDVERLIDRHFKEIKTALDYVNSYVNEKIGCGRESVTTDLNSTAL 178
 QY 171 GLRLRLHGYTVSSDVLNFKDKNGQSPSTANIQIEGIRGVNLFRASLVAPGEXKM 230
 DB 179 GLRLRLHGYTVSSDVLNFKDKNGQSPSTANIQIEGIRGVNLFRASLVAPGEXKM 238
 QY 231 EAETFTKYLREALOKIPASSISLEIRVLEYGHTNLPRLARNYMDVFGHTKXNA 290
 DB 239 EAETFTKYLREALOKIPASSISLEIRVLEYGHTNLPRLARNYMDVFGHTKXNA 297
 QY 291 ---AEKLELAKLEBNIFHSLOERELKHSRWKMGSGSPMTFCHRHVEYVALASCIAP 347
 DB 298 YVRSKLLLELAKLEBNIFHSLOERELKHSRWKMGSGSPMTFCHRHVEYVALASCIAP 357
 QY 348 EPOHSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPEYMKGV 407
 DB 358 EPOHSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPEYMKGV 417
 QY 408 MMVHTVNMARVAEAKGGRDTLNYARQAEACFSPSYOEAQWITGTLPTFEYLENGK 467
 DB 418 IAVYDTVNMARVAEAKGGRDTLNYARQAEACFSPSYOEAQWITGTLPTFEYLENGK 477
 QY 468 VSSAHRPCALOPILTLDPDPDLKEVDPPSKNDLICIILRLGDRCYKADRARGE 527
 DB 478 VSCGRHSALOPILTLDPDPDLKEVDPPSKNDLICIILRLGDRCYKADRARGE 537
 QY 528 ASSISCYKNDPGLTEEDALNHNFMIRDAIRELMWELLKPDNSVPTSCKHAFDISRW 587
 DB 538 ASSISCYKNDPGLTEEDALNHNFMIRDAIRELMWELLKPDNSVPTSCKHAFDISRW 597
 QY 588 HHGVRDGYSPFANVETKSLMRTYIEPVPL 618
 DB 598 HHGVRDGYSPFANVETKSLMRTYIEPVPL 628

RESULT 8
 US-09-360-545-67

; Sequence 67, Application US/09360545
 ; Patent No. 6429014
 ; GENERAL INFORMATION:
 ; APPLICANT: Croceau, Rodney B
 ; APPLICANT: Bohmann, Jorg
 ; APPLICANT: Steele, Christopher L
 ; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 ; FILE REFERENCE: wau13885
 ; CURRENT APPLICATION NUMBER: US/09/360,545
 ; EARLIER FILING DATE: 1999-07-26
 ; EARLIER APPLICATION NUMBER: 60/052,249
 ; EARLIER FILING DATE: 1997-11-07
 ; EARLIER APPLICATION NUMBER: PCT/US98/14528
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 67
 ; LENGTH: 630
 ; TYPE: PRT
 ; ORGANISM: Abies grandis
 US-09-360-545-67

Query Match 69.6%; Score 2264; DB 4; Length 630;
 Best Local Similarity 68.3%; Pred. No. 2.5e-211;
 Matches 435; Conservative 78; Mismatches 98; Indels 26; Gaps 9;
 QY 1 MALSLTPVLSRGL-----SSSHEIKALRRTIPTLIGCRPGKSVASHINMCLTSVAST 54

DB 1 MALVSAP---KSLHKSLSRSTHBLKPLRRTIPTLQMCGRGKSFTPSVMSLTTAVSD 57
 QY 55 DSVORVGNHNSNMDDDFIQLSLSTPGADPYREBRADRLIGVYDIMEFKSLDGC-- 112
 DB 58 DGLORRIGDYNHNSNMDDDFIQLSL-STPYGEPSYERAEKLLGEVYE-MFNSMPSDGSMS 115
 QY 113 --NDLORLLVDDVERLIDRHFKEIKTALDYVNSYVNEKIGCGRESVTTDLNSTAL 169
 DB 116 SPLNDLIRLMMVSSVERLIDRHFKEIKTALDYVNSYVNEKIGCGRESVTTDLNSTAL 175
 QY 170 GLRLRLHGYTVSSDVLNFKDKNGQSPSTANIQIEGIRGVNLFRASLVAPGEXKM 229
 DB 176 SGFRTRLRHGYTVSSDVLNFKDKNGQSPSTANIQIEGIRGVNLFRASLVAPGEXKM 234
 QY 230 DEATFTKYLREALOKIPASSISLEIRVLEYGHTNLPRLARNYMDVFGHTKXNA 285
 DB 235 DEATFTKYLREALOKIPASSISLEIRVLEYGHTNLPRLARNYMDVFGHTKXNA 293
 QY 286 KNKNA---AEKLELAKLEBNIFHSLOERELKHSRWKMGSGSPMTFCHRHVEYVAL 341
 DB 294 KKKRTQYLDSEKLLLELAKLEBNIFHSLOERELKHSRWKMGSGSPMTFCHRHVEYVAL 353
 QY 342 ASCIAFEPHSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPE 401
 DB 354 SSCIAFEPHSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPE 413
 QY 402 YMKGVYMMVHTVNMARVAEAKGGRDTLNYARQAEACFSPSYOEAQWITGTLPTFE 461
 DB 414 YMKGVYMMVHTVNMARVAEAKGGRDTLNYARQAEACFSPSYOEAQWITGTLPTFE 473
 QY 462 YLENGKVSASARPCALOPILTLDPDPDLKEVDPPSKNDLICIILRLGDRCYKAD 521
 DB 474 YLENGKVSASARPCALOPILTLDPDPDLKEVDPPSKNDLICIILRLGDRCYKAD 533
 QY 522 RARGEASSISCYKNDPGLTEEDALNHNFMIRDAIRELMWELLKPDNSVPTSCKHAF 581
 DB 534 RARGEASSISCYKNDPGLTEEDALNHNFMIRDAIRELMWELLKPDNSVPTSCKHAF 593
 QY 582 DISRVMMHGRYRDCYSPFANVETKSLMRTYIEPVPL 618
 DB 594 DISRVMMHGRYRDCYSPFANVETKSLMRTYIEPVPL 630

RESULT 9
 US-09-360-545-2

; Sequence 2, Application US/09360545
 ; Patent No. 6429014
 ; GENERAL INFORMATION:
 ; APPLICANT: Croceau, Rodney B
 ; APPLICANT: Bohmann, Jorg
 ; APPLICANT: Steele, Christopher L
 ; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 ; FILE REFERENCE: wau13885
 ; CURRENT APPLICATION NUMBER: US/09/360,545
 ; EARLIER FILING DATE: 1999-07-26
 ; EARLIER APPLICATION NUMBER: 60/052,249
 ; EARLIER FILING DATE: 1997-11-07
 ; EARLIER APPLICATION NUMBER: PCT/US98/14528
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 627
 ; TYPE: PRT
 ; ORGANISM: Abies grandis
 US-09-360-545-2

Query Match 67.7%; Score 2200.5; DB 4; Length 627;
 Best Local Similarity 66.1%; Pred. No. 3.8e-205;
 Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
 QY 1 MALSLTPVLSRGL-----SSSHEIKALRRTIPTLIGCRPGKSVASHINMCLTSVAST 55


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Db 1 MALVSIPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTSPMSISLATAAPDD 60
Qy 56 SVQRRVGNHNSNIMDDDFIOSLISTPYGADPYRERARLIGEVKDIMFNFSKLEDDG--- 112
Db 61 GVQRRIDYHNSIMDDDFIOSL-STPYGEPYQERAEELIVEVKI-FNSWYLDGRLMS 118
Qy 113 --NDLORLLLVDDVERLGDIDRHFKKEIKTALDYVNSYNNKEKIGCGRESVYTDLNSAL 170
Db 119 SFNDLMQRLMIVDSVERLGIARHFKNETSALDYVFRWENNGIGCGRDSIVTDLNSAL 178
Qy 171 GLRTLRLHGTVSSDVINVFQKNGQSPSTANIQIEGIRGVNLFRASLVAFFGEKYM 230
Db 179 GFTLRLHGTVSSDVINVFQKNGQSPSTANIQIEGIRGVNLFRASLVAFFGEKYM 237
Qy 231 EAETFSKYLREALOKIPASSISLEIRDVLEYGWHTNLPRLERARNYIDTLEKOTSAMLN 287
Db 238 EAETFSKYLREALOKIPVSA-LSQELKPYMEYGMHTNLPRLERARNYIDTLEKOTSAMLN 296
Qy 288 KNAEKLLELAKLEFNFHSLQERELKHVSRMKDSGSPMTFCRHRHVEYALASCIATF 347
Db 297 KNAEKLLELAKLEFNFHSLQERELKHVSRMKDSGSPMTFCRHRHVEYALASCIATF 356
Qy 348 EPOHSGRLGFTKMSHLITVLDNMYDVFGTVDELFTATIKRWDPSAMECLPEYMGVY 407
Db 357 DPKHSARLGFARFKCHLVTVLDDIYDFGTVDELFTATIKRWNSSIEHLPEYMKCVY 416
Qy 408 MMVYHTNEMARVAEKAQSDTLNVARQWACFDSYMOEAKWATATGYPFEEYLENGK 467
Db 417 MMVEYTNELTREAEKQGNRTLNVARQWACFDSYMOEAKWATATGYPFEEYLENGK 476
Qy 468 VSSAHRCALOPILTLDPFPDHLKEVDPPSKINDLICILRLRGDTRCYKADRANGEE 527
Db 477 VSSAYRAVATQPIITLNAMLPDYILKGIDPPSRNDLASSFLRLRGDTRCYKADRANGEE 536
Qy 528 ASSISCYMKONPGLTBEDALNHINFMIRDAIRELWELLKPDNSVPTSKGAPDISRW 587
Db 537 ASSISCYMKONPGSTBEDALNHINAMVNDIIRKELNWEILLASNDNI PMLAKKHADITRAL 596
Qy 588 HHGRRYDGYSPANVETKSLVMTVIE 614
Db 597 HHLYTRDGFVSANKETKCLVMTLE 623
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RESULT 10

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US-09-398-395A-30
; Sequence 30, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772L, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-398-395A-30
```

```
Query Match 67.7%; Score 2200.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 3.8e-205;
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Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
Qy 1 MALSTIPLVSRCL-----SSSHEIKALRRITPTLIGCPGKSVASHINMCLTVASTD 55
Db 1 MALVSIPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTSPMSISLATAAPDD 60
Qy 56 SVQRRVGNHNSNIMDDDFIOSLISTPYGADPYRERARLIGEVKDIMFNFSKLEDDG--- 112
Db 61 GVQRRIDYHNSIMDDDFIOSL-STPYGEPYQERAEELIVEVKI-FNSWYLDGRLMS 118
Qy 113 --NDLORLLLVDDVERLGDIDRHFKKEIKTALDYVNSYNNKEKIGCGRESVYTDLNSAL 170
Db 119 SFNDLMQRLMIVDSVERLGIARHFKNETSALDYVFRWENNGIGCGRDSIVTDLNSAL 178
Qy 171 GLRTLRLHGTVSSDVINVFQKNGQSPSTANIQIEGIRGVNLFRASLVAFFGEKYM 230
Db 179 GFTLRLHGTVSSDVINVFQKNGQSPSTANIQIEGIRGVNLFRASLVAFFGEKYM 237
Qy 231 EAETFSKYLREALOKIPASSISLEIRDVLEYGWHTNLPRLERARNYIDTLEKOTSAMLN 287
Db 238 EAETFSKYLREALOKIPVSA-LSQELKPYMEYGMHTNLPRLERARNYIDTLEKOTSAMLN 296
Qy 288 KNAEKLLELAKLEFNFHSLQERELKHVSRMKDSGSPMTFCRHRHVEYALASCIATF 347
Db 297 KNAEKLLELAKLEFNFHSLQERELKHVSRMKDSGSPMTFCRHRHVEYALASCIATF 356
Qy 348 EPOHSGRLGFTKMSHLITVLDNMYDVFGTVDELFTATIKRWDPSAMECLPEYMGVY 407
Db 357 DPKHSARLGFARFKCHLVTVLDDIYDFGTVDELFTATIKRWNSSIEHLPEYMKCVY 416
Qy 408 MMVYHTNEMARVAEKAQSDTLNVARQWACFDSYMOEAKWATATGYPFEEYLENGK 467
Db 417 MMVEYTNELTREAEKQGNRTLNVARQWACFDSYMOEAKWATATGYPFEEYLENGK 476
Qy 468 VSSAHRCALOPILTLDPFPDHLKEVDPPSKINDLICILRLRGDTRCYKADRANGEE 527
Db 477 VSSAYRAVATQPIITLNAMLPDYILKGIDPPSRNDLASSFLRLRGDTRCYKADRANGEE 536
Qy 528 ASSISCYMKONPGLTBEDALNHINFMIRDAIRELWELLKPDNSVPTSKGAPDISRW 587
Db 537 ASSISCYMKONPGSTBEDALNHINAMVNDIIRKELNWEILLASNDNI PMLAKKHADITRAL 596
Qy 588 HHGRRYDGYSPANVETKSLVMTVIE 614
Db 597 HHLYTRDGFVSANKETKCLVMTLE 623
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RESULT 11

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US-09-887-586A-30
; Sequence 30, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6495354L, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/358,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-887-586A-30
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```

Query Match      67.7%: Score 2200.5; DB 4; Length 627;
Best Local Similarity 60.1%: Pred. No. 3.8e-205;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALISIPPLVRSCL-----SSSHEIKALRRTIPTLIGCRGKSVASHINMCLTSVSTD 55
D 1 MALVISIPPLASKSCRLSKSLISSIHKKPPRTIENLGRRRGKSVTPSMISLATAAPDD 60
QY 56 SVQRVGNVNSHNLMDDFIOQLSTPYGADPYRERADRLIGEVDIMNFKSLSDG--- 112
D 61 GVQRRIIDYHSNIMDDFIOQL-STPYGEPGYQERARLIYEVKI-FNSMYLDDGRILMS 118
QY 113 --NDLQRLLLVDYVERLGIIDRHFKKEIKTALDVVNSYNNKGIICGGRSVTDLNSTAL 170
D 119 SFNDLMQRLMIVDSVERLGIARHFKNETSALDYVFRWEENGICGGRDSIVTDLNSTAL 178
QY 171 GLRTLRHAGTVSSDVNVFQDKNGQFSSSTANIQIEGIRGVNLFRASLVAFPGEKYM 230
D 179 GFRTLRHAGTVSSDVNVFQDKNGQFSSSTANIQIEGIRGVNLFRASLVAFPGEKYM 237
QY 231 EAETFSKYLREALOKIPVSA-LSQEIKFVMEYGMHTNLPRLERANYIDTLEKOTSAMLN 287
D 238 EAETFSKYLREALOKIPVSA-LSQEIKFVMEYGMHTNLPRLERANYIDTLEKOTSAMLN 296
QY 288 KNAEKLELAKLEFNFHSLQERELKRVSRWMDSGSPENTFCRHRVVEYALASCIAP 347
D 297 KNAEKLELAKLEFNFHSLQERELKRVSRWMDSGSPENTFCRHRVVEYALASCIAP 356
QY 348 EPOHSGRLGFTKNSHITVLDMDYVFGTVDELDELFTATIKRMDPSAMECLPEYMKGV 407
D 357 DPKSARLRFPAKCHLVTVLDYIDTFTGIDELFTSAIKRNNSSIEHLPEYMKGV 416
QY 408 MMVYHTVEMARVAEKAQGRDITLVYARQWAEACDSYQWAKWJATGYLPTFEYLENGK 467
D 417 MMVETNELTREAEKQGRDITLVYARQWAEACDSYQWAKWJATGYLPTFEYLENGK 476
QY 468 VSSAHRCALOPILTLIPFPDHLKVEDPFSKNDLICILRLRGDTRCYKADRDGEE 527
D 477 VSSAHRCALOPILTLIPFPDHLKVEDPFSKNDLICILRLRGDTRCYKADRDGEE 536
QY 528 ASSISCYMKONPGLTEDDALNHINFMIRDAIRELNMWELKPDNSVPTSKGAFDISRW 587
D 537 ASSISCYMKONPGLTEDDALNHINFMIRDAIRELNMWELKPDNSVPTSKGAFDISRW 596
QY 588 HHGIRYRDGVSFANVETKSLVMRTVIE 614
D 597 HHGIRYRDGVSFANVETKSLVMRTVIE 623

RESULT 12
US-09-895-752-30
; Sequence 30, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6559297, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 3.0

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; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-895-752-30

Query Match      67.7%: Score 2200.5; DB 4; Length 627;
Best Local Similarity 60.1%: Pred. No. 3.8e-205;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALISIPPLVRSCL-----SSSHEIKALRRTIPTLIGCRGKSVASHINMCLTSVSTD 55
D 1 MALVISIPPLASKSCRLSKSLISSIHKKPPRTIENLGRRRGKSVTPSMISLATAAPDD 60
QY 56 SVQRVGNVNSHNLMDDFIOQLSTPYGADPYRERADRLIGEVDIMNFKSLSDG--- 112
D 61 GVQRRIIDYHSNIMDDFIOQL-STPYGEPGYQERARLIYEVKI-FNSMYLDDGRILMS 118
QY 113 --NDLQRLLLVDYVERLGIIDRHFKKEIKTALDVVNSYNNKGIICGGRSVTDLNSTAL 170
D 119 SFNDLMQRLMIVDSVERLGIARHFKNETSALDYVFRWEENGICGGRDSIVTDLNSTAL 178
QY 171 GLRTLRHAGTVSSDVNVFQDKNGQFSSSTANIQIEGIRGVNLFRASLVAFPGEKYM 230
D 179 GFRTLRHAGTVSSDVNVFQDKNGQFSSSTANIQIEGIRGVNLFRASLVAFPGEKYM 237
QY 231 EAETFSKYLREALOKIPVSA-LSQEIKFVMEYGMHTNLPRLERANYIDTLEKOTSAMLN 287
D 238 EAETFSKYLREALOKIPVSA-LSQEIKFVMEYGMHTNLPRLERANYIDTLEKOTSAMLN 296
QY 288 KNAEKLELAKLEFNFHSLQERELKRVSRWMDSGSPENTFCRHRVVEYALASCIAP 347
D 297 KNAEKLELAKLEFNFHSLQERELKRVSRWMDSGSPENTFCRHRVVEYALASCIAP 356
QY 348 EPOHSGRLGFTKNSHITVLDMDYVFGTVDELDELFTATIKRMDPSAMECLPEYMKGV 407
D 357 DPKSARLRFPAKCHLVTVLDYIDTFTGIDELFTSAIKRNNSSIEHLPEYMKGV 416
QY 408 MMVYHTVEMARVAEKAQGRDITLVYARQWAEACDSYQWAKWJATGYLPTFEYLENGK 467
D 417 MMVETNELTREAEKQGRDITLVYARQWAEACDSYQWAKWJATGYLPTFEYLENGK 476
QY 468 VSSAHRCALOPILTLIPFPDHLKVEDPFSKNDLICILRLRGDTRCYKADRDGEE 527
D 477 VSSAHRCALOPILTLIPFPDHLKVEDPFSKNDLICILRLRGDTRCYKADRDGEE 536
QY 528 ASSISCYMKONPGLTEDDALNHINFMIRDAIRELNMWELKPDNSVPTSKGAFDISRW 587
D 537 ASSISCYMKONPGLTEDDALNHINFMIRDAIRELNMWELKPDNSVPTSKGAFDISRW 596
QY 588 HHGIRYRDGVSFANVETKSLVMRTVIE 614
D 597 HHGIRYRDGVSFANVETKSLVMRTVIE 623

RESULT 13
US-09-903-012B-30
; Sequence 30, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569656, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

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;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 30
;; LENGTH: 627
;; TYPE: PR1
;; ORGANISM: Abies grandis
us-09-903-0128-30

Query Match 67.7%; Score 2200.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 3.8e-205;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

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QY 1 MALSTIPVRSCL-----SSHEIKALRTIPTLIGICPGKSVASHINMCLTSVASTD 55
D 1 MALVSIPLASKSCLRKSLISSIHEHKPPRTIPNLGMRRRGKSVTSMISLATAAPDD 60
QY 56 SVGRVGNHNSNMDDDFIQLISTPYGADPYERADRLIGEVDIMFNFKSLDGG-- 112
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QY 113 --NDLLQRLLLVDDVERLGIIDRHFKKIKTALDYVNSYNMEKIGCGRESVYTDLNSTAL 170
D 119 SFNDLMQRLMIVDSVERLGIARHFKNEITSALDYVFRYWEENGIGCGRDSIVTDLNSTAL 178
QY 171 GLRTLRLHGTVSSDVNLVFKDKNGQFSSSTANIQIEBEIRGVNLPRASLVAAPGEKVM 230
D 179 GFRTRLRHGTVSEVLKARQDONGQFVCSPG-QTBEIRSVNLVPRASLVAAPGEKVM 237
QY 231 EAETFTKYRLREALOKIPASSISLEIRDVLEYGMHTNLPRLERANYMDVFGQHTK--N 287
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D 297 KNAEKLLELAKLEFNI FNSLOQKELOYLRLWMEKESDLPKLTFRHHRHVEYTLASCIAP 356
QY 348 EPOHSGFRIGFTKMSHITVLDMDYDVGTVDELELFTATIKRMDPSAMECLPEYMGVY 407
D 357 DPKHSARLRFAPKACHLVATVDIYDFPGTIDLELFTSAIKRNSSEIHLPEYMGVY 416
QY 408 MMVYHTVENARVAEKAQGRDTLNYARQAEACDSYMOEAKWTATGYLPTFEYELNGK 467
D 417 MMVETYNELTREAEKIQGRNTLNYARKAEAYFDSYMEAKWISNGYLPWFEEYHENGK 476
QY 468 VSSAHRPCALQPIITLIDIPPDHILKEVDPSKNDLICILRLRGDTRCYKADRGEE 527
D 477 VSSAYRVATLQPIITLNLAMPDYILKGI DFPSPRNDLASSFLRLRGDTRCYKADRGEE 536
QY 528 ASSISCYMKDNPGLTEBDALNHINFMIRDAIRELNMELKPDNSVPTSKGADISRVM 587
D 537 ASSISCYMKDNPGSTEBDALNHINAMVNDI IKELNMELLRNSDNI PMLAKHAPDITRAL 596
QY 588 HHGYYRDGYSFANVETKSLVMRTVIE 614
D 597 HHLYIYRDGFSVANKETKCLVMETILLE 623
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RESULT 14
US-09-900-797-30
; Sequence 30, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17

;; PRIOR APPLICATION NUMBER: 60/130,628
;; PRIOR FILING DATE: 1999-04-22
;; PRIOR APPLICATION NUMBER: 60/150,262
;; PRIOR FILING DATE: 1999-08-23
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 30
;; LENGTH: 627
;; TYPE: PR1
;; ORGANISM: Abies grandis
us-09-900-797-30

Query Match 67.7%; Score 2200.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 3.8e-205;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

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D 1 MALVSIPLASKSCLRKSLISSIHEHKPPRTIPNLGMRRRGKSVTSMISLATAAPDD 60
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D 61 GVGRIGDHSNMDDDFIQL--STPYGEPGYERARLLIVEYKKI-FNSMYLDDGLMS 118
QY 113 --NDLLQRLLLVDDVERLGIIDRHFKKIKTALDYVNSYNMEKIGCGRESVYTDLNSTAL 170
D 119 SFNDLMQRLMIVDSVERLGIARHFKNEITSALDYVFRYWEENGIGCGRDSIVTDLNSTAL 178
QY 171 GLRTLRLHGTVSSDVNLVFKDKNGQFSSSTANIQIEBEIRGVNLPRASLVAAPGEKVM 230
D 179 GFRTRLRHGTVSEVLKARQDONGQFVCSPG-QTBEIRSVNLVPRASLVAAPGEKVM 237
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D 238 EAETFTKYRLREALOKIPVSA-LSQELKFVMEYGMHTNLPRLERANYIDTLEKOTSAMLN 296
QY 288 KNAEKLLELAKLEFNI FHSLOERELKHSRWKDCSGSPENTFCRHNVHEYALASCIAP 347
D 297 KNAEKLLELAKLEFNI FNSLOQKELOYLRLWMEKESDLPKLTFRHHRHVEYTLASCIAP 356
QY 348 EPOHSGFRIGFTKMSHITVLDMDYDVGTVDELELFTATIKRMDPSAMECLPEYMGVY 407
D 357 DPKHSARLRFAPKACHLVATVDIYDFPGTIDLELFTSAIKRNSSEIHLPEYMGVY 416
QY 408 MMVYHTVENARVAEKAQGRDTLNYARQAEACDSYMOEAKWTATGYLPTFEYELNGK 467
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D 477 VSSAYRVATLQPIITLNLAMPDYILKGI DFPSPRNDLASSFLRLRGDTRCYKADRGEE 536
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D 537 ASSISCYMKDNPGSTEBDALNHINAMVNDI IKELNMELLRNSDNI PMLAKHAPDITRAL 596
QY 588 HHGYYRDGYSFANVETKSLVMRTVIE 614
D 597 HHLYIYRDGFSVANKETKCLVMETILLE 623
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RESULT 15
US-09-360-545-32
; Sequence 32, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wu113885
; CURRENT APPLICATION NUMBER: US/09/360,545

CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 627
TYPE: PRT
ORGANISM: Abies grandis
US-09-360-545-32

Query Match 67.6%; Score 2197.5; DB 4; Length 627;
Best Local Similarity 60.1%; Pred. No. 7.5e-205;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
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DB 119 SFNDLMORLWVDSVERIGIARHFKNEITSLADYVFRYWEENGIGCGRDSIVTDLNSTAL 178
QY 171 GLTILRLHGYVSSDVNLVFPKXNGQFSTANIOIEGRIGVLNFRASLVAFPGEKYMD 230
DB 179 GFTILRLHGYVSSDVNLVFPKXNGQFSTANIOIEGRIGVLNFRASLVAFPGEKYME 237
QY 231 EAETFSKYLRALOKIPASSILSLERDVLGYGHTNLPRLEARNYMDVFGQHTK--N 287
DB 238 EAFIFSTRYLKALOKIPVSA-LSQEIFVMEYGHNTLPRLEARNYIDLEKDTSAWLN 296
QY 288 KNAEKLELAKLEFNTFHSIQERELKVSRWKDSGSPMTFCHRHVEYYALASCTAF 347
DB 297 KNAEKLELAKLEFNTFHSIQERELKVSRWKDSGSPMTFCHRHVEYYALASCTAI 356
QY 348 EPOHSGFRLGFTKMSHLITVDMDVFGVDELELFTATIKRMDPSAMECLPEYMKGVY 407
DB 357 DPKSAFRLGFAKCHLVTVDDIYDTGTIDELFTSAIKRNNSSIEHLPEYMKGVY 416
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DB 417 MVEFETVNELETRAEAKTQGRATLVNVRKAMEAYFDSYMEBAKWSNGYLPFEEYHENGK 476
QY 468 VSSAHRPCALOPITLIDIPFPDHLKXVDFPSKLNLCIILRLRGDTRCYKADARGE 527
DB 477 VSSAYRAVATLOPILTLNMLKIDFPSRFNDLASSPLRLNGDTRCYKADARGE 536
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DB 597 HHLIYIRDGFSVANKETKLVMETLLE 623

Search completed: July 23, 2004, 09:04:45
Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 09:03:48 ; Search time 50 Seconds
(without alignments) 3870.586 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251
Sequence: 1 MALLSTPLVRSCLSSSHR.....FANVETSLVNRVTEPVPL 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3251	100.0	618	14	US-10-025-145A-65 Sequence 65, Appl
2	2453	75.5	628	9	US-09-887-586A-20 Sequence 20, Appl
3	2453	75.5	628	9	US-09-903-012-20 Sequence 20, Appl
4	2453	75.5	628	10	US-09-900-797-20 Sequence 20, Appl
5	2453	75.5	628	12	US-09-893-820-20 Sequence 20, Appl
6	2453	75.5	628	13	US-10-041-007-22 Sequence 22, Appl
7	2453	75.5	628	14	US-10-025-145A-4 Sequence 4, Appl
8	2264	69.6	630	14	US-10-025-145A-67 Sequence 67, Appl
9	2200.5	67.7	627	9	US-09-887-586A-30 Sequence 30, Appl
10	2200.5	67.7	627	9	US-09-903-012-30 Sequence 30, Appl
11	2200.5	67.7	627	10	US-09-900-797-30 Sequence 30, Appl
12	2200.5	67.7	627	12	US-09-893-820-30 Sequence 30, Appl
13	2200.5	67.7	627	13	US-10-041-007-26 Sequence 26, Appl
14	2200.5	67.7	627	14	US-10-025-145A-2 Sequence 2, Appl
15	2197.5	67.6	627	14	US-10-025-145A-32 Sequence 32, Appl

16	2137	65.7	630	14	US-10-025-145A-78 Sequence 78, Appl
17	2084.5	64.1	637	13	US-10-041-007-28 Sequence 28, Appl
18	2084.5	64.1	637	14	US-10-025-145A-69 Sequence 69, Appl
19	2031.5	62.5	637	9	US-09-887-586A-58 Sequence 58, Appl
20	2031.5	62.5	637	10	US-09-903-012-58 Sequence 58, Appl
21	2031.5	62.5	637	10	US-09-900-797-58 Sequence 58, Appl
22	2031.5	62.5	637	12	US-09-893-820-58 Sequence 58, Appl
23	2031.5	62.5	637	13	US-10-041-007-24 Sequence 24, Appl
24	2031.5	62.5	637	14	US-10-025-145A-6 Sequence 6, Appl
25	1295.5	39.8	581	9	US-09-887-586A-48 Sequence 48, Appl
26	1295.5	39.8	581	9	US-09-903-012-48 Sequence 48, Appl
27	1295.5	39.8	581	10	US-09-900-797-48 Sequence 48, Appl
28	1295.5	39.8	581	12	US-09-893-820-48 Sequence 48, Appl
29	1295.5	39.8	581	13	US-10-041-007-18 Sequence 18, Appl
30	1250.5	38.5	577	14	US-10-025-145A-18 Sequence 18, Appl
31	1240.5	38.2	862	9	US-09-887-586A-44 Sequence 44, Appl
32	1240.5	38.2	862	10	US-09-903-012-44 Sequence 44, Appl
33	1240.5	38.2	862	10	US-09-900-797-44 Sequence 44, Appl
34	1240.5	38.2	862	12	US-09-893-820-44 Sequence 44, Appl
35	1240.5	38.2	862	12	US-10-041-018-386 Sequence 386, App
36	1240.5	38.2	862	13	US-10-041-007-41 Sequence 41, Appl
37	1231	37.9	553	9	US-09-887-586A-50 Sequence 50, Appl
38	1231	37.9	553	9	US-09-903-012-50 Sequence 50, Appl
39	1231	37.9	553	10	US-09-900-797-50 Sequence 50, Appl
40	1231	37.9	553	12	US-09-893-820-50 Sequence 50, Appl
41	1231	37.9	553	13	US-10-041-007-20 Sequence 20, Appl
42	1187	36.5	782	9	US-09-887-586A-46 Sequence 46, Appl
43	1187	36.5	782	9	US-09-903-012-46 Sequence 46, Appl
44	1187	36.5	782	10	US-09-900-797-46 Sequence 46, Appl
45	1187	36.5	782	12	US-09-893-820-46 Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-10-025-145A-65
Sequence 65, Application US/10025145A
Publication No. US2003015861A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Bohnmann, Joerg
APPLICANT: Steele, Christopher L.
APPLICANT: Phillips, Michael A.
TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
FILE REFERENCE: WSR118414
CURRENT APPLICATION NUMBER: US/10/025.145A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 09/360,545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052,249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65
LENGTH: 618
TYPE: PRT
ORGANISM: Abies Grandis
US-10-025-145A-65
Query Match 100.0%; Score 3251; DB 14; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.5e-302;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 181 TVSSDVNLVDFDKNGQFSSSTANIQIEGIRGVNLFRASLVAPEGEKMDAEFTSTKYL 240
QY 241 REALQKIPASSILSLEIRDVLEYGMHTNLPRLEARNYMDVFGQHTKNAAEKLELAKL 300
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QY 301 EFNIFHSLQERELKHVSRWMDSCSPENTFCRHRHVEYALASCIAPFQHSGLRGTGTX 360
DB 301 EFNIFHSLQERELKHVSRWMDSCSPENTFCRHRHVEYALASCIAPFQHSGLRGTGTX 360
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DB 361 MSHLITVLDMDYDVGTVDELELFTATIKRMDPSAMECLPEYMGKVMMVYHTVENMARV 420
QY 421 AEKQGRDTLVYARQAWACFDSYMOEAKWTATGYLPTFEELYENGVSAHRPCALQPI 480
DB 421 AEKQGRDTLVYARQAWACFDSYMOEAKWTATGYLPTFEELYENGVSAHRPCALQPI 480
QY 481 LTLDIPEPDHILKEVDFPSKINDLICITLRLGDTRCYKADRAGEEASISCYMKONG 540
DB 481 LTLDIPEPDHILKEVDFPSKINDLICITLRLGDTRCYKADRAGEEASISCYMKONG 540
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DB 541 LTBEDALNHINFMIRDAIRELNWELKPDNSVPTTSKGAADISRWHEGTRYRDSYFA 600
QY 601 NVEKSLVMRTVIEPVPL 618
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RESULT 2
US-09-887-586A-20
Sequence 20, Application US/09887586A
Patent No. US20020094556A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094556A1, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 628
TYPE: PRT
ORGANISM: Abies grandis
US-09-887-586A-20

Query Match 75.5%; Score 2453; DB 9; Length 628;
Best Local Similarity 75.3%; Fred. No. 5.9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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QY 113 --NDLQRLILVDDVERLIGIDRHFKEIKTALDVNSYMEKGI GCGRESVVTDLNSTAL 170
DB 113 PLNDLQRLILVDDVERLIGIDRHFKEIKTALDVNSYMEKGI GCGRESVVTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVNLVDFDKNGQFSSSTANIQIEGIRGVNLFRASLVAPEGEKMD 230
DB 179 GLRTLRLHGYTVSSDVNLVDFDKNGQFSSSTANIQIEGIRGVNLFRASLVAPEGEKMD 238
QY 231 EAEFTSTKYLREALQKIPASSILSLEIRDVLEYGMHTNLPRLEARNYMDVFGQHTKNA 290
DB 239 EAEFTSTKYLREALQKIPASSILSLEIRDVLEYGMHTNLPRLEARNYMDVFGQHTKNA 297
QY 291 ---AEKLELAKLEFNIFHSLQERELKHVSRWMDSCSPENTFCRHRHVEYALASCIAP 347
DB 298 YVSKSKLELAKLEFNIFHSLQERELKHVSRWMDSCSPENTFCRHRHVEYALASCIAP 357
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DB 598 HHGTRYRDSYFANVETKSLVMRTVIEPVPL 628

RESULT 3
US-09-903-012-20
Sequence 20, Application US/09903012
Patent No. US20020094557A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094557A1, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 628
TYPE: PRT
ORGANISM: Abies grandis
US-09-903-012-20

Query Match 75.5%; Score 2453; DB 9; Length 628;
Best Local Similarity 75.3%; Fred. No. 5.9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;


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DB 1 MALVSTAPLAKSKCLHKSLSISTHELKALSRITPALGMSRRGKSTIPISMSSTTVTDD 60
QY 56 SVORRVGNHNLNDDDFIQLISTPYCAPDYREARADLIGEVKDIMNPFSLDEGCG--- 112
DB 61 GVRRRMGDFHNLNDDDFIQLISTPYCAPDYREARADLIGEVKDIMNPFSLDEGCG--- 118
QY 113 --NDLORLLLVDDVERLIDRHFKEIKTALDVYNSYWNKSGICGSESVTDLNSTAL 170
DB 119 PLNDLIQRLMIVDSLERIGIRHFRDEIKSALDYVSYWGENGICGSESVTDLNSTAL 178
QY 171 GLTRLRLHGYVSSVPLNVPFKDKNGQFSSSTANIOIEGIRGVNLFRASLAFPEKXMD 230
DB 179 GLTRLRLHGYVSSVPLNVPFKDKNGQFSSSTANIOIEGIRGVNLFRASLAFPEKXMD 238
QY 231 EAEFTSTYKLEALOKIPASSISLEIRDVLEYGHTNLPRLEARNYMDVFGQHTKXNA 290
DB 239 EAEFTSTYKLEALOKIPASSISLEIRDVLEYGHTNLPRLEARNYMDVFGQHTKXNA 297
QY 291 --ABKLELAKLEBNIFHSLQERELKHVSRWKMGSGPEMTFCRRHVEYYALASCIAP 347
DB 298 YVKSKELELAKLEBNIFHSLQERELKHVSRWKMGSGPEMTFCRRHVEYYALASCIAP 357
QY 348 EPOHSGFRIGFTQSHLITVLDMDVDFGTDELELFTATIKRMDPSAMECLPEYMKGVY 407
DB 358 EPOHSGFRIGFTQSHLITVLDMDVDFGTDELELFTATIKRMDPSAMECLPEYMKGVY 417
QY 408 MMVHTVEMARVAEKAQGRDTLYARQAMEACFDSYQOEAQWATGTLPFEEYLENGK 467
DB 418 IAVDTVEMARVAEKAQGRDTLYARQAMEACFDSYQOEAQWATGTLPFEEYLENGK 477
QY 468 VSSAHRPCALOPITLDPFPDHILKEVDPSKNDLICIILRLRGDRCKYADARABEE 527
DB 478 VSCGRISALOPITLMDIPFPDHILKEVDPSKNDLICALIRLGRDRCKYADARABEE 537
QY 528 ASSISCYKNDPGLTEBDALNHNFMIDARLREINWELLKPDNSVPTSKGAPDISRW 587
DB 538 ASSISCYKNDPGLTEBDALNHNFMIDARLREINWELLKPDNSVPTSKGAPDISRW 597
QY 588 HHGYYRDRGYSFANVETKSLMRTVIEPVL 618
DB 598 HHGYYRDRGYSFANVETKSLMRTVIEPVL 628

```

RESULT 4

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US-09-900-797-20
; Sequence 20, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Stark, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
; US-09-900-797-20

```

Query Match 75.5%; Score 2453; DB 10; Length 628;
 Best Local Similarity 75.3%; Pred. No. 5.9e-226;
 Matches 473; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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QY 1 MALISTIPVRSCL-----SSHEIKALRTIPTLGI CRPKSVASINMCLTSVASTD 55
DB 1 MALVSTAPLAKSKCLHKSLSISTHELKALSRITPALGMSRRGKSTIPISMSSTTVTDD 60
QY 56 SVORRVGNHNLNDDDFIQLISTPYCAPDYREARADLIGEVKDIMNPFSLDEGCG--- 112
DB 61 GVRRRMGDFHNLNDDDFIQLISTPYCAPDYREARADLIGEVKDIMNPFSLDEGCG--- 118
QY 113 --NDLORLLLVDDVERLIDRHFKEIKTALDVYNSYWNKSGICGSESVTDLNSTAL 170
DB 119 PLNDLIQRLMIVDSLERIGIRHFRDEIKSALDYVSYWGENGICGSESVTDLNSTAL 178
QY 171 GLTRLRLHGYVSSVPLNVPFKDKNGQFSSSTANIOIEGIRGVNLFRASLAFPEKXMD 230
DB 179 GLTRLRLHGYVSSVPLNVPFKDKNGQFSSSTANIOIEGIRGVNLFRASLAFPEKXMD 238
QY 231 EAEFTSTYKLEALOKIPASSISLEIRDVLEYGHTNLPRLEARNYMDVFGQHTKXNA 290
DB 239 EAEFTSTYKLEALOKIPASSISLEIRDVLEYGHTNLPRLEARNYMDVFGQHTKXNA 297
QY 291 --ABKLELAKLEBNIFHSLQERELKHVSRWKMGSGPEMTFCRRHVEYYALASCIAP 347
DB 298 YVKSKELELAKLEBNIFHSLQERELKHVSRWKMGSGPEMTFCRRHVEYYALASCIAP 357
QY 348 EPOHSGFRIGFTQSHLITVLDMDVDFGTDELELFTATIKRMDPSAMECLPEYMKGVY 407
DB 358 EPOHSGFRIGFTQSHLITVLDMDVDFGTDELELFTATIKRMDPSAMECLPEYMKGVY 417
QY 408 MMVHTVEMARVAEKAQGRDTLYARQAMEACFDSYQOEAQWATGTLPFEEYLENGK 467
DB 418 IAVDTVEMARVAEKAQGRDTLYARQAMEACFDSYQOEAQWATGTLPFEEYLENGK 477
QY 468 VSSAHRPCALOPITLDPFPDHILKEVDPSKNDLICIILRLRGDRCKYADARABEE 527
DB 478 VSCGRISALOPITLMDIPFPDHILKEVDPSKNDLICALIRLGRDRCKYADARABEE 537
QY 528 ASSISCYKNDPGLTEBDALNHNFMIDARLREINWELLKPDNSVPTSKGAPDISRW 587
DB 538 ASSISCYKNDPGLTEBDALNHNFMIDARLREINWELLKPDNSVPTSKGAPDISRW 597
QY 588 HHGYYRDRGYSFANVETKSLMRTVIEPVL 618
DB 598 HHGYYRDRGYSFANVETKSLMRTVIEPVL 628

```

RESULT 5

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US-09-893-820-20
; Sequence 20, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A1, Joseph P.
; APPLICANT: Stark, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20

```

LENGTH: 628
TYPE: PRF
ORGANISM: Abies grandis
US-09-893-820-20

Query Match 75.5%; Score 2453; DB 12; Length 628;
Best Local Similarity 75.3%; Pred. No. 5,9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

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QY 1 MALSTIPPLVRSCL-----SSSHEIKALRRTTPTLGIICRPGKSVASHINMCLTSVASTD 55
D 1 MALVSTAPLASKSCJLHSLISSTHEKALSRITPALGMSRGRKSTPISMSSTTVVTD 60
QY 56 SVORRVGNHNSLMDDDPIQSLISTPYGADPYRERARLIGEVNDIMNFSLDEG--- 112
D 61 GVRKRMDFHNSLMDDDVIOQL-PTAYEKSYLERAEKLIGEVKN-MNNSLSLEGLMS 118
QY 113 --NDLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYMNKGIQCGRESVTTDLNSTAL 170
D 119 PLNDLIQRLMIVDSLELGRHFKDEIKSALDYVSYWGENGICGRESVTTDLNSTAL 178
QY 171 GLRTLRLHGTVSSDVNVFKNQKQFSSSTANIQIEGIRGVNLFRASLVAFPGEKMD 230
D 179 GLRTLRLHGTVSSDVNVFKNQKQFSSSTANIQIEGIRGVNLFRASLVAFPGEKMD 238
QY 231 EAETFTSTKYLEALOKIPASSILSLERDVLEYGMHTNLPRLERANMVDVGOHTKNNA 290
D 239 EAETFTSTKYLEALOKIPASSILSLERDVLEYGMHTNLPRLERANMVDVGOHTKNNA 297
QY 291 ---AEKLELAKLEFNI FHSIQERELKHSRWKDSGSPENTFCRHREVEYYALASCIAP 347
D 298 YVSKKLELAKLEFNI FHSIQERELKHSRWKDSGSPENTFCRHREVEYYALASCIAP 357
QY 348 EPQSGRFLGFTKXSHLITVLDMDYVFGVDELELFTATIKRMDPSAMECLPEYMGVY 407
D 358 EPQSGRFLGFTKXSHLITVLDMDYVFGVDELELFTATIKRMDPSAMECLPEYMGVY 417
QY 408 MMVHTNEMARVAEKAQSGDPTLNARQAMEACDPSYQOAKMIAATGYLPTFEELYENGK 467
D 418 IAYDVTNEMAREAEQGRDTLYARBAWEAYIDSTQOEARMIATGYLPSFDEYENGK 477
QY 468 VSSAHRPCALQPIITLDIPFPDHLIKEVDPPSKNDLICIILRLRGDTRCYKADARCEE 527
D 478 VSCGRISALQPIITLDIPFPDHLIKEVDPPSKNDLICALILRLRGDTRCYKADARCEE 537
QY 528 ASSISCYMKDNGLTBEDALNHNFMIRDAIRELWELLKPDNSVPTSKKHADISRW 587
D 538 ASSISCYMKDNGLTBEDALNHNFMIRDAIRELWELLKPDNSVPTSKKHADISRW 597
QY 588 HHGYRBDGVSFANVETKSLMRTVIEPVPL 618
D 598 HHGYRBDGVSFANVETKSLMRTVIEPVPL 628
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RESULT 6
US-10-041-007-22
Sequence 22, Application US/10041007
Publication No. US20020164736A1
GENERAL INFORMATION:
APPLICANT: Matsuda, Seichi P.T.
APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1
CURRENT APPLICATION NUMBER: US/10/041,007
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 628
TYPE: PRF
ORGANISM: Abies grandis

US-10-041-007-22

Query Match 75.5%; Score 2453; DB 13; Length 628;
Best Local Similarity 75.3%; Pred. No. 5,9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

```
QY 1 MALSTIPPLVRSCL-----SSSHEIKALRRTTPTLGIICRPGKSVASHINMCLTSVASTD 55
D 1 MALVSTAPLASKSCJLHSLISSTHEKALSRITPALGMSRGRKSTPISMSSTTVVTD 60
QY 56 SVORRVGNHNSLMDDDPIQSLISTPYGADPYRERARLIGEVNDIMNFSLDEG--- 112
D 61 GVRKRMDFHNSLMDDDVIOQL-PTAYEKSYLERAEKLIGEVKN-MNNSLSLEGLMS 118
QY 113 --NDLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYMNKGIQCGRESVTTDLNSTAL 170
D 119 PLNDLIQRLMIVDSLELGRHFKDEIKSALDYVSYWGENGICGRESVTTDLNSTAL 178
QY 171 GLRTLRLHGTVSSDVNVFKNQKQFSSSTANIQIEGIRGVNLFRASLVAFPGEKMD 230
D 179 GLRTLRLHGTVSSDVNVFKNQKQFSSSTANIQIEGIRGVNLFRASLVAFPGEKMD 238
QY 231 EAETFTSTKYLEALOKIPASSILSLERDVLEYGMHTNLPRLERANMVDVGOHTKNNA 290
D 239 EAETFTSTKYLEALOKIPASSILSLERDVLEYGMHTNLPRLERANMVDVGOHTKNNA 297
QY 291 ---AEKLELAKLEFNI FHSIQERELKHSRWKDSGSPENTFCRHREVEYYALASCIAP 347
D 298 YVSKKLELAKLEFNI FHSIQERELKHSRWKDSGSPENTFCRHREVEYYALASCIAP 357
QY 348 EPQSGRFLGFTKXSHLITVLDMDYVFGVDELELFTATIKRMDPSAMECLPEYMGVY 407
D 358 EPQSGRFLGFTKXSHLITVLDMDYVFGVDELELFTATIKRMDPSAMECLPEYMGVY 417
QY 408 MMVHTNEMARVAEKAQSGDPTLNARQAMEACDPSYQOAKMIAATGYLPTFEELYENGK 467
D 418 IAYDVTNEMAREAEQGRDTLYARBAWEAYIDSTQOEARMIATGYLPSFDEYENGK 477
QY 468 VSSAHRPCALQPIITLDIPFPDHLIKEVDPPSKNDLICIILRLRGDTRCYKADARCEE 527
D 478 VSCGRISALQPIITLDIPFPDHLIKEVDPPSKNDLICALILRLRGDTRCYKADARCEE 537
QY 528 ASSISCYMKDNGLTBEDALNHNFMIRDAIRELWELLKPDNSVPTSKKHADISRW 587
D 538 ASSISCYMKDNGLTBEDALNHNFMIRDAIRELWELLKPDNSVPTSKKHADISRW 597
QY 588 HHGYRBDGVSFANVETKSLMRTVIEPVPL 618
D 598 HHGYRBDGVSFANVETKSLMRTVIEPVPL 628
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RESULT 7
US-10-025-145A-4
Sequence 4, Application US/10025145A
Publication No. US20030175861A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Bohlmann, Joerg
APPLICANT: Steele, Christopher L.
APPLICANT: Phillips, Michael A.
TITLE OF INVENTION: Monocleprene Synthases from Grand Fir (Abies Grandis)
FILE REFERENCE: WSUR118414
CURRENT APPLICATION NUMBER: US/10/025,145A
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 09/360,545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052,249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4

LENGTH: 628
 TYPE: PRT
 ORGANISM: Abies Grandis
 US-10-025-145a-4

Query Match 75.5%; Score 2453; DB 14; Length 628;
 Best Local Similarity 75.3%; Pred. No. 5.9e-226;
 Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALISTPLVRSCL-----SSSHEIKALRTIPTLIGICRPGKSVASHINMCLTSVASTD 55
 DB 1 MALVSTALASKSCLHKSLSISTHELKALISRTIPALGMSRKRKSITPISMSITVITVD 60
 QY 56 SVQRRVGNHYNHMDDDPIQSLISTPYGADPYERADRLIGEVDMFNKSLDEGC--- 112
 DB 61 GVRRRMGDFHNLWDDVIOQL-PTAYEEKSYLAEKELIGEVKN-MFNMSLEDGEIMS 118
 QY 113 --NDLQRLLLVDVERLIGIDRHFKEIKTALDYVNSYNEKIGCGRESVYTDLNSTAL 170
 DB 119 PLNDLIQRLMVDLERLIGIRHFPDEIKSALDYVYSYNGENGICGRESVYTDLNSTAL 178
 QY 171 GLRTLRHGYTVSSDVLANVFKDKNGQFSSTANIQIEGIRGVNLPRASLVAPEGEKYM 230
 DB 179 GLRTLRHGYTVSSDVLPKAFKQNGQFSCSENIQTDEIRGVNLPRASLVAPEGEKIMD 238
 QY 231 EAETFTSTYLAELOKIPASSISLEIRDVLEYGHTNLPRLERANVMYDVFGQHTKNKA 290
 DB 239 EAETFTSTYLAELOKIPASSISLEIRDVLEYGHTNLPRLERANVMYDVFGQHTKNKA 297
 QY 291 ---AEKLELAKLEFNIPHSLOERELKHSRWKMGSGSPMTFCRRHVEYVYALASCIAT 347
 DB 298 YKSKKLELAKLEFNIPHSLOERELKHSRWKMGSGSPMTFCRRHVEYVYALASCIAT 357
 QY 348 EPQSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPEYMKGY 407
 DB 358 EPQSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPEYMKGY 417
 QY 408 MMVHTVNMARVAEAKAGROTLNARQAMEACPDYSYQEAKWITGVLPFEETLENGK 467
 DB 418 IAVDTVNMAREAEAGROTLNARQAMEACPDYSYQEAKWITGVLPFEETLENGK 477
 QY 468 VSSAHRPCALOPILTLDPFDHILKEVDPSKLANDLICIIRLKGDRCYKADARAGE 527
 DB 478 VSCGHRISALOPILTLDPFDHILKEVDPSKLANDLICIIRLKGDRCYKADARAGE 537
 QY 528 ASSISCYKNDPGLTEEDALNHNFMIRDAIRELWELLKPDNSVITSKGAFFDISVW 587
 DB 538 ASSISCYKNDPGLTEEDALNHNFMIRDAIRELWELLKPDNSVITSKGAFFDISVW 597
 QY 588 HHGVRNRCYGFANVETKSLVWRITVIEPVPL 618
 DB 598 HHGVRNRCYGFANVETKSLVWRITVIEPVPL 628

RESULT 8

US-10-025-145a-67
 Sequence 67, Application US/10025145A
 Publication No. US20030175861A1
 GENERAL INFORMATION:

APPLICANT: Croceanu, Rodney B.
 APPLICANT: Bohlmann, Joerg
 APPLICANT: Steele, Christopher L.
 APPLICANT: Phillips, Michael A.
 TITLE OF INVENTION: Monocetene Synthases from Grand Fir (Abies Grandis)
 FILE REFERENCE: WSUR18414
 CURRENT FILING DATE: US/10/025,145A
 PRIOR APPLICATION NUMBER: US 09/360,545
 PRIOR FILING DATE: 1999-07-26
 PRIOR APPLICATION NUMBER: PCT/US98/14528
 PRIOR FILING DATE: 1998-07-10
 PRIOR APPLICATION NUMBER: US 60/052,249
 PRIOR FILING DATE: 1997-07-11

NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 67
 LENGTH: 630
 TYPE: PRT
 ORGANISM: Abies Grandis
 US-10-025-145a-67

Query Match 69.6%; Score 2264; DB 14; Length 630;
 Best Local Similarity 68.3%; Pred. No. 8.2e-208;
 Matches 435; Conservative 78; Mismatches 98; Indels 26; Gaps 9;

QY 1 MALISTPLVRSCL-----SSSHEIKALRTIPTLIGICRPGKSVASHINMCLTSVAST 54
 DB 1 MALVSTALASKSCLHKSLSISTHELKALISRTIPALGMSRKRKSITPISMSITVITVD 57
 QY 55 SVQRRVGNHYNHMDDDPIQSLISTPYGADPYERADRLIGEVDMFNKSLDEGC--- 112
 DB 58 DGLQRRIDGHSNLMDDPIQSL-STPYGEPHYERAKELIGEVKN-MFNMSLEDGEIMS 115
 QY 113 --NDLQRLLLVDVERLIGIDRHFKEIKTALDYVNSYNEKIGCGRESVYTDLNSTAL 169
 DB 116 SPLNDLIERLMMYVSSVERLIGIDRHFKEIKSALDYVYSYNGENGICGRESVYTDLNSTAL 175
 QY 170 GLRTLRHGYTVSSDVLANVFKDKNGQFSSTANIQIEGIRGVNLPRASLVAPEGEKYM 229
 DB 176 GLRTLRHGYTVSSDVLPKAFKQNGQFSCSENIQTDEIRGVNLPRASLVAPEGEKIMD 234
 QY 230 DEAEFTSTYLAELOKIPASSISLEIRDVLEYGHTNLPRLERANVMYDVFGQHTKNKA 285
 DB 235 DEAEFTSTYLAELOKIPASSISLEIRDVLEYGHTNLPRLERANVMYDVFGQHTKNKA 293
 QY 286 KKNKA---AEKLELAKLEFNIPHSLOERELKHSRWKMGSGSPMTFCRRHVEYVYAL 341
 DB 294 KKNKA---AEKLELAKLEFNIPHSLOERELKHSRWKMGSGSPMTFCRRHVEYVYAL 353
 QY 342 ASCTAFEPQSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPE 401
 DB 354 ASCTAFEPQSGFRLGFTKMSHLITVLDMDYDFGVDELELFTATIKRMDPSAMECLPE 417
 QY 402 YMKGVNMYHTVNMAREAEAGROTLNARQAMEACPDYSYQEAKWITGVLPFEETLENGK 461
 DB 414 YMKGVNMYHTVNMAREAEAGROTLNARQAMEACPDYSYQEAKWITGVLPFEETLENGK 477
 QY 462 YLENGKSSARPCALOPILTLDPFDHILKEVDPSKLANDLICIIRLKGDRCYKADARAGE 521
 DB 474 YLENGKSSARPCALOPILTLDPFDHILKEVDPSKLANDLICIIRLKGDRCYKADARAGE 537
 QY 522 ASSISCYKNDPGLTEEDALNHNFMIRDAIRELWELLKPDNSVITSKGAFFDISVW 581
 DB 534 ASSISCYKNDPGLTEEDALNHNFMIRDAIRELWELLKPDNSVITSKGAFFDISVW 593
 QY 582 DISRVMHGRYRRCYGFANVETKSLVWRITVIEPVPL 618
 DB 594 DISRVMHGRYRRCYGFANVETKSLVWRITVIEPVPL 630

RESULT 9

US-09-887-586a-30
 Sequence 30, Application US/09887586A
 Patent No. US20020094556A1
 GENERAL INFORMATION:

APPLICANT: Chappell, Joseph
 APPLICANT: No. US20020094556A1, Joseph P.
 APPLICANT: Stark, Courtney M.
 APPLICANT: Manna, Kathleen R.
 TITLE OF INVENTION: SYNTHASES
 FILE REFERENCE: 07678-025001
 CURRENT APPLICATION NUMBER: US/09/887,586A
 CURRENT FILING DATE: 2001-06-22
 PRIOR APPLICATION NUMBER: 09/398,395
 PRIOR FILING DATE: 1999-09-17
 PRIOR APPLICATION NUMBER: 60/130,628

```

: PRIOR FILING DATE: 1999-04-22
: PRIOR APPLICATION NUMBER: 60/150,262
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 58
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 30
: LENGTH: 627
: TYPE: prt
: ORGANISM: Adies grandis
: JS-09-887-586A-30

```

Query Match	67.7%;	Score 2200.5;	DB 9;	Length 627;
Best Local Similarity	68.1%;	Pred. No. 1e-201;		
Matches 427;	Conservative 77;	Mismatches 106;	Indels 17;	Gaps 7;

Qy	1	MALLSIFPVRASCJ-----SSSHKIKALRPITPLGI	CPQKSCVAVHS	INMCLTSTVASTD	55
Db	1	MALVISISPLASKSCJURKSLISSIHENKPPYRTI	PMLGNRRKRSKST	TPBMSISLATAALDD	60
Qy	56	SVQRVRGVNHSNMLDDDFEIOSLISTPYGAPDYERADRLL	IGEVKDI	IMENFMSLEBDG---	112
Db	61	GVQRRIIGDYHSINIMDDDFIOQL-STPYGEPSPQBERALI	VEVKKI	-FNSMYLDDGRILMS	118
Qy	113	--NDLLQRLLLVYDVERLIGIDRHFKKEIKTALDY	YNASVWNEKGICCGSESVYTDL	INSTAL	170
Db	119	SPNDIMQRLMTVDSVERLIGIARHFQNEJLTSALDY	FRWEEBGICGCGDSIYTDL	INSTAL	178
Qy	171	GLRTLRHGYVSVSDVNLVFKDJKNGQFSSSTANIO	IEGELRGVNLNFRASLVAFPEKXTMD	230	
Db	179	GFRITRLHGYVSPVNLVAFODQNGQFVCSPE-Q	TEGELRSTVNLNFRASLVAFPEKXTME	237	
Qy	231	EAEFTSTYKLEBALOKIPASSITLSLEIRDVLEYGHTNL	PLRLAARNYMDVFGQHTK---	N 287	
Db	238	EAEIFSTRYLKEALOKIPEVSA-LSQEI	KFWMEYGHNTMLPRLEARNYIDTLEKOTSAMJLN	296	
Qy	288	KNAEKELLEKLKENI	FHSIOERLKVSRWKKDSSPEMFPQCHRRIVEYALASCAJAF	347	
Db	297	KNAGKRLLEKLKENI	FNSLOQKELYLRMKKESDLPKLTFAHRHVEFTLASCAJAI	356	
Qy	348	EPOHSGFRLEGTKMSHLITVLDDMDVDFGVDEL	ELFATIKRMDPSAMECLPEXMKGVY	407	
Db	357	DPKISAPFLGFAKKOHLVTVLDDIYDTG	ITIDELBLFISAIKRNNSSSEIHLPEXMKCY	416	
Qy	408	MMVHTVNEMARVAEKAQGRDTLNTARQAMEAC	CFDSYNOEAKWLTGYLPTFEEYLENGK	467	
Db	417	MVVEFETVNELTREAEKTOGRNTLVNVRKAMEA	WYFDSYMEBAKMSINGVYLPMEFEEYHENGK	476	
Qy	468	VSSARPCALPILTLDDIPRPHILKEVD	PPSKNDLJCITLRJLGDPRCYCADARQEE	527	
Db	477	VSSAIRVATLOPILTLNAMPDYILKIGID	IFSRFNDLASSFLRLJGDRCTRYKADDRQEE	536	
Qy	528	ASSISCYMKDNGPLTEEDALNHNINEMIDAI	RELMWELLKPDNSVPTSISKGAFDISRW	587	
Db	537	ASCISCYMKDNGSTEEEDALNHNINAMVNDI	IKELNWEILRSNDNIPMLAKGAFTITBAL	596	
Qy	588	HHGRIYRQCYSPANVETKSLVWRVIE	614		
Db	597	HHLYIYRDGFSVANKETKLVWETTEL	623		

RESULT 10
 US-09-903-012-30
 Sequence 30, Application US/09903012
 Patent No. US20020094557A1
 GENERAL INFORMATION:
 APPLICANT: Chappell, Joseph
 APPLICANT: NO. US20020094557A1, Joseph P
 APPLICANT: Starks, Courtney M.
 APPLICANT: Manna, Kathleen R.
 TITLE OF INVENTION: SYNTASES
 FILE REFERENCE: 07678-025001
 CURRENT APPLICATION NUMBER: US/09/903,012
 CURRENT FILING DATE: 2001-07-11

```

? PRIOR APPLICATION NUMBER: 09/398,395
? PRIOR FILING DATE: 1999-09-17
? PRIOR APPLICATION NUMBER: 60/100,993
? PRIOR FILING DATE: 1998-09-18
? PRIOR APPLICATION NUMBER: 60/130,628
? PRIOR FILING DATE: 1999-04-22
? PRIOR APPLICATION NUMBER: 60/150,262
? PRIOR FILING DATE: 1999-08-23
? NUMBER OF SEQ ID NOS: 58
? SOFTWARE: FASTSEQ For Windows Version 3.0
? SEQ ID NO 30
? LENGTH: 627
? TYPE: prt
? ORGANISM: Abies grandis
? US-09-903-012-30

```

Query Match	67.7%	Score 2300.5	DB 9	Length 627
Best Local Similarity	69.1%	Pred. No. 1e-201		
Matches 427	Conservative 77	Mismatches 106	Indels 17	Gaps 7

QY	1	MAJLSITPVRSCGL-----SSHEIKALARTITPTLGICRGKSVLAHSINNCITLVSATSD	55
Db	1	MAJVSISPLASKSCLRKSLSIISIEHKRPPTYTITNLCMRKRGKSVT9SM5ISLATAPADD	60
QY	56	SVQRVRGNYSNLMDDDFIOGLISTPYGADPYRERADRLIGEVDIMFNFKSLDEGC--	112
Db	61	GVQRIRIGDGHNSINWDDPFIOGL-STPYGEPYSQRAEHLIYEVKKI-FNSWYLDGRILMS	118
QY	113	--NLLQRLILVYDVERLGIIDRHKKEIKTALDLYVNSYMKKIGCGRESVYTDINSTAL	170
Db	119	SFNLMORLMTVDSVERLGIARHKNETSLADYVFRWEBSNGCGGDSITVTDINSTAL	178
QY	171	GLRTLRHGYVSSDVLNVFQDKKGQSFSTANIOIEGIRGVNLFRASLYAFGEKVMYD	230
Db	179	GFRILRLHGYVSEVLKAFQDQNGQFYCSGC-QTGBEIRSVNLVYRASLIAPGEKMYE	237
QY	231	EAEFTSTKYLRREALOKIPASISLSLEIRDVLEYGHTNLPLEKARNYMDVCGQTK--N	287
Db	238	EAEFTSTKYLRREALOKIPVSA-LBOEIKFVMEYGMHTNLPLEKARNYIDTLCKOTSAMLN	296
QY	288	KNAEBKLELAKLEFPNI-FHLSQEBELKHKVSMWSDGSPENTFCRHRHVEYYALASCLAF	347
Db	297	KNAEGKLELAKLEFPNIFNSLOQKELYTLRWMKESDLPKLTTPARHRYVEYTTLASCLAI	356
QY	348	EPQHSFGRLGFTKMSHLITVLDMDYDVGIVDELELFTATIKRWDPASMECLPEXMKGVY	407
Db	357	DPKHSAPRLGPAKMGCHLYTVLVDYIDYDFGTIDELELFTSAIKRWMSSEIHLPEXMKGVY	416
QY	408	MMVYHTYNEAKVAKAKOGRDTLNTYAQAQWACDSTYOGEAKNATVGLPFFEEYLBENGK	467
Db	417	MVVEYETVNELTREAEKTOGRNTLNTYVRKAMAYFDSYNEAKMISNGLLPFMEEBEHENGK	476
QY	468	VSSAHRPCALOPITLTDIPFPDHILKEKVDPSKINDLICILRLRGDPRCYKADARAGEE	527
Db	477	VSSAYRAVATLOPILITLANMPDYILIKGIDFSPSRNDLASSFLRLRGDPRCYKADARAGEE	536
QY	528	ASSISCYMKDNGLTJEDBALNHNIFMTARLREINWELLKEDPNSVPTSKGHAEDISKRW	587
Db	537	ASCISCYMKDNGRSTJEDBALNHNINAMVNDIKEINWELLREISNDNI PMLAKGHAEDITRAL	596
QY	588	HGGRYRDGYSFANVETKSLMYRVIIE 614	
Db	597	HHLYIYRDGFSVANKETKGLWETLLE 623	

RESULT 11
US-09-900-797-30
; Sequence 30, Application US/09900797
; Publication No. US2003087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P
; APPLICANT: No. US2003087406A1, Joseph P
; APPLICANT: Starks, Courtney M.

APPLICANT: Manna, Kathleen R.
 TITLE OF INVENTION: SYNTASES
 FILE REFERENCE: 07678-025001
 CURRENT APPLICATION NUMBER: US/09/900,797
 CURRENT FILING DATE: 2001-07-06
 PRIOR APPLICATION NUMBER: US/09/398,395
 PRIOR FILING DATE: 1999-09-17
 PRIOR APPLICATION NUMBER: 60/130,628
 PRIOR FILING DATE: 1999-04-22
 PRIOR APPLICATION NUMBER: 60/150,262
 PRIOR FILING DATE: 1999-08-23
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 30
 LENGTH: 627
 TYPE: PRT
 ORGANISM: Abies grandis
 US-09-900-797-30

Query Match 67.7%; Score 2200.5; DB 10; Length 627;
 Best Local Similarity 68.1%; Pred. No. 1e-201;
 Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

Qy	1	MALSTITPLVRSRC-----SSSHEIKALRTIPTIGICRPGKSVASHSINMCLTSVASTD	55
Db	1	MALVISISPLAKSKCLRSKLSISSIHENKPPYRTIPMLGRKRGKSVTPKMSISLATPAADD	60
Qy	56	SVORRVGNHNSLMDDDFIQSLISTPYGADYREBRADRLIGEVKDIMNFKSLDEGC---	112
Db	61	GVORRIGDYNHIMDDFIQSL-STPYGEPGYOERAEELIVEVKI-FNSMYLDDGRIMS	118
Qy	113	--NDLQRLLLVDYVERIGIDRHFKKEIKTALDYNSYMNKSGICGGSVYTDINSTAL	170
Db	119	SPNDLMQRLMIVDSYERIGIAHFNKETSALDYFRYWEENGICGGRDSITVDINSTAL	178
Qy	171	GLRTLRHGTVSSDVNLVNFQDKNGQFSTANIQIEGIRGVNLFRASLVAFPEKYM	230
Db	179	GFRTLRHGTVSSDVNLVNFQDKNGQFVCSPG-QTEGIRSVNLVYRASLVAFPEKYM	237
Qy	231	EAETFTKYRLBEALOKIPASSILSLERDYLEYGHNTLPRLEARNYMDVFGQHTK--N	287
Db	238	EAETFTKYRLBEALOKIPASSILSLERDYLEYGHNTLPRLEARNYMDVFGQHTK--N	296
Qy	288	KNAEKLELAKLENIHSLQERELKIVSRWKSSGSPMTFCRHRYEYALASCTAF	347
Db	297	KNAEKLELAKLENIHSLQERELKIVSRWKSSGSPMTFCRHRYEYALASCTAF	356
Qy	348	EPOHSGFRLGFTKSHLITVLDMDYVGTVDLELFTATIKRMDPSAMECLPEYMKGV	407
Db	357	DPKISAFRLGFTKSHLITVLDMDYVGTVDLELFTATIKRMDPSAMECLPEYMKGV	416
Qy	408	MVYHTVNEARVAKAQRDTLVYARQAEACPDYNOEAKWIAATGYLPTFEYELNGK	467
Db	417	MVYHTVNEARVAKAQRDTLVYARQAEACPDYNOEAKWIAATGYLPTFEYELNGK	476
Qy	468	VSSAHRPCALPILTLDPFPDHLIKEVDPPSKNDLCILRLRGDRCTYKADRAEE	527
Db	477	VSSAHRPCALPILTLDPFPDHLIKEVDPPSKNDLCILRLRGDRCTYKADRAEE	536
Qy	528	ASSISCYWKDNPCLTEBDALNHINFMIRDAIRELNMWELKPDNSVPTSCKGAADISRW	587
Db	537	ASSISCYWKDNPCLTEBDALNHINFMIRDAIRELNMWELKPDNSVPTSCKGAADISRW	596
Qy	588	HGGRYRDGYSFANVETKSLVMRTVIE	614
Db	597	HGGRYRDGYSFANVETKSLVMRTVIE	623

RESULT 12
 US-09-893-820-30
 Sequence 30, Application US/09893820
 Publication No. US20040053386A1
 GENERAL INFORMATION:

APPLICANT: Chappell, Joseph
 TITLE OF INVENTION: No. US20040053386A1, Joseph P.
 FILE REFERENCE: 07678-025001
 CURRENT APPLICATION NUMBER: US/09/893,820
 CURRENT FILING DATE: 2001-06-28
 PRIOR APPLICATION NUMBER: US/09/398,395A
 PRIOR FILING DATE: 1999-09-17
 PRIOR APPLICATION NUMBER: 60/100,993
 PRIOR FILING DATE: 1998-09-18
 PRIOR APPLICATION NUMBER: 60/130,628
 PRIOR FILING DATE: 1999-04-22
 PRIOR APPLICATION NUMBER: 60/150,262
 PRIOR FILING DATE: 1999-08-23
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 30
 LENGTH: 627
 TYPE: PRT
 ORGANISM: Abies grandis
 US-09-893-820-30

Query Match 67.7%; Score 2200.5; DB 12; Length 627;
 Best Local Similarity 68.1%; Pred. No. 1e-201;
 Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

Qy	1	MALSTITPLVRSRC-----SSSHEIKALRTIPTIGICRPGKSVASHSINMCLTSVASTD	55
Db	1	MALVISISPLAKSKCLRSKLSISSIHENKPPYRTIPMLGRKRGKSVTPKMSISLATPAADD	60
Qy	56	SVORRVGNHNSLMDDDFIQSLISTPYGADYREBRADRLIGEVKDIMNFKSLDEGC---	112
Db	61	GVORRIGDYNHIMDDFIQSL-STPYGEPGYOERAEELIVEVKI-FNSMYLDDGRIMS	118
Qy	113	--NDLQRLLLVDYVERIGIDRHFKKEIKTALDYNSYMNKSGICGGSVYTDINSTAL	170
Db	119	SPNDLMQRLMIVDSYERIGIAHFNKETSALDYFRYWEENGICGGRDSITVDINSTAL	178
Qy	171	GLRTLRHGTVSSDVNLVNFQDKNGQFSTANIQIEGIRGVNLFRASLVAFPEKYM	230
Db	179	GFRTLRHGTVSSDVNLVNFQDKNGQFVCSPG-QTEGIRSVNLVYRASLVAFPEKYM	237
Qy	231	EAETFTKYRLBEALOKIPASSILSLERDYLEYGHNTLPRLEARNYMDVFGQHTK--N	287
Db	238	EAETFTKYRLBEALOKIPASSILSLERDYLEYGHNTLPRLEARNYMDVFGQHTK--N	296
Qy	288	KNAEKLELAKLENIHSLQERELKIVSRWKSSGSPMTFCRHRYEYALASCTAF	347
Db	297	KNAEKLELAKLENIHSLQERELKIVSRWKSSGSPMTFCRHRYEYALASCTAF	356
Qy	348	EPOHSGFRLGFTKSHLITVLDMDYVGTVDLELFTATIKRMDPSAMECLPEYMKGV	407
Db	357	DPKISAFRLGFTKSHLITVLDMDYVGTVDLELFTATIKRMDPSAMECLPEYMKGV	416
Qy	408	MVYHTVNEARVAKAQRDTLVYARQAEACPDYNOEAKWIAATGYLPTFEYELNGK	467
Db	417	MVYHTVNEARVAKAQRDTLVYARQAEACPDYNOEAKWIAATGYLPTFEYELNGK	476
Qy	468	VSSAHRPCALPILTLDPFPDHLIKEVDPPSKNDLCILRLRGDRCTYKADRAEE	527
Db	477	VSSAHRPCALPILTLDPFPDHLIKEVDPPSKNDLCILRLRGDRCTYKADRAEE	536
Qy	528	ASSISCYWKDNPCLTEBDALNHINFMIRDAIRELNMWELKPDNSVPTSCKGAADISRW	587
Db	537	ASSISCYWKDNPCLTEBDALNHINFMIRDAIRELNMWELKPDNSVPTSCKGAADISRW	596
Qy	588	HGGRYRDGYSFANVETKSLVMRTVIE	614
Db	597	HGGRYRDGYSFANVETKSLVMRTVIE	623

RESULT 15

US-10-025-145A-32
Sequence 32, Application US/10025145A
Publication No. US20030175861A1
GENERAL- INFORMATION:
APPLICANT: Croceau, Rodney B.
APPLICANT: Bohlmann, Joerg
APPLICANT: Steele, Christopher L.
APPLICANT: Phillips, Michael A.
TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
FILE REFERENCE: WSUR118414
CURRENT APPLICATION NUMBER: US/10/025,145A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 09/360,545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052,249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 32
LENGTH: 627
TYPE: PRT
ORGANISM: Abies Grandis
US-10-025-145A-32

Query Match 67.6%; Score 2197.5; DB 14; Length 627;

Best Local Similarity 68.1%; Pred. No. 2e-201;

Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALSTITLVRSCL-----SSHEIKALRTIPTLIGICRPGKSVASHINMCLTSVASTD 55
DB 1 MALVSISPLAKSKSCIRKSLISSIHEKPPYRTIPNLGMRGRKSVTPSMSISLATPAADD 60
QY 56 SVORRVGNHNSLMDDDFIQSLSTPYGAPDYREBRADRLIGEVKDIFMFPKSLBDG--- 112
DB 61 GVORRIGDHYNSINDDDFIQSL-STHYGEPYQERARLIVEVKI-FNSMTLDGRLMS 118
QY 113 --NDLQRLLLVDVVERLIGIDRHFKEIKTALDYVNSYMEKIGCGRESVVTDLNSTAL 170
DB 119 SFNDLMQRLWIVDSYVERLIGARHFNERTSALDYFRYWEENGICGRDSIYTDLNSTAL 178
QY 171 GLRTLRLHGTVSSSVLVNVPFKDKNGQESSSTANIOIEGIRGVNLFRASLVAFPGEKYM 230
DB 179 GFRTLRLHGTVSSPEVLKAFQDQNGQFVCSPG-QTEGIRSVLNLFRASLVAFPGEKYM 237
QY 231 EAEFTSTKYLRALOKIPASSILSLRIDVLYEGWHTNLPRLEARNYMDVFGQHTK--N 287
DB 238 EAEFTSTKYLRALOKIPVSA-LSQELKFWMEYGMHTNLPRLEARNYIDTLEKOTSAMLN 296
QY 288 KNAAEKLELAKLEFNIFHSLQERELKIVSRMKDGSPEMTFCRRHVEYYALASCIATF 347
DB 297 KNAGKLELAKLEFNIFNSLQOKELQYLNRWKSDDLKLTFAHRHVEFYTLASCIATF 356
QY 348 EPOHSGPRLGFTKSHLITVDDMYDVGVDELELFTATIKRMDPSAMECLPEYMKGVY 407
DB 357 DPKHSAFRLGFAKCHLVTLDDIYDTFGTIDELFTSAIKRWSSSEIHLPEYMKGVY 416
QY 408 MMYVHTVEMKARVAEKAQGRDTLNYARQAWACFDSYMOBAKWIATGYLPTFEELYENGK 467
DB 417 MVEFETVNELTREAEKTOGRNTLVYRKAMEAYFDSYMEBAKMSNGYLPFTFEYHENGK 476
QY 468 VSSAHRPCALPILTLIPPDHILKEVDPPSKLNDLICIILRLGDTTCYKADRRAGEE 527
DB 477 VSSAYRVATLQPIILTNLMLPDYILKIGIDPFSRFNDLASSFLRLNGDTRCYKADRRAGEE 536
QY 528 ASSISCYWKDNGULTEBDALNHNIMRDAIRBELMWELLPDNSVPITSKGAAPDISRW 587
DB 537 ASSISCYWKDNGULTEBDALNHNIMVNDIILKELMWELLRSDNIPMLAKGAPDITRAL 596
QY 588 HHGYRVDGVSFANVETSKLVMTVIE 614
HHGYRVDGVSFANVETSKLVMTVIE 614

DB 597 HHLYIRDFSVANKETKCLVMTLLE 623

Search completed: July 23, 2004, 09:09:33
Job time : 51 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 08:55:51 ; Search time 58 Seconds
(without alignments)
3010.592 Million cell updates/sec

Title: US-10-025-145A-65
3251

Perfect score: 1 MALLSTRPLVSRCLSSSHE.....PANVETSLVNRVYIEPVPL 618

Sequence: 1 MALLSTRPLVSRCLSSSHE.....PANVETSLVNRVYIEPVPL 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp19908:.*
2: Geneseqp19908:.*
3: Geneseqp20006:.*
4: Geneseqp20018:.*
5: Geneseqp20028:.*
6: Geneseqp20038:.*
7: Geneseqp20038:.*
8: Geneseqp20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3251	100.0	618	4 AAB69390	Aab69390 Grand fir
2	2453	75.5	628	2 AAB69390	Aab69390 Grand fir
3	2453	75.5	628	3 AAB69390	Aab69390 Grand fir
4	2453	75.5	628	4 AAB69390	Aab69390 Grand fir
5	2264	69.6	630	2 AAB69391	Aab69391 Grand fir
6	2200.5	67.7	627	4 AAB69391	Aab69391 Grand fir
7	2200.5	67.7	627	4 AAB69391	Aab69391 Grand fir
8	2200.5	67.7	627	4 AAB69391	Aab69391 Grand fir
9	2197.5	67.6	627	2 AAB69391	Aab69391 Grand fir
10	2197.5	67.6	627	4 AAB69391	Aab69391 Grand fir
11	2197.5	67.6	627	4 AAB69391	Aab69391 Grand fir
12	2137	65.7	630	4 AAB69392	Aab69392 Grand fir
13	2084.5	64.1	637	4 AAB69392	Aab69392 Grand fir
14	2031.5	62.5	637	2 AAB69392	Aab69392 Grand fir
15	2031.5	62.5	637	2 AAB69392	Aab69392 Grand fir
16	2031.5	62.5	637	2 AAB69392	Aab69392 Grand fir
17	1617.5	49.6	462	3 AAB18044	Aab18044 Pinus rad
18	1617.5	49.6	462	3 AAB18044	Aab18044 Pinus rad
19	1295.5	39.8	580	2 AAY06571	Aay06571 Delta-bel
20	1295.5	39.8	581	2 AAY06571	Aay06571 Delta-bel
21	1295.5	39.8	581	2 AAY06571	Aay06571 Delta-bel
22	1295.5	39.8	581	2 AAY06571	Aay06571 Delta-bel
23	1291.5	39.7	581	2 AAY06569	Aay06569 Delta-bel
24	1267.5	39.0	344	3 AAB18043	Aab18043 Pinus rad
25	1250.5	38.5	577	2 AAB69390	Aab69390 Grand fir

26	1250.5	38.5	577	4 AAB69390	Aab69390 Grand fir
27	1240.5	38.2	862	3 AAY06562	Aay06562 Pacific Y
28	1240.5	38.2	862	3 AAY06562	Aay06562 Pacific Y
29	1240.5	38.2	862	3 AAY06562	Aay06562 Pacific Y
30	1236.5	38.0	662	6 AAB09782	Aab09782 Taxadiene
31	1231	37.9	593	2 AAY06564	Aay06564 Gamma-hum
32	1231	37.9	593	2 AAY06564	Aay06564 Gamma-hum
33	1231	37.9	593	2 AAY06564	Aay06564 Gamma-hum
34	1230	37.8	593	2 AAY06564	Aay06564 Gamma-hum
35	1230	37.8	593	2 AAY06564	Aay06564 Gamma-hum
36	1188.5	36.6	817	2 AAY06566	Aay06566 Grand fir
37	1188.5	36.6	817	2 AAY06566	Aay06566 Grand fir
38	1187	36.5	702	3 AAB69391	Aab69391 Grand fir
39	1187	36.5	702	3 AAY06563	Aay06563 Grand fir
40	1187	36.5	702	3 AAB69391	Aab69391 Grand fir
41	1187	36.5	702	3 AAB69391	Aab69391 Grand fir
42	1187	36.5	817	2 AAY06567	Aay06567 E-alpha-b
43	1187	36.5	817	2 AAY06568	Aay06568 E-alpha-b
44	1187	36.5	817	2 AAY06562	Aay06562 Grand fir
45	1187	36.5	817	6 AAB09781	Aab09781 White fir

ALIGNMENTS

RESULT 1
AAB69390 standard; protein; 618 AA.
ID AAB69390
XX AAB69390;
AC AAB69390;
XX AAB69390;
DT 30-APR-2001 (first entry)
XX Grand fir monoterpene synthase protein fragment SEQ ID NO: 65.
DE Grand fir monoterpene synthase protein fragment SEQ ID NO: 65.
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition.
XX Abies grandis.
OS Abies grandis.
XX WO200107565-A2.
XX WO200107565-A2.
PD 01-FEB-2001.
XX 24-JUL-2000; 2000WO-US020264.
XX 26-JUL-1999; 99US-00360545.
XX (UNITW) UNIV WASHINGTON STATE RES FOUND.
XX Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX WPI; 2001-182782/18.
XX N-PSDB; AAF73411.
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
XX synthesis in plants, e.g. for increasing resistance to pests or for
XX treatment of cancer.
XX Claim 7; Page 150-151; 175pp; English.
XX The present invention provides the protein and coding sequences of
XX monoterpene synthases from the grand fir. These include (-)-camphene
XX synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
XX limonene, (-)-alpha-pinene synthase, limonene synthase, myrcene synthase
XX and pinene synthase. The sequences can be used to produce transgenic
XX plants expressing high levels of the enzymes, resulting in levels which
XX are useful in protecting against and treating cancers, and to confer
XX insect resistance on plants
XX Sequence 618 AA;
SQ

Query Match	100.0%;	Score 3251;	DB 4;	Length 618;
Best Local Similarity	100.0%;	Pred. No. 2.7e-295;		
Matches 618;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	MALSTPLVRSRCSLSHEIKALRRTPTLTGICRPGKSVASHINMCLTSVASTDSVQR	60	
Db	1	MALSTPLVRSRCSLSHEIKALRRTPTLTGICRPGKSVASHINMCLTSVASTDSVQR	60	
Qy	61	VGNVNSINMDDDFIOSLISTPYGADYREBRADRLIGEYKDIINFENKSLLEDGNDLLORL	120	
Db	61	VGNVNSINMDDDFIOSLISTPYGADYREBRADRLIGEYKDIINFENKSLLEDGNDLLORL	120	
Qy	121	LVDDVERLGIDIRHFKEIKETALDYNSWMNEKIGCGRESVTTDLNSTALGRLTLHG	180	
Db	121	LVDDVERLGIDIRHFKEIKETALDYNSWMNEKIGCGRESVTTDLNSTALGRLTLHG	180	
Qy	181	TVSSDVLNVFKDKNGQSFSTANIQTIEGIRGVNLFRASLVAFPGKVMDEAETFSYKL	240	
Db	181	TVSSDVLNVFKDKNGQSFSTANIQTIEGIRGVNLFRASLVAFPGKVMDEAETFSYKL	240	
Qy	241	REALOKTPASSILSLERDYLEYGMHTNLPRLEARNMDFGQHTKNKNAAEKLEIAKL	300	
Db	241	REALOKTPASSILSLERDYLEYGMHTNLPRLEARNMDFGQHTKNKNAAEKLEIAKL	300	
Qy	301	EFNIFHSLOERELKTVSRWMDSGSPENTFCRHRYEYVALASCIAPFEOHSGFRLGFTK	360	
Db	301	EFNIFHSLOERELKTVSRWMDSGSPENTFCRHRYEYVALASCIAPFEOHSGFRLGFTK	360	
Qy	361	MSHLITVLDDMYDVGVTYDELELFTATIKRMDPSAMECLPEYMKGVMMVYHTVNEMAR	420	
Db	361	MSHLITVLDDMYDVGVTYDELELFTATIKRMDPSAMECLPEYMKGVMMVYHTVNEMAR	420	
Qy	421	AEKAGSRDTLVYARQAWACEDPSYMOEAKMINTGYLPTFEEYLENGKXSSAHRPALQPI	480	
Db	421	AEKAGSRDTLVYARQAWACEDPSYMOEAKMINTGYLPTFEEYLENGKXSSAHRPALQPI	480	
Qy	481	LTLDIPEPDHILKEVDPSPKLNDLICTILRLGDRCTKADPARGEBASSISCYMKDNFG	540	
Db	481	LTLDIPEPDHILKEVDPSPKLNDLICTILRLGDRCTKADPARGEBASSISCYMKDNFG	540	
Qy	541	LTEEDALNHINPMIDARIELNWEELKPDNSVPTSCKGAFDISRYMHGYYRDOGSFA	600	
Db	541	LTEEDALNHINPMIDARIELNWEELKPDNSVPTSCKGAFDISRYMHGYYRDOGSFA	600	
Qy	601	NVETKSLVMRTVIEPVL 618		
Db	601	NVETKSLVMRTVIEPVL 618		
RESULT 2				
AAW85701				
ID	AAW85701 standard; protein; 628 AA.			
AC	AAW85701;			
XX				
XX	27-SEP-1999 (first entry)			
XX				
DS	Pinene synthase of grand fir.			
XX				
KW	Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;			
XX	defense; plant seed; oil; meal.			
OS	Abies grandis.			
XX	W09902030-A1.			
FN	21-JAN-1999.			
XX				
PF	10-JUL-1998; 98MO-US014528.			
XX				
RR	11-JUL-1997; 97US-0052249P.			
XX				
PA	(UNIW) UNIV WASHINGTON STATE RES FOUND.			

	Query Match	75.5%; Score 2453; DB 2; Length 628;
	Best Local Similarity 75.3%; Pred. No. 1.9e-220;	
	Matches 475; Conservative 59; Indels 81; Gaps 6;	
XX	Bohlmann J, Steele CL, Croceau RB;	
PI	WP1; 1999-120396/10.	
DR	N-PSDB; AAX08644.	
XX	New isolated gymnosperm monoterpene synthase DNA - obtained from Grand	
PT	fir (<i>Abies grandis</i>), used to provide plants with modified production of	
PT	monoterpenes, e.g. myrcene, limonene or pinene.	
XX	Claim 13; Page 77-79; 121pp; English.	
PS		
XX	Nucleotide sequences encoding myrcene synthase, limonene synthase and	
CC	pinene synthase from Grand fir may be incorporated into any organism	
CC	(e.g. intact plant, animal, microbe), or derived cell culture that	
CC	produces geranyl diphosphate for the production of the aforementioned	
CC	enzymes or their products. The sequences when expressed in transfected	
CC	cells may also be used for the production or modification of flavour and	
CC	aroma properties, improvement of the defense capability, and the alteration	
CC	of other ecological interactions mediated by myrcene, limonene, pinene,	
CC	or their derivatives. In particular they can be used for the production	
CC	of plant seeds for the extraction of oil or meal	
XX		
SQ	Sequence 628 AA:	
QY	1 MALSTIPVRSGL-----SSSHETALRTITTLGICRPGKVAHSINMCLSVASTD 55	
DB	1 MALVSTAPLAKSKSLKSLKSLSTHKLALSTTIALGSRGKSITPSISMSTVTVD 60	
QY	56 SVQRRVGVNHNLMDDDFIOGLISTPYGADPYRRERADLGEVNDIMENFSLDEG-- 112	
DB	61 GVRRRMGDFHNMDDDVIOGL-PTAAEKSYLERAEKLIGEVEN-MFNMSLDEGLMS 118	
QY	113 --NDLQRLLLVDVERLQIDRHFKEKITKALDYVNSYMEKGI GCGHESVYTDNLSTAL 170	
DB	119 PLNLLIQLRLMTVDSLERIGIRHFRKDEIKSLADVYYSWGENGIGCGHESVYTDNLSTAL 178	
QY	171 GLRLRLHGVYSSDVLVNPFQDKNGQFSSTANIOIEGIRGVNLFRASLVAFPGCEKYM 230	
DB	179 GLRLRLHGVYSSDVLFKAFQNGQGSNSNIGTDEIRGVNLFRASLVAFPGCEKIM 238	
QY	231 EAETFTKYLRALQKIPASSIISLIRDLVEYGMHTNLPRLERANYMDVFGQHTKNKA 290	
DB	239 EAETFTKYLRALQKIPVSS-LREIGDVLVEYGMHTNLPRLERANYIQVFGQDTEWTKS 297	
QY	291 --AEKLLIETLAKLEFNFHSIQESELKVSWMWDSQSPENTFCRHRHVEYVYALASCTAF 347	
DB	298 YVKSRLLELAKLEFNFQSLQKRELSLVNWKMSGSPENTFCRHRHVEYVYALASCTAF 357	
QY	348 EPOHSGEFLGFTKMSHLITVLADMDYDVGTVDELFTATIKRWDPSPAMECLPEYMGVY 407	
DB	358 EPOHSGEFLGFTKMSHLITVLADMDYDVGTVDELFTATIKRWDPSPAMECLPEYMGVY 417	
QY	408 MMVYHTNEMARVAEKAQGRPTLNTYAQAQMAACDSYQEKWYATGVLPPFEYELNGK 467	
DB	418 IAVYDVNEMAREAEQAQGRPTLNTYAEBAWAVYIDSYQEARWATGVLPSFEYELNGK 477	
QY	468 VSSAHRPCALOPITLDPFPPDHILKEVDFPSKINDLILCILRLRGDTCYKARARGEE 527	
DB	478 VSCGRHSIALOPITLMDPFPPDHILKEVDFPSKINDLILRLRGDTRCYKARARGEE 537	
QY	528 ASSISICYKNDPGLTEBDALNHNFMTRDAIRLBNMELKEDNSVPTSKGAHDISWV 587	
DB	538 ASSISICYKNDPGLTEBDALNHNFMTRDAIRLBNMELKEDINVPISAKGAHDIAFAF 597	
QY	588 HHGYRYDGVSEANVETKSLIMRVIVBPVL 618	
DB	598 HHGYRYDGVSEANVETKSLIMRVIVBPVL 628	

RESULT 3
AA90837
ID AA90837 standard; protein; 628 AA.
XX
AC AA90837;
XX
DT 25-AUG-2000 (first entry)
XX
DE Grand fir pinene synthase protein sequence SEQ ID NO:20.
XX
KM Synthesis: protein co-ordinate data; active site; modification; terpenoid;
KM 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KM isoprenoid; breeding programme; fragrance; flavour; pheromone;
KM defensive agent; pigment; antitumor; steroid hormone;
KM signal transduction pathway; bile acid; affinity purification;
KM photoreceptor; enzymatic synthesis; nutrient supplement;
KM immunological reagent.
XX
OS Abies grandis.
XX
PN MO200017327-A2.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US021419.
XX
PR 18-SEP-1998; 98US-010093P.
PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT) UNIV KENTUCKY RES DEPT.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappel J, Manna KR, Noel JP, Starks CM;
XX
DR WPI: 2000-292839/25.
DR N-PSDB: AAA38922.
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
PS Claim 102; Page 367-368; 450pp; English.
XX
CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AA90831. (I) contains nine alpha
CC -carbon atoms (aliphatic) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining as side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I), and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, antitumor agents,
CC components of signal transduction pathways, precursors of steroid
CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA38910 to AAA38938 and AA90831 to AA90859 represent
CC sequences used in the exemplification of the present invention
XX
XX Sequence 628 AA;

Query Match 75.5%; Score 2453; DB 3; Length 628;
Best Local Similarity 75.3%; Pred. No. 1.9e-220;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALISTPLVRSPL-----SSSEIKALRRITPTIGCRPKSVASINMCLTSTVASTD 55
DB 1 MALVSTAPLASKSLKSLKSLSTHEKSLSTRIPALGSRKSKSLTTPISMSSTTVATD 60
QY 56 SVORRVGNVNSLWDDDFIQLISTPYGAPYRERADRLIGEVKDIMENFKSLDEGC--- 112
DB 61 GVRRMGDFFHSLNMDDDVIQSL-PTAYEKSGLYERAKLIGEVKN-MRNSMSLEDGELMS 118
QY 113 --NDLQRLLLVDVERLGIQDHFKEIKTALDYVNSWNEKIGICGRESVYTDLSNRL 170
DB 119 PLNDLIQRLWVDSIERLGIHRHFDEIKSLADVYYSWGENGLIGCGRESVYTDLSNRL 178
QY 171 GLRTRLHGYVSSGVNLVFPDKNGQFSTANIOIEGRIGVNLFRASLVAFPEKXMD 230
DB 179 GLRTRLHGYVSSGVNLVFPDKNGQFSTANIOIEGRIGVNLFRASLVAFPEKXMD 238
QY 221 EAEFTSTYKLEALQKIPASSLSLEIRDLVEYGMHTNLPRLRANVMDVFGQHTKNNA 290
DB 229 EAEFTSTYKLEALQKIPASSLSLEIRDLVEYGMHTNLPRLRANVMDVFGQHTKNNA 297
QY 291 ---AEKLELAKLEFNITHSIQERELKAVSRMKDSSPEMTCFCHRRVETALASCIAF 347
DB 298 YKSKQLLELAKLEFNITHSIQERELKAVSRMKDSSPEMTCFCHRRVETALASCIAF 357
QY 348 EPOHSGFRLGFTIASHLITVDMDVDFGTVDDELPTATIKRMDPSAMECLPEYMKGY 407
DB 358 EPOHSGFRLGFTIASHLITVDMDVDFGTVDDELPTATIKRMDPSAMECLPEYMKGY 417
QY 408 MMVYHTVEMARVAKAGRDITLVYARQWACFDSYQOAKWIAATGYLPTFEVYLENGK 467
DB 418 IAVYDTVEMARVAKAGRDITLVYARQWACFDSYQOAKWIAATGYLPTFEVYLENGK 477
QY 468 VSAHRPCLQPIITLDIPFPDHLIKEVDPPSKNDLICILRLRGDRCKADARABEE 527
DB 478 VSCGRISALQPIITLDIPFPDHLIKEVDPPSKNDLICILRLRGDRCKADARABEE 537
QY 528 ASSISCYWKNPGLTEBDALNHINFMIDARLELWELLKPDNSVPIYSKKAAPDISHW 587
DB 538 ASSISCYWKNPGLTEBDALNHINFMIDARLELWELLKPDNSVPIYSKKAAPDISHW 597
QY 588 HNGRYRDGYSFANVETKSLVMTVIEPVPL 618
DB 598 HNGRYRDGYSFANVETKSLVMTVIEPVPL 628
RESULT 4
AAB69371
ID AAB69371 standard; protein; 628 AA.
XX
AC AAB69371;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-pinene synthase SEQ ID NO: 4.
XX
KM Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KM terpinolene synthase; insect resistance; nutrition.
XX
OS Abies grandis.
XX
PN MO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX

DR WPI; 2001-182782/18.
XX N-PSDB; AAF73372.
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
XX Claim 66; Page 110-112; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
CC
XX
SQ Sequence 628 AA;

Query Match 75.5%; Score 2453; DB 4; Length 628;

Best Local Similarity 75.3%; Pred. No. 1,9e-220; Mismatches 81; Indels 16; Gaps 6;

Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALSTIPLVSRSCV-----SSSHEIKALRRITPTLGI CRPGKSAHSMCLTSVASTD 55
DB 1 MALVSTAPLAKSKCLHKSLSISTHEKALSRITPALGMSRRGKSTPSSSTTVVTD 60
QY 56 SVQRRVGNHNSLMDDDPFIQSLISTPYGAPDYERADRLISEVKDIMPNFSLDEGC-- 112
DB 61 GVRRRMGDFHSLMDDDVIOQL-PTAYEKSYSLSRAEKLIEVKN-MENSMSLDEGLMS 118
QY 113 --NDLQRLILVDVERLIGIDRHFKEIKTALDYVNSYWNKGI GCGRESVTTDLNSTAL 170
DB 119 PLNDLQRLILVDVERLIGIDRHFKEIKTALDYVNSYWNKGI GCGRESVTTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQEGIRGVNLFRASLVAFPGEKYM 230
DB 179 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQEGIRGVNLFRASLVAFPGEKYM 238
QY 231 EAEFTSTKYLRALOKIPASSISLEIRDVLEYGWHTNLPRLERANVMDVFGQHTKNA 290
DB 239 EAEFTSTKYLRALOKIPASSISLEIRDVLEYGWHTNLPRLERANVMDVFGQHTKNA 297
QY 291 ---AEKLELAKLAEFNIFHSLQERELKHSRWKMDSGSPENTFCRRHVEYYALASCI 347
DB 298 YVSKKLELAKLAEFNIFHSLQERELKHSRWKMDSGSPENTFCRRHVEYYALASCI 357
QY 348 EPQSGFRIGFTKMSHLITVLDMYDVFGVDELELFTATIKRMDPSAMECLPEYMGVY 407
DB 358 EPQSGFRIGFTKMSHLITVLDMYDVFGVDELELFTATIKRMDPSAMECLPEYMGVY 417
QY 408 MMVHTVNMARVAEKAQGRPTLNYARQAWACPDSPYQEAQKATATGLTPFEETLEN 467
DB 418 IAVVDVNMARVAEKAQGRPTLNYARQAWACPDSPYQEAQKATATGLTPFEETLEN 477
QY 468 VSSAHPFCALOPITLDPFPDHLIKEVDPSKINDLICTILRLAGDRCKADARAGEE 527
DB 478 VSCGRHSALOPITLDPFPDHLIKEVDPSKINDLICTILRLAGDRCKADARAGEE 537
QY 528 ASSISCTMKDNGLTEDBALNHINFMIRDAIRELNMELKPDNSVPTSKGAPDISRW 587
DB 538 ASSISCTMKDNGLTEDBALNHINFMIRDAIRELNMELKPDNSVPTSKGAPDISRW 597
QY 588 HHGRYRDGYSPANVETKSLVMTYIESEVPL 618
DB 598 HHGRYRDGYSPANVETKSLVMTYIESEVPL 628

RESULT 5
ID AAB69391 standard; protein, 630 AA.
XX

AC AAB69391;
XX
XX 30-APR-2001 (first entry)
DT
XX
DB Grand fir monoterpene synthase protein fragment SEQ ID NO: 67.
XX
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition.
XX
XX Abies grandis.
XX
XX MO200107565-A2.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000MO-US020264.
XX
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIV) UNIV WASHINGTON STATE RES FOUND.
XX
XX Steele CL, Bohlmann J, Crocrau RB, Phillips MA;
XX
XX WPI; 2001-182782/18.
DR N-PSDB; AAF73412.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
PT
XX
XX Claim 12; Page 154-156; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
CC
XX
SQ Sequence 630 AA;

Query Match 69.6%; Score 2264; DB 4; Length 630;

Best Local Similarity 68.3%; Pred. No. 1e-202; Mismatches 98; Indels 26; Gaps 9;

Matches 435; Conservative 78; Mismatches 98; Indels 26; Gaps 9;

QY 1 MALSTIPLVSRSCV-----SSSHEIKALRRITPTLGI CRPGKSAHSMCLTSVAST 54
DB 1 MALVSSAP---KSCLAHKSLSIRSTHEKALSRITPTLGMCRGKSTPSSVMSLTTAVSD 57
QY 55 SVQRRVGNHNSLMDDDPFIQSLISTPYGAPDYERADRLISEVKDIMPNFSLDEGC-- 112
DB 58 DGLQRRIGDHSNLMDDPFIQSL-STPYGAPDYERADRLISEVKDIMPNFSLDEGC-- 115
QY 113 --NDLQRLILVDVERLIGIDRHFKEIKTALDYVNSYWNKGI GCGRESVTTDLNSTA 169
DB 116 SPLNDLIERLMDVSVRLIGIDRHFKEIKTALDYVNSYWNKGI GCGRESVTTDLNSTA 175
QY 170 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQEGIRGVNLFRASLVAFPGEKYM 229
DB 176 SGFTTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQEGIRGVNLFRASLVAFPGEKYM 234
QY 230 DEATFTSTKYLRALOKIPASSISLEIRDVLEYGWHTNLPRLERANVMDVFGQHT--- 285
DB 235 EAEFTSTKYLRALOKIPASSISLEIRDVLEYGWHTNLPRLERANVMDVFGQHT--- 293
QY 286 KNKNA---AEKLELAKLAEFNIFHSLQERELKHSRWKMDSGSPENTFCRRHVEYYAL 341
DB 294 KKKRTQYLDSEKLELAKLAEFNIFHSLQERELKHSRWKMDSGSPENTFCRRHVEYYAL 353
QY 342 ASCTAEPQSGFRIGFTKMSHLITVLDMYDVFGVDELELFTATIKRMDPSAMECLPE 401


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PR 23-AUG-1999; 99US-0150262P.
XX
XX (KENT ) UNIV KENTUCKY RES DEPT.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Chappel J, Manna KR, Noel JP, Scarke CM;
XX
XX MPI; 2000-292839/25.
DR N-PSDB; AAA38927.
XX
XX Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
XX Claim 117, Page 390-392; 450pp; English.
XX
CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC -carbon atoms (aliphac) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom ) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining aa side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I), and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, antitumor agents,
CC components of signal transduction pathways, precursors of steroid
CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity (and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
CC sequences used in the exemplification of the present invention
XX
XX Sequence 627 AA:
SQ
Query Match 67.7%; Score 2200.5; DB 3; Length 627;
Best Local Similarity 68.1%; Pred. No. 9.1e-197;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
QY 1 MALVSIPLVRSCL-----SSSHEIKALRRTIPTLGIICRPGKSAVSHINMCLTSVASTD 55
DB 1 MALVSIPLASKSKCLRSLSISIHENKPPYRTIPNLGRRGKSVTSPMSISLTAAPDD 60
QY 56 SVQRVGNHNSNLMDDDFIQSLISTPYGADPYRERADRLIGEVDIMFNFKSLDGG--- 112
DB 61 GVQRRIQDGHNSNIMDDDFIQSL-STPYGEPGYQERARLIVEVKKI-FNSMYLDDGRILMS 118
QY 113 --NDLLQRLILVNDERLIDRHRKKEIKTLDVYNSVWNKKGICCGGSAVYTDLNSIAL 170
DB 119 SFNDLMQRLWLVDSVERLGIARHFKNETTSALDYVFRWENNGICGGDSIVTDLNSTAL 178
QY 171 GLRTLRHAGVYSSDVNLVFKDKNGQSFSTANIQIEGIRGVNLFRASLVAFGEKYMVD 230
DB 179 GFTLRHAGTVSEVLKAFQDQNGQFVCSPG-QTEGIRSVNLVRLASLAFGEKYM 237
QY 231 EAETFSKYLRREALQKIPASSILSLIRDLVLEYGMHTNLPRLERANVMDFGQHTK---N 287
DB 238 EAETFSKYLRREALQKIPVSA-LSQEIKFVMEYGMHTNLPRLERANVIDTLEKDSAVLN 296
QY 288 KNAEKULELAKLEFNFIHSIOERELKIVSRWMDSSGPENTFCRHRYVEYYALASCIAT 347
DB 297 KNAKKLLELAKLEFNFIHSNQOKELQYLLRWKRESDPKLTJFARHRYVEYYTASCIAT 356
QY 348 EPQSGRLGRTKSHLITVLDMDVYGVDELLELFTATIKRMDPSAMECLPEYMKGVY 407
DB 357 DPKSARLRIGFARKCHLVTVDDIYDTFGTIDLELFLPSAIKRNSSSIEHLPEYMKGVY 416
QY 408 MMVYHTVNEARVAEKAQGRDTLNVARQWEACFDSYMQEAKWLTATGYLPTFEEYLENGK 467
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DB 417 MVVFETVNELTREAKTQGRNTLNVYKAWEAYPDSTMEAKWISNGYLPWFEEYHENGK 476
QY 468 VSSAHRPCALOPTLTLDIPFPDHLKEVDPPSKUNDILICILRLRGDTRCKADRAGEE 527
DB 477 VSSAVRAVLTQPIITLWMLPDTYLGIDIPPSRNDLASSFRLRGDTRCKADRAGEE 536
QY 528 ASSISCYMKDNPGLTEBDALNHIFMIRDAIRELWELKPDNSVPIITSKGAFDISRW 587
DB 537 ASSISCYMKDNPSTEDDALNHIAVMNDIIKELNWEILSNNDI PMLAKGHAFDITRAL 596
QY 588 HHGRRYDGYSPANVETKSLVMTVIE 614
DB 597 HHLYYRDGFSVANKETKLVMTILE 623
RESULT 8
AAB69370
ID AAB69370 standard; protein; 627 AA.
XX
XX AAB69370;
AC 30-APR-2001 (first entry)
DT Grand fir myrcene synthase SEQ ID NO: 2.
DE
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition.
XX
XX Abies grandis.
OS
XX WO200107565-A2.
PN
XX 01-FEB-2001.
PD
XX 24-JUL-2000; 2000WO-US020264.
PE
XX 26-JUL-1999; 99US-00360545.
PR
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.
PA Steele CL, Bohlmann J, Croteau RB, Phillips MA;
PI
XX MPI; 2001-182782/18.
DR N-PSDB; AAF73371.
DB New nucleic acid encoding monoterpene synthases, for increasing terpene
FT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
XX Claim 58; Page 106-107; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
XX Sequence 627 AA:
SQ
Query Match 67.7%; Score 2200.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 9.1e-197;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
QY 1 MALVSIPLVRSCL-----SSSHEIKALRRTIPTLGIICRPGKSAVSHINMCLTSVASTD 55
DB 1 MALVSIPLASKSKCLRSLSISIHENKPPYRTIPNLGRRGKSVTSPMSISLTAAPDD 60
QY 56 SVQRVGNHNSNLMDDDFIQSLISTPYGADPYRERADRLIGEVDIMFNFKSLDGG--- 112
```



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XX Grand fir monoterpene synthase protein fragment SEQ ID NO: 32.
DE
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
XX terpinolene synthase; insect resistance; nutrition.
OS
XX Abies grandis.
XX
XX W0200107565-A2.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000MO-US020264.
XX
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
XX Steele CL, Bohmann J, Croteau RB, Phillips MA;
XX
XX WPI; 2001-182782/18.
XX
XX N-PSDB; AAF73391.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
XX synthesis in plants, e.g. for increasing resistance to pests or for
XX treatment of cancer.
XX
XX
XX Disclosure; Page 138-139; 175pp; English.
XX
XX
XX The present invention provides the protein and coding sequences of
XX monoterpene synthases from the grand fir. These include (-)-camphene
XX synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
XX limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
XX and pinene synthase. The sequences can be used to produce transgenic
XX plants expressing high levels of the enzymes, resulting in levels which
XX are useful in protecting against and treating cancers, and to confer
XX insect resistance on plants
XX
XX
XX Sequence 627 AA:
SQ
Query Match 67.6%; Score 2197.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 1.7e-196;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
QY 1 MALVSTIPVSRSL-----SSSHEIKALARTIPTLIGCRPGKSAVSIINMCLTNSVSTD 55
DB 1 MALVSTIPVSRSL-----SSSHEIKALARTIPTLIGCRPGKSAVSIINMCLTNSVSTD 55
QY 56 SVQRKRVGNVSNLWDDDFIOGLISTPYGAPDYRERADRLIGEVDIMENFQSLDGG--- 112
DB 61 GVGQRIDVNSINWDDDFIOGLISTPYGAPDYRERADRLIGEVDIMENFQSLDGG--- 112
QY 113 --NDLRLRLVLDVVERKLDIRHFKKIKTALDYVNSYWNKKGICGGRSVYTLNSTAL 170
DB 119 SFNDLMORLWVDSVERLGIARHFKNETSALDVFRWENNGICGGRDSIVTDLNSTAL 178
QY 171 GLRTLRHAGTVSSDVNVFQDKNGQFSSSTANIOIEGIRGVNLFRASVAFPGKMD 230
DB 179 GFTLRHAGTVSSDVNVFQDKNGQFSSSTANIOIEGIRGVNLFRASVAFPGKMD 230
QY 231 EAETFSKYLRREALQKIPASSILSLAIRDVLYEGMHTNLPRLBARNVYDFGQHTK--N 287
DB 238 EAETFSKYLRREALQKIPVSA--LSQELKFVMEYGMHTNLPRLBARNVYDFLEKOTSAMLN 296
QY 288 KNAAEKLELAKLEFNFHSLQERELKAVSRWMDSGSPENTFCRHRHVEYALASCTAF 347
DB 297 KNAEKKLELAKLEFNFHSLQERELKAVSRWMDSGSPENTFCRHRHVEYALASCTAI 356
QY 348 EPOHSGRLGFTKMSHITVDDMYDVGVDELFLFATIKRMDPSAMECLPEYMGVY 407
DB 357 DPKHSAIRLGFARAKCHLVTVDDIYDTFGITIDELFLFSAIKRWMSSEIEHLPEYMKCVY 416
```

```
QY 408 MMYHTVNEARVAEKAQGRDTLNVARQAEACFDSYMOEAKVIATGYLPTFESEYLENGK 467
DB 417 MVVEFETVNELTREAEKTOGRNTLNVYRKAEAVFDSYMEBAKVISNGYLPFTFESEHENGK 476
QY 468 VSSNHRCAQPIITLIDIPRPHILKEVDPSPKNDICITILRLRGTRCYKADRAGEE 527
DB 477 VSSAYRAVTLQPIITLNVAMPDYLKIGIDPPSRNDLASSFLRLRGTRCYKADRAGEE 536
QY 528 ASISCYMKDNPGLTEBDALNHFIRDAIRBLMELKPDNSVPTTSKXAFDISRW 587
DB 537 ASCISCYMKDNPSTEDALNHINAMVNDIILKELMELLSNDNIPLMAKKAHDITRAL 596
QY 588 HHGYYRPGYSPANVETKSLVMRTVIR 614
DB 597 HHLYYRDGFSVANKETKLMETILRE 623
RESULT 11
ABB79395
ID ABB79395 standard; protein; 627 AA.
XX
XX ABB79395;
XX
XX 13-AUG-2002 (first entry)
XX
XX Taxadiene synthase homologous protein sequence w85710.
XX
XX Taxane; taxane synthase; taxadiene synthase; cycostatic; anticancer;
XX enzyme.
XX
XX Unidentified.
XX
XX W0200240694-A2.
XX
XX 23-MAY-2002.
XX
XX 16-NOV-2001; 2001WO-DK000763.
XX
XX 17-NOV-2000; 2000DK-00001730.
XX
XX 29-NOV-2000; 2000US-0253843P.
XX
XX (NOVO ) NOVOZYMES AS.
XX
XX
XX Vind J;
XX
XX WPI; 2002-471624/50.
XX
XX Heterologous production of taxane analogs related compound useful as
XX anticancer agent involves cloning a full-length taxane synthase pathway
XX from a taxan-producing organism into a taxane-resistant host cell.
XX
XX Example 3; Fig 1; 60pp; English.
XX
XX The present invention describes the heterologous expression of taxane
XX analogues, comprising cloning a DNA sequence comprising a taxane
XX synthase pathway, making a DNA construct in which the DNA sequence is
XX under control of regulatory elements, introducing the DNA construct into
XX a host cell, growing the host cell to produce taxane analogues, and
XX recovering the required taxane from the culture medium. Also described:
XX (1) an isolated DNA sequence comprising the taxane synthase pathway;
XX (preferably taxol synthase pathway); (2) an expression vector comprising
XX the isolated DNA sequence; and (3) a host cell comprising a taxane
XX synthase pathway derived from a taxane-producing organism, plant or
XX tissue, the taxane synthase pathway is foreign to the host cell. The
XX taxane analogues have cytostatic activity, and so can be used as
XX anticancer agents. The present sequence represents a taxadiene synthase
XX homologous protein, which is given in an example from the present
XX invention
XX
XX Sequence 627 AA:
SQ
Query Match 67.6%; Score 2197.5; DB 5; Length 627;
Best Local Similarity 68.1%; Pred. No. 1.7e-196;
```


ID AAB69392 standard; protein; 637 AA.
XX
XX AAB69392:
XX
30-APR-2001 (first entry)
XX
DE Grand fir monoterpene synthase protein fragment SEQ ID NO: 69.
XX
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KM terpinolene synthase; insect resistance; nutrition.
XX
OS Abies grandis.
XX
XX W0200107565-A2.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000MO-US020264.
XX
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
XX Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX
XX WPI; 2001-182782/18.
XX
XX N-PSDB; AAF73413.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
XX
XX Claim 54; Page 159-161; 175pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
XX
SQ Sequence 637 AA:
Query Match 64.1%; Score 2084.5; DB 4; Length 637;
Best Local Similarity 64.9%; Pred. No. 7.1e-186;
Matches 417; Conservative 80; Mismatches 115; Indels 31; Gaps 13;
QY 1 MALSLIRPL-VSRSC-----LSSSHEIKAL--RRITPTLIGICRPGKSAHSINMCLTSTA 52
DB 1 MALSLISLVQPKSCGKSLISSNVOKALCISTAVPLTRRRKOKALV--INMKTIVS 58
QY 53 STDS-----VQRRVGNVHNSLMDDPTQSLISTPYGAPDYRERADRLIGEYKDIWPNF-- 105
DB 59 HRDNGGCGVLRRIADHHPNLMEDDPFQSL-SSPYGSSSYERAVTVVEEYKE-MFNSIP 116
QY 106 --KSLEGGNDLORLLLVNDVERLGIDRHFKKEIKTALDVNSVNMKE-GICGGRSIV 162
DB 117 NNNELFSSQNDLRLMMVDSIERLGIDRHQNEIRVALDVVSYWKEKGIIGGRDSTF 176
QY 163 TDINSTALGLRTLRHAGTVSSDVLANVFKDNGQFSSSTANIQIGEI-RGYANTFRASLV 221
DB 177 PDINSTALARTLRHAGVNSDVLEFRKQKGFACPA-ILTSGQITRSTVLANVRSVLV 235
QY 222 APFGKVMDEAFETSTYKLRALOKIPASSILSLERIDVLEYGHTNLPRLEANNVDVF 281
DB 236 APFGKVMDEAFETSTYKLRALOKIPASSILSLERIDVLEYGHTNLPRLEANNVDVF 294
QY 282 GQHTKMK-----AAKLELATLEFRIFHSLOBERLKVSRWVKSGSPGMTFCRRH 335
DB 295 GQDSYESSNEMPVNTQKLKLARLEFIFHSILOBERLKVSRWVKSGSSHLFTRRH 354

QY 336 VEXYALASCIAPFEPHSGFRLGFTKMSHLITVLDMYVGVDELELFTATIKRMPSPA 395
DB 355 VEXYTMASCSIMBPKSAPFLGFTKCHLLTVLDMYVDTGTDELQFTTAFRKMDLSE 414
QY 396 MECLPEYMKGVYMMVHTTVEMARVAEKAQGRDTLNTARQAMFACPSYQOEAQVITGY 455
DB 415 TKCLPEYMKGVYMMVHTTVEMARVAEKAQGRDTLNTARQAMFACPSYQOEAQVITGY 474
QY 456 LPFEEYLENGKVSASARPCALPILTLDPFPHLKEVDPSKNDLICIIRLRGDT 515
DB 475 LPFEEYLENGKVSASARPCALPILTLDPFPHLKEVDPSKNDLICIIRLRGDT 534
QY 516 RCYKADRARGEASISCYMKDNPGLTEBDALNHINFMIRDAIRELWELLKPDNSVPT 575
DB 535 RCYKADRARGEASISCYMKDNPGLTEBDALNHINFMIRDAIRELWELLKPDNSVPT 594
QY 576 SKKHAFDISRVHMGIRYRDCYGFANVETSLVMKTYIEPVPL 618
DB 595 SKKHAFDISRVHMGIRYRDCYGFANVETSLVMKTYIEPVPL 637
RESULT 14
ID AAW85702 standard; protein; 637 AA.
XX
XX AAW85702:
XX
XX 27-SEP-1999 (first entry)
XX
XX Limonene synthase of grand fir.
XX
XX Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
KM defense; plant seed; oil; meal.
XX
XX
XX Abies grandis.
XX
XX W09902030-A1.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98MO-US014528.
XX
XX 11-JUL-1997; 97US-0052249P.
XX
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
XX Bohlmann J, Steele CL, Croteau RB;
XX
XX WPI; 1999-120396/10.
XX
XX N-PSDB; AAX08645.
XX
XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (Abies grandis), used to provide plants with modified production of
PT monoterpenes, e.g. myrcene, limonene or pinene.
XX
XX
PS Claim 14; Page 82-84; 121pp; English.
XX
XX Nucleotide sequences encoding myrcene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by myrcene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
XX
SQ Sequence 637 AA:
Query Match 62.5%; Score 2031.5; DB 2; Length 637;
Best Local Similarity 63.6%; Pred. No. 6.6e-181;

Matches	409;	Conservative	84;	Mismatches	119;	Indels	31;	Gaps	14;
QY	1	MALISTPL-VSRSC-----LSSSHEIKAL--RRTIPLGICRPGKSVASHINNCLTISVA	52						
DB	1	MALISTVSLQVPSKCGKSLISSNVOKALCISTAVPTLRMRROKALV--INMKLTFTVS	58						
QY	53	STDS-----VORRGVGNHSNLMDDDFIOQLISTYTGADYERADRILGEVYDLMFNF--	105						
DB	59	HRDNGGCVLQRIADHPNLMEDDFIOQL--SSPYGSSYSERATVVEEYKE--MFSNIP	116						
QY	106	--KSLBDGNDLQRLLLVDVERLIGIDRHFKEIKTALDVNSYVNEK--GIGGRESV	162						
DB	117	NNRRLFGSQNDLRLMMVDSIERLQIDRHFQNEIRVALDVYSYWEKEGIGGRDSTF	176						
QY	163	TDLNSTALGRTLRHGTVSSDVLNFKDNKGOPSSTANIQIEGEI--RGVNLPRASLV	221						
DB	177	PDLNSTALARTLRHLHGYNSSDVLVEYFKDEKGFACPA--ILTGGQITRSVLTNLYRASLV	235						
QY	222	AFPEKVMDEAEFTSTKYLRALOKIPASSILSLSEIRVLEYGWHTNLPRLAANYMDVF	281						
DB	236	AFPEKVMDEAEFTSASTLKKVLOKIPVSN--LSGEIEVLEYGWHTNLPRLAANYLEVY	294						
QY	282	---GQHTKNKVA---AEKLELAKLEFNIFFHSLOERELKHVSRRWKDGSPEMTFCRRH	335						
DB	295	EQSGYESTLNEMPRVNMKKLQALAKLEFNIFFHSLOERELQSISSRWKSGSQLTFTRRH	354						
QY	336	VEYYALASCIAPFPOHSGFRIGFTKMSHLITVLDMDYFEGTVDEBELFTATIKRMDPSA	395						
DB	355	VEYTMASCIISMPLKHSAPFMEFVVCGLVTLVDIYDTFGTNNELQFTDAIKRMDIST	414						
QY	396	MECLPEYMKVGVNMYHTVNMARVAEKAQRDLTNVAKOMECFQDSMEAKWINTGY	455						
DB	415	TRMLPEYMKVGVNMYLOCINEMVEAEKTOGRDMLNITQNMELPDTFMEAKWISSY	474						
QY	456	LPTFEVLENGKVSASRRPCALQPLITLDIPFPDHIKEVDFPSKXNDLIIILRLRGT	515						
DB	475	LPTFEVLENGKVSASRRPCALQPLITLDIPFPDHIKEVDFPSKXNDLIIILRLRGT	534						
QY	516	RCYADPARGEASISCTYMKDNGLTEDLNLHINFMIRALIRLWELLKPDNSVPT	575						
DB	535	RCYADPARGEASISCTYMKDNGLTEDLNLHINFMIRALIRLWELLKPDNSVPT	594						
QY	576	SKKIAFDISRYMHGVRDGYSFANVETKSLNMTVEPEVPL	618						
DB	595	SKKIAFDITRAFHVYKTRDGTIVSNNEIKNLVMTKVLLEPLAL	637						
RESULT 15									
AA90859									
ID	AA90859	standard; protein; 637 AA.							
AC	AA90859;								
DT	25-AUG-2000	(first entry)							
DE	Grand fir limonene synthase protein sequence SEQ ID NO:58.								
KW	Synthase; protein co-ordinate data; active site; modification; terpenoid;								
KW	3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;								
KW	isoprenoid; breeding programme; fragrance; flavour; pheromone;								
KW	defensive agent; pigment; antitumour; steroid hormone;								
KW	signal transduction pathway; bile acid; affinity purification;								
KW	photoreceptor; enzymatic synthesis; nutrient supplement;								
KW	immunological reagent.								
OS	Abies grandis.								
PN	W0200017327-A2.								
PD	30-MAR-2000.								
PF	17-SEP-1999; 99WO-US021419.								

PR	18-SEP-1998;	98US-010993P.
PR	22-APR-1999;	99US-010628P.
PR	23-AUG-1999;	99US-010628P.
PA	(KENT) UNIV KENTUCKY RES DEPT.	
PA	(SALK) SALK INST BIOLOGICAL STUDIES.	
PI	Chappell J, Manna KR, Noel JP, Starks CM;	
DR	WPI; 2000-292839/25.	
DR	N-PSDB; AAA38938.	
PT	Novel terpene synthase enzymes, useful for producing terpene	
PT	hydrocarbons, e.g. fragrances or antitumor agents, are derived from known	
PT	enzymes by specific amino acid alterations.	
XX	Claim 104; Page 448-450; 450pp; English.	
CC	The present invention describes an isolated terpene synthase (1)	
CC	comprising a region with at least 20% identity to region 265-535 of a 548	
CC	amino acid (aa) sequence (1a), given in AA90831. (1) contains nine alpha	
CC	-carbon atoms (alphaC) that have interatomic distances, between each	
CC	other, within tabulated ranges, have a centre point (within a sphere of	
CC	radius 2.3 Angstrom) within tabulated ranges, and have an ordered	
CC	arrangement of R groups (defining as side chains), excluding specific	
CC	tabulated arrangements (tables given in the specification). (1), and	
CC	related enzymes, are used to produce a wide range of terpenoids (e.g.	
CC	cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,	
CC	flavours, pheromones, defensive agents, pigments, antitumour agents,	
CC	components of signal transduction pathways, precursors of steroid	
CC	hormones and bile acids, as photoreceptors and as co-factor side chains.	
CC	Some synthases with little or no catalytic activity (and nucleic acids	
CC	encoding them) are used as controls in the analysis of products formed by	
CC	enzymatic synthesis; as nutrient supplements; for affinity purification	
CC	of isoprenoids; or to develop immunological reagents or nucleic acids for	
CC	monitoring expression of terpene synthase or inheritance of the gene in	
CC	plant breeding programs. The new synthases may produce novel terpene	
CC	products. AA90831 to AA90838 and AA90831 to AA90859 represent	
CC	sequences used in the exemplification of the present invention	
XX	Sequence 637 AA;	
QY	Query Match	63.5%; Score 2031.5; DB 3; Length 637;
QY	Best Local Similarity	63.6%; Pred. No. 6.6e-181;
QY	Matches	409; Conservative 84; Mismatches 119; Indels 31; Gaps 14;
QY	1 MALISTPL-VSRSC-----LSSSHEIKAL--RRTIPLGICRPGKSVASHINNCLTISVA	52
DB	1 MALISTVSLQVPSKCGKSLISSNVOKALCISTAVPTLRMRROKALV--INMKLTFTVS	58
QY	53 STDS-----VORRGVGNHSNLMDDDFIOQLISTYTGADYERADRILGEVYDLMFNF--	105
DB	59 HRDNGGCVLQRIADHPNLMEDDFIOQL--SSPYGSSYSERATVVEEYKE--MFSNIP	116
QY	106 --KSLBDGNDLQRLLLVDVERLIGIDRHFKEIKTALDVNSYVNEK--GIGGRESV	162
DB	117 NNRLFGSQNDLRLMMVDSIERLQIDRHFQNEIRVALDVYSYWEKEGIGGRDSTF	176
QY	163 TDLNSTALGRTLRHGTVSSDVLNFKDNKGOPSSTANIQIEGEI--RGVNLPRASLV	221
DB	177 PDLNSTALARTLRHLHGYNSSDVLVEYFKDEKGFACPA--ILTGGQITRSVLTNLYRASLV	235
QY	222 AFPEKVMDEAEFTSTKYLRALOKIPASSILSLSEIRVLEYGWHTNLPRLAANYMDVF	281
DB	236 AFPEKVMDEAEFTSASTLKKVLOKIPVSN--LSGEIEVLEYGWHTNLPRLAANYLEVY	294
QY	282 ---GQHTKNKVA---AEKLELAKLEFNIFFHSLOERELKHVSRRWKDGSPEMTFCRRH	335
DB	295 EQSGYESTLNEMPRVNMKKLQALAKLEFNIFFHSLOERELQSISSRWKSGSQLTFTRRH	354
QY	336 VEYYALASCIAPFPOHSGFRIGFTKMSHLITVLDMDYFEGTVDEBELFTATIKRMDPSA	395
DB	355 VEYTMASCIISMPLKHSAPFMEFVVCGLVTLVDIYDTFGTNNELQFTDAIKRMDIST	414

```

QY      396  MCELPYWKGYMMYYHHVHNEAARVAEKQOGSDLTLYAQAOWAPACDPSYMOEKATATGY  455
Dh      415  TRMLPEYKGYMMDIYQCIENNEVEBEKTKQGDMLATYIONAEALPDTMOEAKMSSSY  474
QY      456  LPTEBEYLENGKVSASAHRCALQPIITLTDIPEPDHILKEVDPPSKUNDIICITLRGDT  515
Dh      475  LPTEBEYILKNKAVSSGSRATLQPIITLTDVLPEDYITIGIDYPSRNNELASSITLRGDT  544
QY      516  RCYKADRARGEBASSISCYMKONPGITTEEDALNHINFMIRDAIRELNWELKXDNSVPI  575
Dh      535  RCYKADRARGEBASSISCYMKDHPGISEEDDALNHINAMSDALRELNWELRDSKSPIS  594
QY      576  SKKHAFDISRVWHNGRYRDGSPANVERKSLVMRTVIEBPVL  618
Dh      595  SKKHAFDITRAFHVYKTRDGTIVSNKTLNLMVKVLVEBPVL  637

```

Search completed: July 23, 2004, 09:02:26
Job time : 60 secs

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OM protein - protein search, using sw model

Run on: July 23, 2004, 09:00:27 ; Search time 21 Seconds
(without alignments)
2830.779 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251

Sequence: 1 MALLSTPLVSRSLSSSH.....FANVETKSLVWRTYIEPVPL 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	724.5	22.3	599	2 A48863	limonene cyclase -
2	717.5	22.1	554	2 S68366	(+)-delta-cadinene
3	717.5	22.1	554	2 S68365	(+)-delta-cadinene
4	689.5	21.2	591	2 H84633	probable limonene
5	669.5	20.6	520	2 A56118	verispiradiene syn
6	656	20.2	600	2 F71434	probable limonene
7	641.5	19.7	550	2 T03714	5-epi-aristolochin
8	632	19.4	559	2 T08174	sesquiterpene cycl
9	615.5	18.9	548	2 T06266	germacrene C synth
10	614.5	18.9	548	2 T06265	germacrene C synth
11	586.5	18.0	1024	2 G71434	probable limonene
12	569	17.5	632	2 B86723	hypothetical prote
13	536	16.5	598	2 H86460	hypothetical prote
14	504.5	15.5	785	2 G96825	hypothetical prote
15	504.5	15.5	785	2 T52059	ent-kaurene syntha
16	497.5	15.3	608	2 G86443	probable terpene s
17	486.5	15.0	789	2 T09672	ent-kaurene syntha
18	483	14.9	582	2 C71424	hypothetical prote
19	481	14.8	530	2 G96588	hypothetical prote
20	437.5	13.5	598	2 T00509	probable verispira
21	427.5	13.1	421	2 C96642	hypothetical prote
22	426	13.1	598	2 F96684	probable terpene s
23	425	13.1	350	2 C56118	ent-kaurene syntha
24	423.5	13.0	801	2 T06783	hypothetical prote
25	415.5	12.8	573	2 T05328	hypothetical prote
26	408	12.5	802	2 D85035	ent-kaurene synthe
27	406.5	12.5	612	2 T05331	hypothetical prote
28	405	12.5	870	2 A96637	hypothetical prote
29	404.5	12.4	823	2 T02959	kaurene synthase A

30	404	12.4	383	2 D71424	hypothetical prote
31	401	12.3	535	2 T06285	hypothetical prote
32	393.5	12.1	596	2 T05329	hypothetical prote
33	359.5	11.1	300	2 B56118	verispiradiene syn
34	320.5	9.9	471	2 T06287	hypothetical prote
35	185.5	5.7	203	2 H96525	probable terpene c
36	133	4.1	1941	2 T30554	ubiquitin-protein
37	125	3.8	1296	2 T40645	botulinum neurotox
38	120.5	3.7	943	2 B72015	metalloproteinase,
39	120.5	3.7	942	2 C86610	insulinase family/
40	120	3.7	834	2 T19010	hypothetical prote
41	119.5	3.7	1077	2 A97306	superfamily II DNA
42	117.5	3.6	1187	2 J50347	hypothetical prote
43	117.5	3.6	1493	2 A38218	GAP-associated pro
44	116	3.6	455	2 AG0189	adenylosuccinate 1
45	116	3.6	576	2 AC1384	phosphomannomutase

ALIGNMENTS

RESULT 1

A48863
limonene cyclase - spearmint
C.Species: Mentha spicata (spearmint)
C.Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999
C.Accession: A48863
R.Colby, S.M.; Alonso, W.R.; Katsahira, E.J.; McGarvey, D.J.; Croteau, R.
J. Biol. Chem. 268, 23016-23024, 1993
A.Title: 4S-limonene synthase from the oil glands of spearmint (Mentha spicata). cDNA 1st
A.Reference number: A48863 ; MUID:94043077; PMID:8226816
A.Accession: A48863
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-599 <COL>
A.Cross-references: GB:L13459; NID:G410229; PIDN:AA037366.1; PID:G410230
C.Superfamily: verispiradiene synthase 1

Query Match	22.3%	Score 724.5;	DB 2;	Length 599;
Best Local Similarity	31.7%	Pred. No. 4.1e-43;		
Matches 197;	Conservative 114;	Mismatches 249;	Indels 61;	Gaps 16;
13	SCSSHEIKALRTIPITGICRPGKSVASHINMCTSVASTSDSVQRVGNVSNLWDD	72		
20	TCLQPSH-----FKSPKLLSTNSSRSRLRVYCSSQLT-----ERRSGYNSRMVYN	71		
73	FIOSLISTPYGAPYRE-----RADRLIGEYQDIMFNKSLDEGNDLQRLLVDDVER	127		
72	FIOGULS-----DYKEDKHVIRASELVTLVK-----MELEK-ETDQIRQLBLDDLQR	118		
128	LGIDRHFKKEIKYTLTD-----YVNSYNNKKGIGCGRESVVDINSTALGLTLRLHG	179		
119	MGLDHDFNEMKEKLLSSLYLDHYYKNPFPEE-----BDLVSTSLAFILRHG	168		
180	YTVSSDVLNVFKDNGGFSSTANIQIEGEIRGVNLFPSASLVAPFGKVMDEATFSTKY	239		
169	FQVAGVDFDSFANEGERKES-----LSDDTRGGLQLVPSALTLBGETTLESABFAKPF	224		
240	LREALOKIPASSIISLEIRDVLEXGWHNTNLPRLFARNYMDVFGGHTYKNKAEXKLEIAK	299		
225	LEEKVNEGVGDGLTLRLAYSLDIPLHWIRIKRPAPVWIE---WYRKRPDMNPVLEIAI	281		
300	LEFNIFHSLOREIKHYSRWKXDSGSE-NTFCCHRYVEYVALASCLAFEOHSGFRIGF	358		
282	LDLNIIVAQFSEIKESFRMRNRNGFVEKLPFADRLVECFYMTGIIIEPQHASAKTMM	341		
359	TKMSHLITVLDMDVFGTVEDELEFATIKRMDPSAMECLPEYMKGVYNNVYTVNEMA	418		
342	GKVAALITVIDIDYDVTGLELEQFTDILRRWINSIDQLPDVMOQLFLANNFVDDTS	401		
419	RVAEKAQGRDTLNTARQAWKACFDSYQOAKWIAATGYLPTEFYELNGKVSAAHPCALQ	478		
402	YDVNKEKGVNVIPLYRSWDLADKYNVEARWFGGHKPSLEEVLEN-SMOSISGPCMLT	460		

Qy 479 PILTLIDPDPHILKE--VDPFSKINDLI---CIIIRLGRDTRCYAKADRAGEASISISCY 534
Db 461 HIF---FRVYDSFKREYVDSIKYKHDLVWSSPVLRLADDTGTVEEVSRCQVPSKLOCY 517
Qy 535 MKDNPGLTEDALNINFMIRDAIRELWMLLPDONSVPITSSKKAAPDISFVHHGYR 594
Db 518 MSDY--NASEARAKHVKWLIAEVMKKMAERVSXOSPFGKDFICGADVIGRAQLMYHNG 576
Qy 595 DGYSFANVETKSLVMRTVIEP 615
Db 577 DGHGTQHPHIIHQOMTRTLFEF 597

RESULT 2
S68366
(+)-delta-cadinene synthase isozyme Xc14 - Gossypium arboreum
C/Species: Gossypium arboreum
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C/Accession: S68366
R/Chen, X.Y.; Chen, Y.; Heinstein, P.; Davison, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A/Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A/Reference number: S68365; MUID:96132653; PMID:8554317
A/Accession: S68366
A/Molecule type: mRNA
A/Residues: 1-554 <CHB>
A/Cross-references: EMBL:U23205; NID:G1045313; PIDN:AAA93065.1; PID:G1045314
A/Experimental source: cultivar Nanking
C/Superfamily: vetispiradiene synthase 1
C/Keywords: phytoalexin biosynthesis

Query Match 22.1%; Score 717.5; DB 2; Length 554;
Best Local Similarity 31.9%; Pred. No. 1.1e-42;

Matches 184; Conservative 108; Mismatches 241; Indels 43; Gaps 14;

Qy 51 VASTDSVQRRVGNVSNLMDDPFIQSLISTPYGAPD-----YERADRLIGEYKDIMFN 104
Db 14 LSSNKDEMRKPADQPSIMGDLFL-----NCPDKNIDAEKRGQQLKEBYR----- 60
Qy 105 FKSLDEGNDLQRLLLVDVERLGIDRHFKKEIKTALDYVNSYWNKGIGCGRESVYTD 164
Db 61 -KMTVAPMANSTQCLAFIDSVQRLGVSYHFTKEIDELE--NIYHN-----NNDAMND 110
Qy 165 LNSTALGLRTLRHGTVSSDVLVNFQDKGQFSTANIOEGEIRGYLNFRAVLVAF 224
Db 111 LYTTSILRRLREHGFVNSCDVFNKFKDQGNFKSS---VTSVKGLELYQASYLAVH 166
Qy 225 GEKVMDEAEFTSTKYLRALOKIPASSILSLERIDVLEYGWHYMLPRLAARNYMDVFGQH 284
Db 167 GEDILDEAISTFTYHLSLAVASLDP--LSSEVSHALQKQIRRGLPVREAHYLSVY-QD 223
Qy 285 TKKNAAEKLELAKLEFNIFHSIOERELKXVSRWKD--SGSPMTFCRHRYVEYALAS 343
Db 224 IESHN--KVLLEFAKIDFNMLQFLHRELSLSIRWMDLPQRLPYARDRVVGYPWIS 281
Qy 344 CIAEPHSGRGLFTKMSHLITVLDYVFGVDELELFTATIKRMDPSAMECLPEYM 403
Db 282 GYVEPEYSLGRKMLTKYIMASIVDDYDSYATYEEILPYTKAIERMDIKCIDELPEYM 341
Qy 404 KGYVMYVHTVNEARVAEKAQGRDITLVARQAEACFDSYMOEAKWITATGYLPTFEYL 463
Db 342 KPSYKALLDYEEVQLVAEHGRQYRVEYAKNMIRLAQSIVLAKNTLQNYKSFEEFK 401
Qy 464 ENGVSSAHRPCALQPIITL-DIPEPHILKEVDPSKLANDLICIIIRLGDTRCYADR 522
Db 402 ANALPTCGYAMLAITSFVGMGDIVTPETFKWAANDP-KIIQASTIICRFMDVVAEHKFKH 460
Qy 523 ARGEASISICYMDNPGLTEDALNINFMIRDAIRELWMLLPDONSVPITSSKKAAPD 582
Db 461 RREDDCAIECYMEBY-GVTAQEAIVDVNKKVSESAMKQVNAEFLKP-TEMTEVYLRSLN 518
Qy 583 ISRVVHHGYRRDGYSPFANVETKSLVMRTVIEPVL 618

Db 519 LARVMDVLYREBGDYTYVGRKAAGKITSLLIEPVAL 554

RESULT 3

(+)-delta-cadinene synthase isozyme Xc1 - Gossypium arboreum
C/Species: Gossypium arboreum
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C/Accession: S68365
R/Chen, X.Y.; Chen, Y.; Heinstein, P.; Davison, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A/Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A/Reference number: S68365; MUID:96132653; PMID:8554317
A/Accession: S68365
A/Molecule type: mRNA
A/Residues: 1-554 <CHB>
A/Cross-references: EMBL:U23206; NID:G1045311; PIDN:AAA93064.1; PID:G1045312
A/Experimental source: cultivar Nanking
C/Superfamily: vetispiradiene synthase 1
C/Keywords: phytoalexin biosynthesis

Query Match 22.1%; Score 717.5; DB 2; Length 554;
Best Local Similarity 31.8%; Pred. No. 1.1e-42;

Matches 183; Conservative 107; Mismatches 243; Indels 43; Gaps 14;

Qy 51 VASTDSVQRRVGNVSNLMDDPFIQSLISTPYGAPD-----YERADRLIGEYKDIMFN 104
Db 14 LSSNKDEMRKPADQPSIMGDLFL-----NCPDKNIDAEKRGQQLKEBYR----- 60
Qy 105 FKSLDEGNDLQRLLLVDVERLGIDRHFKKEIKTALDYVNSYWNKGIGCGRESVYTD 164
Db 61 -KMTVAPMANSTQCLAFIDSVQRLGVSYHFTKEIDELE--NIYHN-----NNDAMND 110
Qy 165 LNSTALGLRTLRHGTVSSDVLVNFQDKGQFSTANIOEGEIRGYLNFRAVLVAF 224
Db 111 LYTTSILRRLREHGFVNSCDVFNKFKDQGNFKSS---VTSVKGLELYQASYLAVH 166
Qy 225 GEKVMDEAEFTSTKYLRALOKIPASSILSLERIDVLEYGWHYMLPRLAARNYMDVFGQH 284
Db 167 GEDILDEAISTFTYHLSLAVASL--DHPLEEVSHALQKQIRRGLPVREAHYLSVY-QD 223
Qy 285 TKKNAAEKLELAKLEFNIFHSIOERELKXVSRWKD--SGSPMTFCRHRYVEYALAS 343
Db 224 IESHNKA--LLEFAKIDFNMLQFLHRELSLSIRWMDLPQRLPYARDRVVGYPWIS 281
Qy 344 CIAEPHSGRGLFTKMSHLITVLDYVFGVDELELFTATIKRMDPSAMECLPEYM 403
Db 282 GYVEPEYSLGRKMLTKYIMASIVDDYDSYATYEEILPYTKAIERMDIKCIDELPEYM 341
Qy 404 KGYVMYVHTVNEARVAEKAQGRDITLVARQAEACFDSYMOEAKWITATGYLPTFEYL 463
Db 342 KPSYKALLDYEEVQLVAEHGRQYRVEYAKNMIRLAQSIVLAKNTLQNYKSFEEFK 401
Qy 464 ENGVSSAHRPCALQPIITL-DIPEPHILKEVDPSKLANDLICIIIRLGDTRCYADR 522
Db 402 ANALPTCGYAMLAITSFVGMGDIVTPETFKWAANDP-KIIQASTIICRFMDVVAEHKFKH 460
Qy 523 ARGEASISICYMDNPGLTEDALNINFMIRDAIRELWMLLPDONSVPITSSKKAAPD 582
Db 461 RREDDCAIECYMEBY-GVTAQEAIVDVNKKVSESAMKQVNAEFLKP-TEMTEVYLRSLN 518
Qy 583 ISRVVHHGYRRDGYSPFANVETKSLVMRTVIEPVL 618
Db 519 LARVMDVLYREBGDYTYVGRKAAGKITSLLIEPVAL 554

RESULT 4

H84633
probable limonene cyclase (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C/Accession: H84633

[illegible]

Db 16 EEIRPVPDPSPSLGDRFLSPSINDQVETKKAQ-----ETIEPLKEQTRSM 63
Qy 110 DGGNDLRLLLVDDVERLGIDRHFKEIKTALDYV--NSYWNKEGIGCGRESVTDL 168
Db 64 ASGRLESTLWLDIVRIELGIAVHEKEIDELDIRIYENSNFEG-----DYYNDLCTC 118
Qy 169 ALGLRTJLHGYTVSSDVLANFKDKNGQSPSSANIQIGSEIRGVNLPRASIVAPGEKV 228
Db 119 RLQRFLLQHGQVNLISLTKFSKFLDNGRKLKES---LSDVGLISLVEASHVSHGEDI 174
Qy 229 MDEAETPSTKYLRREALQKIPASSISLEIRDVLEYGHTNLPRLEARNYMDVFGCHTRNK 288
Db 175 LEDLAFSTHLESAITPLEYR--LKEQVRHLEBSLHKGIPIRIIGPFISSVYDQAIK 232
Qy 289 NAAKLELALAEFNIFFHSLOERELKHYSRWKXGSGSP--MTFCRHVEYALASCIAP 347
Db 233 N--VLLRFAPALDYMLQMLHKQELAEVSRWKXGSP--MTFCRHVEYALASCIAP 290
Qy 348 EPOHSGPRLGFTKMSHLITVLDMDVGVYDELELFTATIKRMDPSAMECLPEYMKGY 407
Db 291 EPOHSGPRLGFTKMSHLITVLDMDVGVYDELELFTATIKRMDPSAMECLPEYMKGY 347
Qy 408 MMYHTVEMARVAEKAQGRD---TLNVARQAMEACDPSYQAKWATATGYLPTFEYL 463
Db 348 -ISYKALIDLYKDYEKEMSRDGRSHVYVYAKERLELVKSVNIEAKWPIEGHMPASAYL 406
Qy 464 ENKYSASHPCALQPIITLIDIPPDHILKEVDP--SKLNDLI--CI--ILRLQDTRCY 518
Db 407 RNAFVTTYYVLTATTSYLGM-----KYAKEQGFEMLSKPKILEGCVTICVIDDIATY 460
Qy 519 KADBARGEASSISCYMKDNPGLTEEDALNHNIFIRAIRLAMELKKPDMSVPTSK 578
Db 461 EVEKRGSLSTGIECTMYRDSVSTGE--AMAKFOEGESGCMKIDNGMLRP--TPIMEPLS 518
Qy 579 HAPDISRVHMGYRY--RDGYSFANVETKSLVMTATYE 614
Db 519 RLNLARLVDTYKGNEDGYTHPEKVIKPHIIMAVD 555

RESULT 9

106266
germacrene C synthase - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T06266
R:Colby, S.M.; Crook, J.; Dowdle-Rizzo, B.; Lemaux, P.G.; Croteau, R.
Proc. Natl. Acad. Sci. U.S.A. 95, 2216-2221, 1998
A:Title: Germacrene C synthase from Lycopersicon esculentum cv. VFNT Cherry tomato: cDNA
A:Reference number: Z15576; MUID:98151492; PMID:9482865
A:Accession: T06266
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-548 <COL>
A:Cross-references: EMBL:AF035631; NID:g2967688; PIDN:AAC3943.1; PID:g2967689
A:Experimental source: cultivar VFNT
C:Superfamily: vetispiradiene synthase 1

Query Match 18.9%; Score 615.5; DB 2; Length 548;
Best Local Similarity 27.0%; Pred. No. 1.7e-35;
Matches 159; Conservative 136; Mismatches 229; Indels 65; Gaps 16;
Qy 52 ASTDSVORVGNYSNLMDDDFI-----QSLSTPYGADYRERADRLIGEVKDI 103
Db 3 ASSADKCRPLANFSPVGVHFLSYTHETNOEKVE---VDEYKETIRKMLVETCD-- 55
Qy 104 NFKSLDEGNDLRLLLVDDVERLGIDRHFKEIKTALDYV--NSYWNKEGIGCGRES 160
Db 56 -----NSTQKVLIDAMQRLGAVYHFDNEIETSIQNI FPASSKQNDND----- 98
Qy 161 VTDLNLSTALGRLTLRLHGYTVSSDVLANFKDKNGQSPSSANIQIGSEIRGVNLFRASL 220
Db 99 --NNILYVSLRFRLVROQGHYMSDVFQKFTNQDCKFET---LTNDVQGLISLVEASH 152

Qy 221 VAFPEKVMDEAFSTKYLRREALQKIP--ASSISLEIRDVLEYGHTNLPRLEARNYMD 279
Db 153 LVRNNEELTEALFTTHLESIVSNLSNNNSLVEVGEALTOPIRMTLPFGAKRTIS 212
Qy 280 VFGCHTRKNNAEK--LELAKLEFNIFFHSLOERELKHYSRWKXGSGSPMTFCRHVEY 337
Db 213 IY----ENNDAHHLILKFAKLDPMKQPHQRELSLDTLRWKDIDPANKYVYARDLVE 268
Qy 338 YVALASCIAPFQHSGLFGLTKMSHLITVLDMDVGVYDELELFTATIKRMDPSAME 397
Db 269 CYFWILGYFPEKYSRARKMTKVLNLSIIDTDFDAVATPEDELTFDAILQRMANAD 328
Qy 398 CLPEYMKGVMMVYHTVEMARVAEKAQGRDPLNVARQAMEACDPSYQAKWI--ATGYL 456
Db 329 SIQYRPAVQALDIYSEMEQVLSKEGKLDVRYAKEMKLVRAVFKETOMLDCDHI 388
Qy 457 PTFEYLENGYSSASHPCALQPIITLIDIPPDHILKEVDP--SKLNDLI--CI--ILRL 511
Db 389 PKYEQVENALVSGY-----NMISTTCLVGEIEEFTSHETFEWMLNSESIVRASALIRA 443
Qy 512 RQDTRCYADBARGEASSISCYMKDNPGLTEEDALNHNIFM--IRDAIRLAMELKKPD 569
Db 444 MMDIVGHDEDEFGHVASLIECYMKDYGASKOE--TYIKFLKEVTNAMKIDINKQFSRP- 499
Qy 570 NSVPTSKKHAFLISRVHMGYRYRDGYSFANVETKSLVMTATYEVPVL 618
Db 500 TEVPMFLVRLVNLTRVADTLTKEDQYSTAKGKLMNIPILISVKI 548

RESULT 10

106265
germacrene C synthase, epidermal - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T06265
R:Colby, S.M.; Crook, J.; Dowdle-Rizzo, B.; Lemaux, P.G.; Croteau, R.
Proc. Natl. Acad. Sci. U.S.A. 95, 2216-2221, 1998
A:Title: Germacrene C synthase from Lycopersicon esculentum cv. VFNT Cherry tomato: cDNA
A:Reference number: Z15576; MUID:98151492; PMID:9482865
A:Accession: T06265
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-548 <COL>
A:Cross-references: EMBL:AF035630; NID:g2967686; PIDN:AAC3943.1; PID:g2967687
A:Experimental source: cultivar VFNT
C:Superfamily: vetispiradiene synthase 1

Query Match 18.9%; Score 614.5; DB 2; Length 548;
Best Local Similarity 26.8%; Pred. No. 2e-35;
Matches 158; Conservative 137; Mismatches 229; Indels 65; Gaps 16;
Qy 52 ASTDSVORVGNYSNLMDDDFI-----QSLSTPYGADYRERADRLIGEVKDI 103
Db 3 ASSADKCRPLANFSPVGVHFLSYTHETNOEKVE---VDEYKETIRKMLVETCD-- 55
Qy 104 NFKSLDEGNDLRLLLVDDVERLGIDRHFKEIKTALDYV--NSYWNKEGIGCGRES 160
Db 56 -----NSTQKVLIDAMQRLGAVYHFDNEIETSIQNI FPASSKQNDND----- 98
Qy 161 VTDLNLSTALGRLTLRLHGYTVSSDVLANFKDKNGQSPSSANIQIGSEIRGVNLFRASL 220
Db 99 --NNILYVSLRFRLVROQGHYMSDVFQKFTNQDCKFET---LTNDVQGLISLVEASH 152
Qy 221 VAFPEKVMDEAFSTKYLRREALQKIP--ASSISLEIRDVLEYGHTNLPRLEARNYMD 279
Db 153 LVRNNEELTEALFTTHLESIVSNLSNNNSLVEVGEALTOPIRMTLPFGAKRTIS 212
Qy 280 VFGCHTRKNNAEK--LELAKLEFNIFFHSLOERELKHYSRWKXGSGSPMTFCRHVEY 337
Db 213 IY----ENNDAHHLILKFAKLDPMKQPHQRELSLDTLRWKDIDPANKYVYARDLVE 268
Qy 338 YVALASCIAPFQHSGLFGLTKMSHLITVLDMDVGVYDELELFTATIKRMDPSAME 397

Db 269 CFWITLGYPEEPKXSRARKNMTKYNLNTLSIIDDFDPAATATDELVTDFDIALQRRDANAD 328
 QY 398 CLPEYMKGVYMMVYHTTVNEMARVAEKAQGRDTLTVARQAMEACPDSTYMOEAKMI-ATGYL 456
 Db 329 SIQPMFPAVYQALDLIDYSEMEQVLSKEGKLDPRVYAAKNEKMLVRAVPEKOTMINDCHI 388
 QY 457 PTPEEYLVNGKVSASHRCALQPLITLIDIPPPDHLEKVDPEPSKUNDI-----CIIRL 511
 Db 389 PKREYQVNAIVASQY-----MMISTTCLVGIIEEISHETEWMLNBSVIYRASALLRA 443
 QY 512 RGDTRCYKADBARGEAASSISGCKMDNPGLTTEEDALNHNFM--IRDAIRELAMELLKPD 569
 Db 444 MNDIYGHDEDEGRGHVASTLICYMKDYGASKOE--TYIKELKEVTYNAKMDINKQFRP- 499
 QY 574 NSVPTSKGAHFDISRVMHNGRYRDPDGSFANVEKSLVMTVIEPVL 618
 Db 500 TEVPEFVIERVNLTRVADTLTYKENDTYNAKGLKNNINSILIESVKI 548
 RESULT 11
 G71434
 probable limonene cyclase - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 A:Variety: Columbia
 C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
 C:Accession: G71434
 R:Bayan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirp
 P.; Wedder, H.; Wedler, E.; Wandut, R.; Weltzienegger, T.; Pohl, T.M.; Terry, N.; Giehl
 avanagh, T.; Hempel, S.; Kotzer, P.; Entian, K.D.; Rieger, M.; Schaefer, M.; Funk, B.
 Nature 391, 485-488, 1998
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
 ehoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Reehman, S.; An
 C.; Chalwatiz, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis tha
 A:Reference number: A71400; MUID:98121113; PMID:9461215
 A:Accession: G71434
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1024 <BEV>
 A:Cross-references: GB:297341; NID:g22444991; PID:e327011; PID:g2245029
 C:Genetics:
 A:Map position: 4COP9-4G3845
 Query Match 18.0%; Score 586.5; DB 2; Length 1024;
 Best Local Similarity 30.2%; Pred. No. 4.8e-33;
 Matches 163; Conservative 109; Mismatches 195; Indels 73; Gaps 17;
 QY 86 DYREPADLLIGBKIMNFKSLBDGNDLQRLLYNDVERLIGDRHFKKEIKTALDLY 145
 Db 5 DIVEVVTLLKQGVSKML-----NETGGLBQELIDTLQLGVSHPEDIKKTLNV 57
 QY 146 NSYMKGIGCGRESVVT-----DLNSTALGLRTLRHGYTSSDVLNVFKDNGQFSSTA 201
 Db 58 ----HVKNVRAHKORIDNRMGDLVATLLEPRLRQH-----DY-----FDGNI 97
 QY 202 NIQIBG-EIRGYLNFPRASLVAFPEBKWMDAETSTYLR---EALOKIASSTLSIEI 257
 Db 98 GVDLDLQKIKGLISLYEASYSTRIIDTKLKSIIYTYRLKREYEVNNNETKSYTLRRMV 157
 QY 258 RDVLEYGHTNLPRLAEANVMDVFGQ-HTKNNAALEKLELAKLEFNIFHLSQERELGHV 316
 Db 158 IHALEMPHRRVGRLEAMWYIEVGERIDM-----PILLELAKUDFNVOAMHODELSKL 213
 QY 317 SRWKDQSG-SPEMTFCRRHRYEYVALASCIAPFQHSQSPRLGFTYMSHLITVLDMDYVF 375
 Db 214 SSWMSTKLITKLIDVRDRIRTEGYSSVGWMEPEFAHROKLTFRVFLITIIDIDYDI 273
 QY 376 GTVLELELFTATIKWDSAMECLPEYMKGVYMMVYHTTVNEMARVAEKAQGRDTLTVARQ 435
 Db 274 GLEELQPLFTTVKMDVNRLEELPNMKLCTFLCVNSIENOIGYFVLBDKGFNVIPLYKE 333
 QY 436 AMEAFDSDYMOEAKMIATGYLPTPEEYLVNGKVSAS-----HRPCALQPLITLDI--PF 487

Db 334 SWADCTTFLKAAKAYKSGYKPNFEYQNGWISSVPTLLHLFCLLSD-QTLIDIGSY 392
 Qy 488 PDHLKEVDPSFKANDLICIIIRLQGD-----TFCYADRRARGEASSISCTYMKD 537
 Db 393 NHSVRS-----SATILRIANDLATSTSVSHGFTTYNTEELRAGDTMKVQCMMHE 442
 Qy 538 NPGLEEDALNINIMIRDAIRELNWELLKPNNSVITSKGAFAIDISRVWHGGRYRDGY 597
 Db 443 T-GASEASRAVITQIIIGVAMDDLAME--KSCRLHQGFLEAANLGRVACVYQYGDGH 499

 RESULT 12
 B96723
 Hypoetical protein F205.19 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C:Accession: E96723
 R:TitleLogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizcar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.-
 C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marzalli,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: AB6141; MUID:21016719; PMID:11130712
 A:Accession: E96723
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-632 <STO>
 A:Cross-References: GB:AE005173; NID:g2194130; PIDN:AAB61105.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: P205.19
 A:Map position: 1
 C:Superfamily: vetispiradiene synthase 1

 Query Match 17.5%; Score 569; DB 2; Length 632;
 Best Local Similarity 26.5%; Pred. No. 4e-32;
 Matches 174; Conservative 120; Mismatches 276; Indels 86; Gaps 18;

 Qy 10 VSRSC----LSSHEIKALRTIPTLTGICRPGKSVASHINMC-----TSVASDSVGRV 61
 Db 16 LSRLLCRLWLSSSYVPLKSSLSFSRFPK-----LCVRAATNTDDSTTRSF 68
 Qy 62 GNYHGNLWDDDFIOGLISTPYGAPDRERAD--RLIGVADIMFNFKSLDEGDNDLQRL 119
 Db 69 TPHPPSLWGHHTLSASV-----NOTEMDLMROIEALKPIY-NMLLPICNGADAKKIT 120
 Qy 120 LINDVVERLIGIDRHKKEIKTALDVYNSYWNKEGICGGBSVTDLNSTLGLRTLRHG 179
 Db 121 CFIHITVLSIGVSYHBEKIVEFLKAFENIEDMIDCKED---DIYVASIIFRVFLYG 176
 Qy 160 YTVSS-----DVLTNPFQDKKGQSFSTANTQIEGIRGLNIFRA 218
 Db 177 HTITBELHTITSYFPFLIFHTCMCYDIPNRKFGDGNFRKCLN----DVRGMLSPYEA 232
 Qy 219 SLVAFPGKWDDEAETFTSTKYLRAL--OKIPASSILSLIRDVLEYGWHNLPRLEARN 276
 Db 223 SHFGTTTDEILEEAMSPQKHLEFLVGEKAKHYPIHTKLIQALYLPQNFNLEIIVARE 292
 Qy 277 YMDVGGQHTKKNAAEKLELAKLEFNIFHSLOERLKVSPRWK--DGSPEMTFCRHR 334
 Db 293 YIDFELFEDNH--EMLKLAKLNFRLOLOTYIQDLKTLTITWKELDLVSKIPVYFRER 349
 Qy 335 HVEYVALASCIAPFEOHSGFRLGFTMSHLITVLDMDYVFGTVDBELFTATIKRWDPS 394
 Db 350 LAEPFMAITGIYEEQYSARIMLAKSIILVDIVNTFPDYVGTIDEXSLVQAIERDSD 409
 Qy 395 AMECLPEYKGVYMMVYHTVNEMARVAEKAQGRDITLNYARQAMBACDSTMOEAKMYATG 454
 Db 410 AVDVLPDYIKVVFRTTFDLFEKLEEVVSSEASFTMQVAYEOLRIIMKGKLOEEMWNRG 469

455 YLPFEEYLENGKVSASARPCALQILTLDD-IIPPD-----HILKEVDEPSKLANDLICIL 509
470 HLPHEEYIEVGASTAG-----EVLAMPTIPMGDAAGVGVYELRSRPLTALFPAKS 524
510 RLRLDTRCYKADRRAGEEASISCYMKONPGLTEEDA-----LNIHINFIKDAIRELN 562
525 RLRLDITATYEMRGDVCNINCNTYKQHK-VSEEEACIEFEKKTNNHS-----KMN 576
563 MELIKPNSVPTISKKAHFDISRVHMHGRRYRDGVSFAVETSKLIMVTIEPVPL 618
577 EEFLKAKAFIPILHILRPVLYNGRLADVCKYGDGYTFAGEKIKOYITSLYVDLITL 632

RESULT 13

H86460
hypothetical protein Fl4W2.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: H86460
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86460
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-598 <STO>
A:Cross-references: GB:AE005172; NID:G9665095; PIDN:AF97286.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: velispiradiene synthase 1

Query Match 16.5%; Score 536; DB 2; Length 598;
Best Local Similarity 27.4%; Pred. No. 7.8e-30;
Matches 162; Conservative 123; Mismatches 254; Indels 52; Gaps 17;
44 INMLCVTASTDSQVRKGNTHS--NLMDPFIOSLSTPYGADPYRERADRLIGEVDI 101
44 LNLGVKASCKTSQVSSRPLPHSAPDLMGHIL-----SVPTENSEFPTLETETESI 95
102 MFNFKS-LEDSGNLLRLLLVDVERLGDHFKKEIKTALDY-----VNSYMEKIGIC 156
96 KPKVRNMLMSHKTDEKICILHILICGTHTYFEKEIEETLEQAFKLDMLFTDE---- 151
157 GRESVVNDLNSALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEBEIRGVNL 216
152-----DLETTALMFVEFRLYGHKISCDVDRFKGVADAKFE---HLVSDVAGMLQLY 201
217 RASLVAPGKGVMDAETFSKYRLREAL--OKIPASSLSLEIFDVLEYGMHTNLPRL 274
202 EAAHLATPFEITLDEALSF-TRYHLESLAGQAATAPIH-SHHIINALYKPRFLKMEI 259
275 RNVDVVGQHTKNGNAEKLLELAKLEFNIPHSLOERELKHVSRRMKDQSGSP-EMTF 333
260 REYIHFF-----QKSGHETILIKFPAKLNPFQQLHYRELKTLTKMKDIDLPTK 315
334 RHVEYVALASCIAPGPHSGFRIGFTKMSHLITVLDMDYDVGVDELFTATIKRMDP 393
316 RLLETFIGVAVVLEPHYSIGRIATKVSQYIVVMDTCDAYGTFSEVRSILDSLERMD 375
394 SNAECLPEYMGKVMYHTYENMAVAEKAQGR-----DTLANARQAMECFSPYQEA 448
376 GAIIDLKPSCLRTIVQISIVETMEDIER-EMKPRGRSSVQDVETEEKIKMGRA---Y 430
449 KWIATGYLPTFEEYLENGKVSASARPCALQILTLDDIPFDHILKEVDPSKLANDLIC 508

431 KMAAGHVPTFDQDIETELGDSGGRCPAMYSFIMEDDEENQTNAMFKSKRMALASVI 490
509 LRLDTRCYKADRRAGEEASISCYMKONPGLTEEDA-----LNIHINFIKDAIRELN 568
491 FRLTNDIAGFEERARRGCVVGVANCYVQH-NVTKELAVREIKKIRINNYIMMEEF 549
569 DN-SVPTISKKAHFDISRVHMHGRRYRDGVSFAVETSKLIMVTIEPVPL 618
550 KSVSRPIVLR--CFNIVRLVNLVEEGDNFTNPKGLDITLSLFPHEPL 598

RESULT 14

G96825
hypothetical protein T8K14.12 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96825
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96825
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-785 <STO>
A:Cross-references: GB:AE005173; NID:G94835764; PIDN:AD030231.1; GSPDB:GN00141
C:Genetics:
A:Gene: T8K14.12
A:Map position: 1

Query Match 15.5%; Score 504.5; DB 2; Length 785;
Best Local Similarity 28.8%; Pred. No. 2e-27;
Matches 152; Conservative 105; Mismatches 230; Indels 41; Gaps 15;
114 DLQRLLLVDVERLGDHFKKEIKTALDVNSYMEKIGICGRESVNTDNLSTALGLR 173
270 DQYRLSTIYVLESGLDRDFTKIKSILDETYWLR-----GDEICDLATCALAFR 324
174 TLRHGYTVSSDVLNVFKDKNGQFSSTANIQIEBEIR---GVNLFRASLVAPGKGYMD 230
325 LLLHAGVDVGYDPLKPFABSSG-FSDT---LEGVYKNTFSVLELFPKA-QSYPHESAL 378
231 EAEPFSTKYRLREALOKIPASSI---LSLEIRDVLEYGMHTNLPRLERANMYDVGQHT 286
379 KQCCMTQYQLEMLSSWVKSVRDYKKEVEDLAPPSYASLERSRSHRRI-LNGSAVE 437
287 NKNAAB-----KLLELAKLEFNIPHSLOERELKHVSRRMKDQSGSPMTFCRRH 335
438 NTRVTKTSYRLNICTSDILKLAVDNPFQCSIRREBERLDRIIVENRLODELFAKOKL 497
336 VEYVALASCIAPGPHSGFRIGFTKMSHLITVLDMDYDVGVDELFTATIKRMDPSA 395
498 AYCFSGAATLPSLELDARISMAKGVLTIVVDPDFDVGSKSELELJHLVEKMDLNG 557
396 M-ECLPEYMGKVMYHTYENMAVAEKAQGRPTLVYARQAWACPDSTYQEAQKATG 454
558 VPEYSSHVELIFSVLADDTLLETGDKAFYQGRVTHIYIWDLLKSMLEKLEWSSDK 617
455 YLPFEEYLENGKVSASARPCALQILTLDDIPFDHILKEVDPF--SKNDLJCILRLR 512
618 STPLEIDYENAYISFALGPIVLPATYILIGPRLP---KIVDSQYQYLYLVYTMGRLL 674
513 GDRFCYKADRRAGEEASISCYMK-DNPGLTEEDALNHNIFMIRDAIRELWELLKPDNS 571
675 NDIGFGRSAEG-KLNAVSLHMGHERDNRSKVEYIISMKGIAERKREELHKLVLBEKGS 733

```
Qy      572 VPITSKKIAF-DISRWVHHGYYRRDGYSPANVETKSLVMRTVIEPVL 618
      | | | | | | | | | | | | | | | | | | | | | |
Db      734 VVPRECKEAFLLKMSKVLNLFYRKDDG--FTSNDIMSLVKSVIYEPVSL
      | | | | | | | | | | | | | | | | | | | | | |
```

RESULT 15

ent-kaurene synthase (EC 2.5.1.-) [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C/Accession: T52059
C/Yamaguchi, S.; Sun, T.; Kawaide, H.; Kamiya, Y.
J. Am. Chem. Soc. 117: 1227-1230, 1995

Query Match	15.5%	Score 504.5	DB 2	Length 785
Best Local Similarity	28.8%	Pred. No. 2e-27		
Matches 152; Conservative	105	Mismatches 230	Indels 41	Gaps 15

Qy	114	DLORLLVDDVERGIGIRHPEKEIKTALDVYNSWNEKGKIGCGSESVTDLNSPALGIR	173
Db	270	DÖYARLSITVLEBSIGIDRODFTEIKSLIDREYRWLR-----GBELCIDLATCALAFR	324
Qy	174	TLRLHGTVSSDVLVNFKDNGQFSSTANIQGEIR--GYLNIFRSLVAFPECKYMD	230
Db	325	LILLAHGYVSDYDPLKPFABESG-FSDT-----LEGYKNTFSVLEJPFKAA-OSYPHESALK	378
Qy	231	EAEFSTKYLEALÖKI PASSI-----LSLEIRDVLEYGQHTLPTLEARNVWDVGQATK	286
Db	379	KÖCMTKOYLEMELSWVKTSYVRDKYLLKEVEDALAFSYASLESNDHRKI-LNGSAVE	437
Qy	287	MKNAAE-----KLEBLAKLEFNI FSLÖREBLKHVSRWKDGSPEMTECRHRH	335
Db	438	NTRVTKTSYRLHNICTSDILKLAVDPDFNFCOSIHREEMERLDRIWENRLÖELKFAKOQL	497
Qy	336	VEYVALMSCLAFEPHOGSFLGFTGMSHLITVLDMDVYFVGVDLEFTATIKEMDQSA	395
Db	498	AYCPSGATLTFSPELSDARISMAKGYVLTIVDDPFIVDGSKELEMLIHLEWMDIANG	557
Qy	396	M-ECLPEYMKGVMMVYHTVNEEMAVAEKAOGRDILANARQAMEACFDSYMOEAKMIATG	454
Db	558	VPEXSEHVEIIFSVLRDTILETGDKAFYQGRNVTHIIVKIMLDLMSKMLEAEMSSDK	617
Qy	455	YLFFPEEILENGKYSASRRCALQPIILDLIPFRPHILKEVDF--SKLNDLICILILAR	512
Db	618	STPSLEDMEANAYISFALGPIVLPRATYLLIGPLPE--KTVDSHOYNÖLYKLVSTMGRLL	674
Qy	513	GDTRCYKADRARGEASSISCYCM-DNEGLTPEEDLNLNINFMIRAIRIELNMLLETKPNUS	571
Db	675	NDIGQFKRESABG-KLNAVSLMHKMERONRSKEVILIEBCKGLAEKRREELHKLVLBEKGS	733
Qy	572	VPIISKHAFF-DISRWVHHGYRIYDGYFANVETYSLVKRYTIVIEVPL	618
Db	734	VVPECKEAFUKMSKVNLVFRKDDG--FTSNDLMSLVKSVIYEEVSL	779

Search completed: July 23, 2004, 09:04:15
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 08:56:41 ; Search time 13 Seconds
(Without alignments)
2475.335 Million cell updates/sec

Title: US-10-025-145A-65

Sequence: 1 MALLSTPLVSRCLSSHE.....FANVETSLVWRTYIEPVL 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2453	75.5	628	1	TSDB1 ABIGR
2	2200.5	67.7	628	1	TSDB1 ABIGR
3	2031.5	62.5	637	1	TSDB1 ABIGR
4	1240.5	38.2	862	1	TASV1 TAXBR
5	1238.5	38.1	862	1	TASV1 TAXBA
6	1209.5	37.2	862	1	TASV1 TAXCH
7	717.5	22.1	554	1	DCS1 GOSAR
8	717.5	22.1	554	1	DCS2 GOSAR
9	701.5	21.6	554	1	DCS3 GOSAR
10	699.5	21.5	555	1	DCS3 GOSAR
11	692.5	21.3	554	1	DCS1 GOSAR
12	667	20.5	601	1	CAS5_RICCO
13	644.5	19.8	548	1	SEAS_TOBAC
14	133	4.1	1941	1	UBR1_KLUDIA
15	125	3.8	1295	1	BXA2_CLOBO
16	117.5	3.6	1513	1	GRLF_BAT
17	114	3.5	456	1	PUR8_ECOLI
18	111.5	3.4	602	1	LEPA_HELPY
19	110	3.4	2875	1	RRLP_TSWVL
20	109.5	3.4	1513	1	GRLF_HUMAN
21	108.5	3.3	570	1	ESRA_BACNA
22	108.5	3.3	1061	1	CCS3_YEAST
23	107	3.3	815	1	CCS3_YEAST
24	105.5	3.2	428	1	SVS_PASNU
25	105.5	3.2	1026	1	YVW6_YEAST
26	105.5	3.2	1026	1	MYV6_YEAST
27	105	3.2	1790	1	VIT_ANTGR
28	104.5	3.2	570	1	CHLB_PINTH
29	104.5	3.2	570	1	ESRA_BACRA
30	104.5	3.2	1500	1	GRLF_CANFA
31	104	3.2	1510	1	MUKB_HAEIN
32	103.5	3.2	598	1	SYD_LACPL
33	103.5	3.2	822	1	VZA_BMV

34	103	3.2	666	1	NEBU_HUMAN	P20929 homo sapien
35	102.5	3.2	567	1	YER2_MERTJA	O56823 methanococ
36	102.5	3.2	1085	1	CASR_BOVIN	P33384 bos taurus
37	102.5	3.2	2364	1	SPCO_HUMAN	Q01082 homo sapien
38	102	3.1	592	1	SYD_THETN	O8ra17 thermoaer
39	102	3.1	700	1	LSHR_RAT	P16235 rattus norv
40	102	3.1	4036	1	RRLP_DUGBV	O66431 dudge virus
41	101.5	3.1	692	1	IFP2_OCEIH	O66431 oceanobacil
42	101.5	3.1	820	1	SUS2_TUGE	Q41607 tulipa gesn
43	101	3.1	1277	1	IFB3_YEAST	Q03690 saccharomyc
44	100.5	3.1	418	1	YER8_SCHPO	O14303 schizosacch
45	100.5	3.1	519	1	YMP4_YEAST	Q04347 saccharomyc

ALIGNMENTS

RESULT 1	ID	TSDB1 ABIGR	STANDARD	PRT	628 AA.
AC	O24475	TSDB1 ABIGR	STANDARD	PRT	628 AA.
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Pineene synthase, chloroplast precursor (EC 4.2.3.14) (Beta-geraniolene synthase) ((-)-(1S,5S)-pinene synthase).				
GN	Ag3.18.				
OS	Abies grandis (Grand fir).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
CC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.				
OX	NCBI_TaxId=46611;				
RN	[1]				
RP	SEQUENCE FROM N. A. AND CHARACTERIZATION.				
RA	MEDLINE=97413772; PubMed=9268308;				
RX	Bohlmann J., Steele C.B., Crocneau R.;				
RT	"Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";				
RL	J. Biol. Chem. 272:21784-21792(1997).				
CC	- FUNCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene (C10) olefins biosynthesis. A mixture of alpha-and beta-pinene is produced by this enzyme.				
CC	- CATALYTIC ACTIVITY: Geranyl diphosphate = pinene + diphosphate.				
CC	- COFACTOR: Manganese and potassium.				
CC	- PATHWAY: Oleosteroidosis.				
CC	- SUBCELLULAR LOCATION: Chloroplast.				
CC	- INDUCTION: By wounding.				
CC	- SIMILARITY: Belongs to the terpene synthase family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; U87909; AAB710E5.1; -.				
CC	HSSP; Q40577; SEAT.				
CC	InterPro; IPR008930; Terp_cyc_toroid.				
CC	InterPro; IPR001906; Terp_synth-like.				
CC	InterPro; IPR005630; Terpene_synth_C.				
CC	InterPro; IPR008949; Terpenoid_synth.				
CC	Pfam; PF01397; Terpene_synth; 1.				
CC	Pfam; PF03936; Terpene_synth; 1.				
CC	Lyase; Manganese; Transic peptide; Chloroplast.				
CC	TRANSIT				
CC	CHAIN				
CC	ACT_SITE				
CC	ACT_SITE				
CC	ACT_SITE				
CC	SEQUENCE				

Query Match 75.5%; Score 2453; DB 1; Length 628;
Best Local Similarity 75.3%; Pred. No. 3e-158;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALISTPLVRSGL-----SSSHEIKALRTTPTLGI CRPGKSVANSINMCLTQSVASTD 55
DB 1 MALVSTPLASKSCLHRSLSISTHETKALSRITPALGMSRGRKSGITSISMSSTTVVTD 60
QY 56 SVORVGNHNSNMDDDPFIOSLSTPGADPRERARLIGEVNDIMNPFSLDGG--- 112
DB 61 GVRKRWDDFHSNMDDDVIOSL-PTAYEKSYLEAEKLIQEVKN-MFNSMSLEDGLMS 118
QY 113 --NDLQRLLVDDVERLIGIDRHFKKEIKTALDVNSYMNKEGIGCGRESVYTDLNSTAL 170
DB 119 PLNDLIGRLMIVDSLEHGLIHRHFKDEIKSALDVYYSWGMNGIGCGRESVYTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLVNFKDNGQFSSSTANIQIBEGIRGVNLPRASLVAFFGEKYM 230
DB 179 GLRTLRLHGYTVSSDVLFKAFKQNGQFSSSBNIQTDEIRGVNLPRASLVAFFGEKIMD 238
QY 231 EAEFSTRKYREALOKIPASSILSLERDVLEGMHNTLPRLEARNYMDVFGCHTKKNA 290
DB 239 EAEFSTRKYREALOKIPVSS-LSREIGDVEYGMHTYLPRLERKNYIQVFQDTEKTS 297
QY 291 ---AEKLELAKLEFNFHSLQERELKHVSRRMWDGSGPEMTFCRRHVEYYALASCI 347
DB 298 VVSKKULELAKLEFNFHSLQERELSLVYMWKESGPEMTFCRRHVEYYALASCI 357
QY 348 EPOHSGRLGFTKMSHLITVLDNMYDFGVYDELFTATIKRWDPSAMECLPEYMKGVY 407
DB 358 EPOHSGRLGFTKMSHLITVLDNMYDFGVYDELFTATIKRWDPSAMECLPEYMKGVY 417
QY 408 MMVYHTNEMARVAREKQGRDITLVYARQAECDSYMOEAKWTATGLPTFEYLENGK 467
DB 418 IAVDITNEMAREBEKQGRDITLVYAREAMAYIDSTOEBKMATGYLSPFDEYENK 477
QY 468 VSSAHRPCALOPTITLDIPPPDHILKEVDPSKINDLICILRLRGDTRCYKADRANGEE 527
DB 478 VSCHRISALOPTITLMOIPPPDHILKEVDPSKINDLICILRLRGDTRCYKADRANGEE 537
QY 528 ASSISCYMKONPGLTBEDALNHNFMTRDAIRLBNWELKPDNSVPTSKGAFDISRW 587
DB 538 ASSISCYMKONPGVSEBEDALNHNFMTRDAIRLBNWELKPDINVPISAKGAFDIARAF 597
QY 588 HHGYRYDGYSFANVETKSLVMTVIEBPVL 618
DB 598 HHGYRYDGYSFANVETKSLVMTVIEBPVL 628

RESULT 2
TS2D ABIGR STANDARD; PRT: 627 AA.

AC 024474;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myrcene synthase, chloroplast precursor (EC 4.2.3.15).
GN AG2.2.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxId=46611;
RN [1]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohlmann J., Steele C.U., Croteau R.;
RT "Monoterpene synthases from grand fir (*Abies grandis*). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-
(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RT J. Biol. Chem. 272:21784-21792(1997).
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene

CC (C10) olefins biosynthesis.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = myrcene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleoresinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By wounding.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; U87908; AAB71084.1; -.
DR HSSP; Q40577; SEAS.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR Pfam; PF01397; Terpene synth; I.
DR Pfam; PF03936; Terpene synth_C; 1.
DR Lyase; Manganese; Transf. peptide; Chloroplast.
KW TRANSIT ?
FT CHAIN 1 627
FT ACT_SITE 523 523 MYRCENE SYNTHASE.
FT ACT_SITE 600 600 BY SIMILARITY.
FT ACT_SITE 604 604 BY SIMILARITY.
SQ SEQUENCE 627 AA; 72478 MW; 2E0DA492B0C971PD CRC64;

Query Match 67.7%; Score 2200.5; DB 1; Length 627;
Best Local Similarity 68.1%; Pred. No. 3.4e-141;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALISTPLVRSGL-----SSSHEIKALRTTPTLGI CRPGKSVANSINMCLTQSVASTD 55
DB 1 MALVSTPLASKSCLHRSLSISTHETKALSRITPALGMSRGRKSGITSISMSSTTVVTD 60
QY 56 SVORVGNHNSNMDDDPFIOSLSTPGADPRERARLIGEVNDIMNPFSLDGG--- 112
DB 61 GVRKRWDDFHSNMDDDVIOSL-STPYGEPSTOERARLLIVEVKI-FNSNYLDDGLMS 118
QY 113 --NDLQRLLVDDVERLIGIDRHFKKEIKTALDVNSYMNKEGIGCGRESVYTDLNSTAL 170
DB 119 SPNDLIGRLMIVDSVEHGLIARHFKDEIKSALDVYYSWGMNGIGCGRDSVYTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLVNFKDNGQFSSSTANIQIBEGIRGVNLPRASLVAFFGEKYM 230
DB 179 GLRTLRLHGYTVSSDVLFKAFKQNGQFSSSBNIQTDEIRGVNLPRASLVAFFGEKIME 237
QY 231 EAEFSTRKYREALOKIPASSILSLERDVLEGMHNTLPRLEARNYMDVFGCHTK---N 287
DB 238 EAEFSTRKYREALOKIPVSA-LSQETKFWEGMHNTLPRLEARNYIDTLEKDTSAMLN 296
QY 288 KNAEKLLELAKLEFNFHSLQERELKHVSRRMWDGSGPEMTFCRRHVEYYALASCI 347
DB 297 KNAGKULELAKLEFNFHSLQERELSLVYMWKESGPEMTFCRRHVEYYALASCI 356
QY 348 EPOHSGRLGFTKMSHLITVLDNMYDFGVYDELFTATIKRWDPSAMECLPEYMKGVY 407
DB 357 EPOHSGRLGFTKMSHLITVLDNMYDFGVYDELFTATIKRWDPSAMECLPEYMKGVY 416
QY 408 MMVYHTNEMARVAREKQGRDITLVYARQAECDSYMOEAKWTATGLPTFEYLENGK 467
DB 417 MMVYHTNEMAREBEKQGRDITLVYAREAMAYIDSTOEBKMATGYLSPFDEYENK 476
QY 468 VSSAHRPCALOPTITLDIPPPDHILKEVDPSKINDLICILRLRGDTRCYKADRANGEE 527
DB 477 VSSAHRPCALOPTITLTMIPPPDHILKEVDPSKINDLICILRLRGDTRCYKADRANGEE 536
QY 528 ASSISCYMKONPGLTBEDALNHNFMTRDAIRLBNWELKPDNSVPTSKGAFDISRW 587


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DB 537 ASCSCMKONPGSTEDALNHNAMVNDIKELNELLRSDNINPMUAKGHADITRAL 596
QY 588 HHGYYRDGYSFANVETKSLVMTVIE 614
DB 597 HHLYYRDGFSVANKETKLVMTITLE 623

RESULT 3
TSID3_ABIGR STANDARD; PRT; 637 AA.
AC 022340;
DT 28-FEB-2003 (Rel. 41, Last Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (-)-(4S)-limonene synthase, chloroplast precursor (EC 4.2.3.16).
GN AG10.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=4611;
RN 11
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RA MEDLINE=9741372; PubMed=9268308;
RA Bohmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase."
RL J. Biol. Chem. 272:21784-21792(1997).
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC response to insect attack or other injury. Involved in monoterpene
CC (c10) olefin biosynthesis.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = limonene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleoresinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By wounding.
CC -1- SIMILARITY: Belongs to the terpene synthase family.

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CC -----
DR EMBL: AF06193; AAB70907.1; -
DR InterPro: IPR008930; Terp_cyc_toroid.
DR InterPro: IPR001906; Terp_synth-like.
DR InterPro: IPR005630; Terpene_synth_C.
DR InterPro: IPR008949; Terpenoid_synth.
DR Pfam: PF01397; Terpene_synth_C.1.
DR Pfam: PF03936; Terpene_synth_C.1.
DR Lysase: Manganese; Transit peptide; Chloroplast.
KM TRANSIT 1
FT CHAIN 1
FT ACT_SITE 533 637 CHLOROPLAST (POTENTIAL).
FT ACT_SITE 533 637 (-)-(4S)-LIMONENE SYNTHASE.
FT ACT_SITE 610 610 BY SIMILARITY.
FT ACT_SITE 614 614 BY SIMILARITY.
SQ SEQUENCE 637 AA; 73477 MW; 8E80CD9DDE86898 CRC64;

Query Match 62.5%; Score 2031.5; DB 1; Length 637;
Best Local Similarity 63.6%; Pred. No. 9.2e-130;
Matches 409; Conservative 84; Mismatches 119; Indels 31; Gaps 14;

QY 1 MALISTPL-VSRSC-----LSSSHEIKAL--RTIPLGICRPGKSVASHINMCTLSVA 52
DB 1 MALISTVLOVPKSCGLKSLISSNVQALCISTAVPLRKRROKALV--INMKTIVS 58
QY 53 STDS-----VORVGNVHSLMDDFIOGLISTPYGADYERARLIGEVKDIWPNF-- 105
DB 59 HRDNGGCVLORRIADHHPNLMEDDFIOGL--SSPYGSSYSERAEATVEEYVE--MFSNP 116

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QY 106 --KSLDGGNDLRLVLDVVERLGIDRHKKEIKTALDVYNSYMEK-GIGGGRSV 162
DB 117 NNRRLPGSNDLRLVMDVSIERLGIDRHFQNEIRVALDVYISYMEKEGIGGRDSTF 176
QY 163 TDLNSTALGRTLLHGYTVSSDVLNFKDNQGFSSPANIQIGEI-RGYLNFRASLV 221
DB 177 PDLNSTALARTLLHGYTVSSDVLNFKDQGFHACPA-ILTEGQITRSVLNIRASLV 235
QY 222 APFGKYMDEATVSTIKYLRALOKIPASSILSLIRVDVLEYGHNTNLPRLRANVMVF 281
DB 236 APFGKYMDEATVSTIKYLRALOKIPASSILSLIRVDVLEYGHNTNLPRLRANVMVF 294
QY 282 ---GQHTKNKA---AKLTLELAKLEFNIHPSLGERELKSRMKSGSPMTFCRRH 335
DB 295 EQSGYSEINEMPNMMKLQJLALFELFHSLLQJRELQISRWKSGSSQLFTFRH 354
QY 336 VEYVALASCIAPFQHSFRLGFTKMSHLTVLDMYDFCTVDELEFTATIKRMDPSA 395
DB 355 VEYTMASCIAPFQHSFRLGFTKMSHLTVLDMYDFCTVDELEFTATIKRMDST 414
QY 396 MECLPEYKGVYMMVYHTNEMARVAEKAQGRDTLNTARQWEACFDSYMOEAKVIATGY 455
DB 415 TRMLPEYKGVYMMVYHTNEMARVAEKAQGRDTLNTARQWEACFDSYMOEAKVIATGY 474
QY 456 LPTREYVLENGKVSARPCALOPILTLDPFPDHIKEVDPSPKANDLICIIIRLRGDT 515
DB 475 LPTREYVLENGKVSARPCALOPILTLDPFPDHIKEVDPSPKANDLICIIIRLRGDT 534
QY 516 RCYADPARGEEASISCYMKDNPGLTEEDALNINFMIRDAISELNMELKPNVSVEIT 575
DB 535 RCYADPARGEEASISCYMKDNPGLTEEDALNINFMIRDAISELNMELKPNVSVEIT 594
QY 576 SKKIAFDISRVHNGYRDGYSFANVETKSLVMTVIEPVL 618
DB 595 SKKIAFDITRAFIHVYKRDGYTVSNMNETKVLNMTKVLVLEPLAL 637

RESULT 4
TASY_TAXBR STANDARD; PRT; 862 AA.
ID TASY_TAXBR
AC 041594; 094FV8;
DT 28-FEB-2003 (Rel. 41, Last Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase).
GN TDC1.
OS Taxus brevifolia (Pacific yew).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX NCBI_TaxID=46220;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE=96199163; PubMed=6621577;
RA Wildung M.R., Croteau R.B.;
RT "A cDNA clone for taxadiene synthase, the diterpene cyclase that
RT catalyzes the committed step of taxol biosynthesis."
RL J. Biol. Chem. 271:9201-9204(1996).
RN 12
RP SEQUENCE FROM N.A.
RA MEDLINE=21297238; PubMed=11404343;
RA Trapp S.C., Croteau R.B.;
RT "Genomic organization of plant terpene synthases and molecular
RT evolutionary implications."
RL Genetics 158:811-832(2001).
CC -1- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid
CC intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
CC parent olefin with a taxane skeleton.
CC -1- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene +
CC diphosphate.
CC -1- PATHWAY: Taxol biosynthesis; first step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.

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DR EMBL: U48796; AAC49310.1; -
DR EMBL: AF326519; AAK83566.1; -
DR HSSP: Q40577; SEAU.
DR InterPro: IPR008930; Terp_cyc_toroid.
DR InterPro: IPR001906; Terp_synth-like.
DR InterPro: IPR005630; Terpene synth_C.
DR InterPro: IPR008949; Terpenoid synth.
DR Pfam: PF01397; Terpene synth_1.
DR Pfam: PF03936; Terpene synth_C; 1.
KW Taxol biosynthesis; Lyase.
FT ACT_SITE 758 758 BY SIMILARITY.
FT ACT_SITE 835 835 BY SIMILARITY.
FT ACT_SITE 839 839 BY SIMILARITY.
FT CONFLICT 148 148 L -> V (IN REF. 2).
FT CONFLICT 767 767 A -> V (IN REF. 2).
SQ SEQUENCE 862 AA; 98303 MW; 9141B59780CD79A1 CRC64;

Query Match 38.2%; Score 1240.5; DB 1; Length 862;
Best Local Similarity 42.6%; Pred. No. 3.9e-76;
Matches 269; Conservative 109; Mismatches 205; Indels 49; Gaps 10;

QY 23 ALARTEPTLGICRPG-----KSAVHSINMCUTSV-ASTDSVQRRVGNVHNL-----W- 69
DB 240 ALLOKAKALGINLVDLPFIKYLSTREARLTDSAAADNIPAMMLNLEGLREVIMNK 299
QY 70 -----DDDFIOGLSTPYGAPDYRRADRLIGEVDMNPFSLBEGN-----D 114
DB 300 IMRFQSGKGSFLSPASTACVLMN-----TGBEKCFITLNNLLDFGCGVCPCMTSID 351
QY 115 LLQRLLLVDVERLGIDRHFKKEIKTALDVNYSYMNKIGCGRESVVTDLNLTALGLRT 174
DB 352 LLRLSLVDNIENHIGIRHFKQELKALDYYRHMSEGIOMGWSLPLDNTALGLRT 411
QY 175 LRLHGYVSSDVLANVFQDKNGQFSSTANIQTGEGIRGVNLFRASLVAFPEKYMDEAET 234
DB 412 LRHMGVNVSSDVLANVFPDENGRFFSSAG-QTHVELRSVNLFRASDLAFPERAMDARK 470
QY 235 FSTYULREAL-QKIPASSILSLERDVLEYGMHNTLPRLAARNYMDVCG-----H 284
DB 471 FAERYLREALTKLSTNFKLEIYVEYEPWHSIPRLKRSYIDSYDNYVMQRTLY 530
QY 285 TKNRNAEKLLELAKLEFNI FHSLOERELKVASRWKDSGSPENTPCRHRHVEYVALASC 344
DB 531 RMPSLNSKCELAKLDPENIVQSLHQBELKLTLMWKSQMAIDNFRHRAVEY--FSS 588
QY 345 IAFEPQSGRFLGRTKSHLITVLDMDVGVYDELELFTATTKRDPMSMECLPEYMK 404
DB 589 ATEPEVSATRTIAFTKIGCLQVLDPDMADIPATIDELKSFTEGVYKMDTSLHETPREMOQ 648
QY 405 GVYVVVHTVEMRAVAKAGSDTLNVARQAECPDSYMQBAKMLATGLVLPFEETLB 464
DB 649 TCFYVWKLMEEVNNDVYKVGSRMLAHIRKPELYFRNCYQOEBWLEAGYIPFEETLK 708
QY 465 NGKVSASARPCALOPILTLDPDPDHLKEVDPSKLNLDLCIILRLGDTRCYKADRAR 524
DB 709 TYAIVSGLGPELTQPIILMGLVLDVYVEKHYPSNMNELVSLMRLLNDTKYQAEKAR 768
QY 525 GEARSSTSCWKDNPGLTEEDALNHNFMIRDAIRELWELLKQDNSVPTISKHAPDIS 584
DB 769 GQASAGLACWKDNPGLTEEDAIKHCIVVDRAKLEASFYEYKPSNDIPMCKSKFIMLR 828
QY 585 RVWHGVRYPDGYSAFANVETKSLWRVTIEBV 616
DB 829 LCVQIFKFIIDGIGIANEELIKDYIRKQYIDPI 860

RESULT 5

TASY TAXBA
ID TASY TAXBA STANDARD; PRT; 862 AA.

AC Q93YA3
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase).
GN TDC1 OR TASY.
OS Taxus baccata (English yew).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX NCBI_TaxID=25629;
RN [1]
RP SEQUENCE FROM N.A.

RA Goehard B.;
RL Thesis (2001), Technische Universitet Berlin, Germany.
CC -1- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid
CC intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
CC parent olefin with a taxane skeleton.
CC -1- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene +
CC diphosphate.

CC -1- PATHWAY: Taxol biosynthesis; first step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.

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CC or send an email to license@isb-sib.ch).

DR EMBL: AJ320538; CAC4273.1; -
DR InterPro: IPR008930; Terp_cyc_toroid.
DR InterPro: IPR001906; Terp_synth-like.
DR InterPro: IPR005630; Terpene synth_C.
DR InterPro: IPR008949; Terpenoid synth.
DR Pfam: PF01397; Terpene synth_1.
DR Pfam: PF03936; Terpene synth_C; 1.
KW Taxol biosynthesis; Lyase.
FT ACT_SITE 758 758 BY SIMILARITY.
FT ACT_SITE 835 835 BY SIMILARITY.
FT ACT_SITE 839 839 BY SIMILARITY.
SQ SEQUENCE 862 AA; 98048 MW; B37835AFDDCIDE CRC64;

Query Match 38.1%; Score 1238.5; DB 1; Length 862;
Best Local Similarity 42.4%; Pred. No. 5.3e-76;
Matches 273; Conservative 110; Mismatches 206; Indels 55; Gaps 13;

QY 15 LSSSHEI--KALARTPTLGICRPG-----KSAVHSINMCUTSV-ASTDSVQRRVGNVHS 66
DB 230 LSPDFEILFPALLQKAKALGINLPYDLPFIKSLSTREALTIVSAAADNIPAMMLALE 289
QY 67 NL-----W-----DDDFIOGLSTPY--YGAPDYRRADRLIGEVDMNPFSLBEGN-----IM 102
DB 290 GLEBEIVDMNIMRFQSGKGSFLSPASTACVLMNTGD--EKCFITLNNLLDFGCGVCPCM 347
QY 103 ENFNSLEDDGNDLLQRLLYVDVERLGIDRHFKKEIKTALDVNYSYMNKIGCGRESV 162
DB 348 YSI-----DLERLSLVNDNIENHIGIRHFKQELKALDYYRHMSEGIOMGWSLPLDNTALGLRT 399
QY 163 TDLNSTALGLRTLRHGYVSSDVLANVFQDKNGQFSSTANIQTGEGIRGVNLFRASLVAF 222
DB 400 PDLNTTALGLRTLRHGYVSSDVLANVFPDENGRFFSSAG-QTHVELRSVNLFRASDLAF 458
QY 223 FPEGKVMDEAETSTYKLEAL-QKIPASSILSLERDVLEYGMHNTLPRLAARNYMDVF 281
DB 459 FPDGAMDDARKFAEPLRDALATKISTNFKLEIYVEYEPWHSIPRLKRSYIDSYDNYVMQRTLY 518
QY 282 GQ-----HTKNRKAELKLELAKLEFNI FHSLOERELKVASRWKDSGSPENTPCR 332

Query Match	37.2%	Score 1209.5	DB 1	Length 862
Best Local Similarity	41.9%	Pred. No. 4,9e-74		
Matches 270	Conservative 110	Mismatches 209	Indels 55	Gaps 12
15	LSSSHEI-KALREITPTGTGRPG----	KSVAHSIMMCLTSV-ASTDSVORRGNYHS	66	
230	LSPDFEIIPEPALCKAKAGINLPDLPEIKYLSITTREARLTDVSAADNIPANNLNALB		289	
67	NL-----W-----	DDFIQSISTPYGADPYRERADRLIGEVKIMFNFKS--LE	109	
290	GLEEVMDMKIMRFQSKSGSFLSSPAST-----	ACVLMTNGDEKCFEFLNNLLVX	339	
110	DGS-----NDLQRLILVYDVERLGIDRHKKEIKITALDLYVNSYNNKEKIGCGRESVY	162		
340	FGGCVPCWMSIDLIERLSLVNDIMEHGIQGRHKFOEIKYALDLYVNHMBEIRGIMWRDSELY	399		
163	TDNLSALGARTLEFLIGYVSSDVLNVFQDKNGQSESTANIQIEGEIGVLLFPASVLA	222		
400	PDNLATLALGRLTLETHGIVYSSDVLNVFPDEKGRFPSSAG-QTHVLSVYLFPASDLA	458		
223	FPBEKMDAETFPSTYLREAL-QKIPASSISLEIRVLEFGWHTNLPLEARYMDF	281		

RESULT 7			
DCSL_GOSAR			
ID	DCSL_GOSAR	STANDARD;	PRT; 554 AA.
AC	039761;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	(+)-delta-cadinene synthase isozyme XCI (BC 4.2.3.13) (D-cadinene synthase).		
OS	Gossypium arboreum (Tree cotton).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucotids II; Malvales; Malvaceae; Malvoideae; Gossypium.		
OX	NCBI_TaxID=29729;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nanking;		
RX	MEDLINE=66132653; PubMed=8554317;		
RA	Chen X.-Y., Chen Y., Hainstein P., Davison V.J.;		
RT	"Cloning, expression, and characterization of (+)-delta-cadinene synthase, a catalyst for cotton phytoalexin biosynthesis.",		
RT	Arch. Biochem. Biophys. 324:255-266(1995).		
CC	1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl		

CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+) -
CC delta-cadinene + diphosphate.
CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U23206; AAA93064.1; -.
DR PIR: S68365; S68365.
DR HSSP: Q40577; SEAU.
DR InterPro: IPR008930; Terp_cyc_toroid.
DR InterPro: IPR001906; Terp_synth-like.
DR InterPro: IPR005630; Terpene synth_C.
DR InterPro: IPR008949; Terpenoid synth.
DR Pfam: PF01397; Terpene_synth_I.
DR Pfam: PF03936; Terpene_synth_C; 1.
DR Lyase; Multigene family.
FT ACT_SITE 451 451 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
FT ACT_SITE 531 531 BY SIMILARITY.
SQ SEQUENCE 554 AA; 64137 MW; 59D6922DDPDPCAF CRC64;

Query Match 22.1%; Score 717.5; DB 1; Length 554;
Best local Similarity 31.8%; Pred. No. 4,7e-41;
Matches 183; Conservative 107; Mismatches 243; Indels 43; Gaps 14;

51 VASDVSQVRKGNVNSLMDPFIQSLISTRYGAPD-----YRBRDRLLGEXKDIMFN 104
14 LSSNKKDEMRPRADQPSIWGDLFL-----NCPDKNIDAEFERHQQLKEEVR----- 60
105 FKSLEDGNDLQRLLLVLDVVERLGIDRHFKEIKITLADVNSYWEKIGICGREGSVTVD 164
61 -KMTVAMMANSTQCLAFIDSVQRLGVSHTFKETEDLE- -NITHN-----NNDAEND 110
165 LNSTALGLRTLRLLHGTVSSDVLVNFKDKNGQSPSTANIQEGEIRGVNLFRASLVAFP 224
111 LYTTSIFRLRLREHGFWNSCDVFNKFKDQGNFKXS-----VTSVDRGLBELYQASLYRVH 166
225 GEKMDAEFTSTYLRALQKIPASSILSLERIDVLEYGWHTNLPRLRANWMDVGOH 284
167 GEDILDEAISTTTHLSLAVASL--DHPLEEVSHALKQSIIRGLPRVEARHYSVY-QD 223
285 TKNKRAAEKLELAEFIHSLQERELKHSVRWMD-SGSPENTPFCRRHVEYVALAS 343
224 IESHNKA--LLEPAKIDFNMLQFLHRKELSEICRMWMDLDRQRLPYARQDVVSGYFIS 281
344 CIAEPHSGRRLFTYKMSHLITVLDNMYVFGIVDELELFTATITKMDPSAMCCLPRYM 403
282 GVEPEPOYSILRKMLTKVIAVASIVDDTVSYATYBELIPYTNAIERWDICIDIEPEYM 341
404 KGVMMVYHTYENARVAEKAQGRDNLNVARQAMWACDSYMOAKMTATGYLPTPEEYL 463
342 KPSTKALLDVVEEVAQLAEHGRQRYEYAKNAMIRLAQSYLVEKMTLONKYSFEFK 401
464 ENGVSSAHRPCALQPIILT-DIEPDIHLEKVDPPSKLNDLICILRLADGTCTYKADR 522
402 ANALPTCGYMLATTSFVGMGDIYTPETFKWASDP-KIQASNTICFMDVAEHKFKH 460
523 ARGEASSISCYMKONPGLTEEDALNHNFMIRDAIRELNWELLKPDNSVPTSKGAFD 582
461 RREDDCAIEBCYMEY-GVTAQEAUVDFVFNKVESAMKDLNDFLKP-TEMPTEVLNLSIN 518
583 ISRWHHGYRRDGYSPANVETKSLVMKTVLEPVL 618
519 LARVMVLYRREGDGYTVGKAKAGGITSLLIEPIAL 554

RESULT 8

DCS2_GOSAR

ID_DCS2_GOSAR STANDARD; PRT; 554 AA.

AC Q39760;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (+)-delta-cadinene synthase isozyme XC14 (EC 4.2.3.13) (D-cadinene
synthase).
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_Taxid=29729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nanking;
RX MEDLINE=96132653; PubMed=8554317;
RA Chen X.-Y., Chen Y., Heinsteain P., Davison V.J.;

RT "Cloning, expression, and characterization of (+)-delta-cadinene
synthase, a catalyst for cotton phytoalexin biosynthesis."
RL Arch. Biochem. Biophys. 324:255-266(1995).
CC -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl
CC diphosphate (FPP) to (+)-delta cadinene.
CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+) -
CC delta-cadinene + diphosphate.
CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
CC -1- first (committed) step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----

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CC -----

DR EMBL: U23205; AAA93065.1; -.
DR PIR: S68366; S68366.
DR HSSP: Q40577; SEAU.
DR InterPro: IPR008930; Terp_cyc_toroid.
DR InterPro: IPR001906; Terp_synth-like.
DR InterPro: IPR005630; Terpene synth_C.
DR InterPro: IPR008949; Terpenoid synth.
DR Pfam: PF01397; Terpene_synth_I.
DR Pfam: PF03936; Terpene_synth_C; 1.
DR Lyase; Multigene family.
FT ACT_SITE 451 451 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
FT ACT_SITE 531 531 BY SIMILARITY.
SQ SEQUENCE 554 AA; 64158 MW; A88974665E0F6B2B CRC64;

Query Match 22.1%; Score 717.5; DB 1; Length 554;
Best local Similarity 31.9%; Pred. No. 4,7e-41;
Matches 184; Conservative 108; Mismatches 241; Indels 43; Gaps 14;

51 VASDVSQVRKGNVNSLMDPFIQSLISTRYGAPD-----YRBRDRLLGEXKDIMFN 104
14 LSSNKKDEMRPRADQPSIWGDLFL-----NCPDKNIDAEFERHQQLKEEVR----- 60
105 FKSLEDGNDLQRLLLVLDVVERLGIDRHFKEIKITLADVNSYWEKIGICGREGSVTVD 164
61 -KMTVAMMANSTQCLAFIDSVQRLGVSHTFKETEDLE- -NITHN-----NNDAEND 110
165 LNSTALGLRTLRLLHGTVSSDVLVNFKDKNGQSPSTANIQEGEIRGVNLFRASLVAFP 224
111 LYTTSIFRLRLREHGFWNSCDVFNKFKDQGNFKXS-----VTSVDRGLBELYQASLYRVH 166
225 GEKMDAEFTSTYLRALQKIPASSILSLERIDVLEYGWHTNLPRLRANWMDVGOH 284
167 GEDILDEAISTTTHLSLAVASLDYR--LSBEVSHALKQSIIRGLPRVEARHYSVY-QD 223

QY 285 TKKNAAEKLELAKLEFNIFHSIQERELKRVSRMKD-SGSPMTFCRRHVEYALAS 343
 DB 224 IESNN--KVLLEFAKIDFNWQOLHREKLEISIRWKKDLPQKLPYARDVVGVEYFIS 281
 QY 344 CIAEPHSGRFLCFTKMSHLITVLDMDYVGFVDELELFTATIKRNDPAMECLPEYM 403
 DB 282 GYVEPEYSLGRKMLTKVIMASIVDDTYSATYEELIPTTKAERNDICIDELPEYIM 341
 QY 404 KGYVMYHTVEMARVAEKAQGRDTLNYARQAMEACPSYMOEAKVIATGYLPPEEYL 463
 DB 342 KPSYKALLDYVEEMEQVAKHGRQYRVAYAKNMRILASVYLAERMTLQNYKESFEFFK 401
 QY 464 ENGVSSAHRPCALQPIITL-DIPEPDHILKEVDPFSKNDLICILIRBDTCYKADR 522
 DB 402 ANALPTGYMALITSPFGMDIVTPETFKWAANDP-KTIQASTTICRFMDVAEHKCH 460
 QY 523 ARGEASSISCYMDONPGLTEEDALNHNFMIRDAIRELNWELKPDNSVPTSKHAFD 582
 DB 461 RREDDCAIECTMEY-GVTAQEAIVDPNKHVESAMKDVNKEPLKP-TEMETVLANSLN 518
 QY 583 ISRVNHHGYRYRDGYSFANVETKSLVMTVIEPVPL 618
 DB 519 LARVMDVLYREGDYTYVGAAGITSLLIEPVAL 554
 RESULT 9
 DCS4 GOSAR STANDARD; PRT; 554 AA.
 ID DCS4 GOSAR 049853;
 AC 049853;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE (+)-delta-cadinene synthase isozyme C2 (EC 4.2.3.13) (D-cadinene synthase).
 GN CAD1-C2.
 OS Gossypium arboreum (Tree cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids II; Malvales; Malvaceae; Malvoidae; Gossypium.
 OC NCBI_TaxID=29729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nanking.
 RA Meng Y., Jia J., Liu C., Liang W., Zhou X., Heinstein P., Chen X.-Y.; Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RL CC -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl diphosphate (FPP) to (+)-delta-cadinene.
 CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-delta-cadinene + diphosphate.
 CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
 CC -1- FIRST (committed) step.
 CC -1- SIMILARITY: Belongs to the terpene synthase family.
 CC -----
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 CC -----
 CC EMBL, Y16432; CAA76223.1; -.
 DR HSSP; Q40577; SEAU.
 DR InterPro; IPR008930; Terp_cyc_toroid.
 DR InterPro; IPR001906; Terp_synth-like.
 DR InterPro; IPR005630; Terpene synth C.
 DR InterPro; IPR008949; Terpenoid synth.
 DR Pfam; PF01397; Terpene_synth; I.
 DR Pfam; PF03936; Terpene_synth_C; 1.
 DR Lyase; Multigene family.
 KM ACT_SITE 451 451 BY SIMILARITY.
 FT ACT_SITE 527 527 BY SIMILARITY.

FT ACT SITE 531 531 BY SIMILARITY.
 SQ SEQUENCE 554 AA; 64117 MM; 35DD660D3E838AAC CRC64;
 Query Match 21.6%; Score 701.5; DB 1; Length 554;
 Best Local Similarity 31.5%; Pred. No. 5.6e-40;
 Matches 179; Conservative 108; Mismatches 238; Indels 43; Gaps 14;
 QY 59 RRVGNYSNMLDDPFIQSUSTPYGARD-----YRBAORLIEVMDIMNPFSLDEGG 112
 DB 22 RPKADFPSPIMGDFPL-----NCPDNIDACTEKHQQLKEEVR-----KVIAPM 67
 QY 113 NDILQRLILVDVVRILGIDRHFKKEIKTALDYVSNYWNKGIIGCGRESVVDLNSTALGL 172
 DB 68 ANSTOKLAFIDVGRVGRVSHFTKEIDEL-NIYN-----NDAENDVITTSIRF 118
 QY 173 RFLRHAGTVSSDVLNFKDNGQPSSTANIQIEGIRGVNLFRASLVAFPEKMDFA 232
 DB 119 RLRLHEGVNASCDFNNFKQEQGNFKSS---VTSVQGLLELYOASYLRVHGEDIIDEA 174
 QY 233 ETEFTKILRELQKIPASSILSLERDYLEGWHITNLPRLEARNYMDVFGQHTKNAAE 292
 DB 175 ISFTNHLISLAVSL--DHPUSEEVSHALKQSIIRGGLPRVFAHYLSVY-ODISHNKA- 230
 QY 293 KLEELAKLEFNIFFSLQERELKRVSRMKD-SGSPMTFCRRHVEYALASCIAFEFOH 351
 DB 231 -LLEFAKIDFNWQOLHREKLEISIRWKKDLPQKLPYARDVVGVEYFISGYVEFOY 289
 QY 352 SGFRLGFTKMSHLITVLDMDYVGFVDELELFTATIKRNDPAMECLPEYMKGVMMVY 411
 DB 290 SLGRKMLTKVIMASIVDDTYSATYEELIPTTKAERNDICIDELPEYMKSSYKALL 349
 QY 412 HTVEMARVAEKAQGRDTLNYARQAMEACPSYMOEAKVIATGYLPPEEYLENGKSSA 471
 DB 350 DVYKMEQOLVAHERQYRVAYAKNMRILASVYLAERMTLQNYKESFEFFKALNLPFG 409
 QY 472 HRPALQPIITL-DIPEPDHILKEVDPFSKNDLICILIRBDTCYKADRARGEASS 530
 DB 410 YAMALITSPFGMDIVTPETFKWAANDP-KTIQASTTICRFMDVAEHKCHGRRREDDCA 468
 QY 531 ISCYMDONPGLTEEDALNHNFMIRDAIRELNWELKPDNSVPTSKHAFDISRVNHHG 590
 DB 469 IECYMEY-GVTAQEAIVDPNKHVESAMKDVNKEFOKP-TEMETVLANSLNARVMDVL 526
 QY 591 YRYRDGYSFANVETKSLVMTVIEPVPL 618
 DB 527 YREGDYTYVGAAGITSLLIEPVAL 554
 RESULT 10
 DCS3 GOSAR STANDARD; PRT; 555 AA.
 ID DCS3 GOSAR 043714;
 AC 043714;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE (+)-delta-cadinene synthase isozyme A (EC 4.2.3.13) (D-cadinene synthase).
 GN CAD1-A.
 OS Gossypium arboreum (Tree cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucosids II; Malvales; Malvaceae; Malvoidae; Gossypium.
 OC NCBI_TaxID=29729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nanking.
 RA Meng Y., Jia J., Liu C., Liang W., Zhou X., Heinstein P., Chen X.-Y., Wang M., Chen Y., Davison V.J., Heinstein P.; MEDLINE=97060798; PubMed=8904844;
 RT "Cloning and heterologous expression of a second (+)-delta-cadinene synthase from Gossypium arboreum.";
 RL J. Nat. Prod. 59:944-951 (1996).
 CC -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl diphosphate (FPP) to (+)-delta-cadinene.

CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+) -
 CC delta-cadinene + diphosphate.
 CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
 CC first (committed) step.
 CC -1- SIMILARITY: Belongs to the terpene synthase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X96429; CAA65289.1; -.
 DR EMBL: U27535; ABA41259.1; -.
 DR HSSP: Q40577; SEAT.
 DR InterPro: IPR008930; Terp_cyc_toroid.
 DR InterPro: IPR001906; Terp_synth_1like.
 DR InterPro: IPR005630; Terpene_synth_C.
 DR InterPro: IPR008949; Terpenoid_synth.
 DR Pfam: PF01397; Terpene_synth; 1.
 DR Pfam: PF03936; Terpene_synth_C; 1.
 DR Lyase; Multigene family.
 FT ACT_SITE 452 452 BY SIMILARITY.
 FT ACT_SITE 528 528 BY SIMILARITY.
 FT ACT_SITE 532 532 BY SIMILARITY.
 SQ SEQUENCE 555 AA; 64103 MW; 7060C4F9D99412P9 CRC64;

Query Match 21.5%; Score 699.5; DB 1; Length 555;
 Best Local Similarity 31.1%; Pred. No. 7.7e-40;
 Matches 181; Conservative 104; Mismatches 241; Indels 49; Gaps 14;

QY 56 SVQRVGNVNSNMDDPFIQSILSTPYGAP-----YREARDLIGEVDIMNF 105
 DB 18 SENPKADPFHGIGMDMFTI-----CPDTIDATELOYEE--LKQVR----- 59
 QY 106 KSLEDGNDLQRLRLVDDVERLGIDRHFKKEIKTALDYVNSYWNKGIIGGRESVVDL 165
 DB 60 KMIWEPPVDSNQKLPFIDAVQRLGVSYHFEKEIDELENIYRDNI-----NNDADTDL 112
 QY 166 NSTALGLRTLRLHGTVSSDVLVNFKDKNGQFSSTANIQIGETRGVNLFRASIVAPFG 225
 DB 113 YTTALRRLRLREHGFDISCDAFNFKDEAGNFKAS---LTSVQGLLELYEASVYRVHG 168
 QY 226 EKWDEAEFTSTKYLREALOKIPASSISLEIRDLVEXGMHTNLPRLEARYVMVFGQHT 285
 DB 169 EDLDEAISTFTAQITLALPTL--HHPLSEOVGHALKOSIRRGDPRVARNFISITV-ODL 225
 QY 286 KNRKAAREKLELAKLEFNIHFSLQERELKGVSRWVKD--SGSPENTFCRRHVEYYALASC 344
 DB 226 ESHN--KSLQFAKIDFVLQLLRKELSEICRWMMKDLDFRKLPFADRVVEGVFWIMG 283
 QY 345 IAFEPQHSGLFGTGRKSHLITVLDMDVDVGVYDELELFTATIKRMPSPMECLPEYMK 404
 DB 284 VFEPQVSLGKMLTKYVAMASIVDVTYSATYDELTPYNAIERMDIKCMNDLPNTMK 343
 QY 405 GVYVWVHTVEMARVAKAQRD--TLNVARQAWBACDSTMOEAKWATGYLPFFEEYVL 463
 DB 344 ISTYALNLVHEMQLAN--QGRQRYEYAKKAMIRLVQATILAKKTHQYKPTFEER 402
 QY 464 ENGRVSSAHPRCALQPIITLDIPPDHILKEVDPSPKLNLDLICIILRLGRDTCYKADRA 523
 DB 403 DNALPFGYALMALITAFVGMEGVITPEFVKMAASDPKIKASTIICRMDDIAEHKFNHR 462
 QY 524 RGEBASSISCTMKNGPGLTEBDALNINFMRLDAIRELWELLRPDNSVPTTSKKHADI 583
 DB 463 REDDCSAIECTMKQY--GVTAQEAINEFNKIHSSSKVNEBEFLK--TEMPFVLCRSINTL 520
 QY 584 SRVWHGGRVADGSPFAVETKSLVMRTVIEPVPL 618
 DB 521 ARVMDVLYRBDGTYTHGAKAKGGITSLIDPITQI 555

RESULT 11
 ID DCSI GOSHI STANDARD; PRT; 554 AA.
 AC P9365;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE (+)-delta-cadinene synthase (EC 4.2.3.13) (D-cadinene synthase).
 GN CNU1.
 OS Gossypium hirsutum (Upland cotton).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 CC NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Westburn M;
 RA Davis E.M., Chen Y.-S.,
 RT "cDNA sequence of a (+)-delta-cadinene synthase gene induced in
 RT Gossypium hirsutum L. by bacterial infection.";
 RL (In) Plant Gene Register PGR98-040.
 RN [2]
 RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RX MEDLINE=96351891; PubMed=8728715;
 RA Davis E.M., Tsuji J., Davis G.D., Pierce M.L., Eissenberg M.;
 RT "Purification of (+)-delta-cadinene synthase, a sesquiterpene cyclase
 RT from bacteria-inoculated cotton foliar tissue.";
 RL Phytochemistry 41:1047-1055(1996).
 CC -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl
 CC diphosphate (FPP) to (+)-delta-cadinene.
 CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+) -
 CC delta-cadinene + diphosphate.
 CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
 CC first (committed) step.
 CC -1- INDUCTION: By bacterial infection.
 CC -1- SIMILARITY: Belongs to the terpene synthase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U88318; AAC12784.1; -.
 DR HSSP: Q40577; SEAU.
 DR InterPro: IPR008930; Terp_cyc_toroid.
 DR InterPro: IPR001906; Terp_synth_1like.
 DR InterPro: IPR005630; Terpene_synth_C.
 DR InterPro: IPR008949; Terpenoid_synth.
 DR Pfam: PF01397; Terpene_synth; 1.
 DR Pfam: PF03936; Terpene_synth_C; 1.
 DR Lyase.
 FT ACT_SITE 451 451 BY SIMILARITY.
 FT ACT_SITE 527 527 BY SIMILARITY.
 FT ACT_SITE 531 531 BY SIMILARITY.
 SQ SEQUENCE 554 AA; 64019 MW; 8BCCT8AD8CA5B816 CRC64;

Query Match 21.3%; Score 692.5; DB 1; Length 554;
 Best Local Similarity 31.1%; Pred. No. 2.3e-39;
 Matches 179; Conservative 113; Mismatches 241; Indels 43; Gaps 15;

QY 51 VASTDSVQRVGNVNSNMDDPFIQSILSTPYGAP-----YREARDLIGEVDIMNF 104
 DB 14 USSNKDEMRRKADQPSIWGDFL-----NCPDKNIIDAFYTKRQQLKEVYRKMI-- 63
 QY 105 KSLEDGNDLQRLRLVDDVERLGIDRHFKKEIKTALDYVNSYWNKGIIGGRESVVDL 164
 DB 64 ---VAPMANSTL-KLAFIDSVQGLGVSYHFKKEIDELE--NIYHN-----NNDLEND 110
 QY 165 LNSTALGLRTLRLHGTVSSDVLVNFKDKNGQFSSTANIQIGETRGVNLFRASIVAPFG 224

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Db 111 LYTSLAFRLREHGFHSCVFNKFKDEGNFSS-----VTSVRGLLELYKQSYLRVH 166
Cc 225 GEKYMDEAFETSTYKYLEBALOKIPASSILSLERDVEYGMHNLPRLEANNMDFVQOH 284
Cc 167 GEDILDEAISTPSNHLISLAVALS--DHPLSEVSHALKQSIIRGLPRVEAHYLSVY-QD 223
Cc 285 TKNNAEKLELAKLEFNIFHSLOERELKHVSWMVD--SSPEMTFCRHHVVEYALAS 343
Cc 224 IESHN--KVLLEFAKIDFNMVOLLRRELSEISRMWMDLDFORKLPVARDVVEGYFWIS 281
Cc 344 CIAEPHSGFRLEFTKMSHLITVLDMMYDVGTVDELELFTATIKRMDPSAMECLPEYM 403
Cc 282 GYVEPEYSLGRKMLTKVIMASIVDQDYDYSATYBELIPTNAIERDICIDELPEYM 341
Cc 404 KGVMMYVHTVEMARVAEKAQGRDTLNYARQAECPDSYMOEAKVIATGYLPEEYL 463
Cc 342 KPSYKALLDVEEWEQVVAEHGRQYVEYAKNAMIRLQSYLVEARWTLQNYKESFEFK 401
Cc 464 ENGVSSAHRPCALQPIITL-DIEPPHILKEVDPFSLNDLICILRLRDTCCYRDR 522
Cc 402 ANALPTCGYMLAITSFVGMDIVTPEPFKWAANDP-KIQASTTICRFMDVTEHKR 460
Cc 523 ARGEASSISCYMDNPGLTEDALNHNFMIRDAIRELWELKPDNSVPTSCKAFD 582
Cc 461 RREDSCAIECTMEY-GVTAQEAIVDFNKNVESAMKDVNGFLKP-TEMTEVLANSIN 518
Cc 583 ISRVMHGGRYRDYGSFANVETKSLVMRTIEPVPL 618
Cc 519 LARVMQVLYREGDGYTVGKAAGITSLIEPIAL 554

RESULT 12
CASS_RICCO STANDARD; PRT; 601 AA.
ID CASS_RICCO STANDARD; PRT; 601 AA.
AC P59287;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Casbene synthase, Chloroplast precursor (EC 4.2.3.8).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaceae;
OC Ricinus.
OC NCBI_TaxID=3988;
OX 11
RN SEQUENCE FROM N.A.
RX MEDLINE=9435958; PubMed=8078910;
RA Mau C.J., West C.A.;
RT "Cloning of casbene synthase cDNA: evidence for conserved structural
RT features among terpenoid cyclases in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8497-8501(1994).
RN [21]
RP CHARACTERIZATION.
RX MEDLINE=97115639; PubMed=8954576;
RA Hill A.M., Cane D.E., Mau C.J., West C.A.;
RT "High level expression of Ricinus communis casbene synthase in
RT Escherichia coli and characterization of the recombinant enzyme.";
RL Arch. Biochem. Biophys. 336:283-289(1996).
CC -1- FUNCTION: Catalyzes the cyclization of geranylgeranyl diphosphate
CC to casbene, a diterpene phytoalexin with antibacterial and
CC antifungal activity.
CC -1- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = casbene +
CC diphosphate.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By oligogalacturonide fragments released by fungal
CC infection. Detected after 5 h of incubation with the pectic
CC fragments and reaches a maximum after 10-12 h.
CC -1- MISCELLANEOUS: The Km of this enzyme is 1.9 micromol.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
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Cc or send an email to license@ebi.ac.uk).
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Query Match 20.5%; Score 667; DB 1; Length 601;
Best Local Similarity 29.8%; Pred. No. 1,36-37;
Matches 174; Conservative 132; Mismatches 230; Indels 48; Gaps 19;

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47 CLTIVASTDVSQVRGVNHSNLMDDDFIQSLISFPYGAIDYERADRLIGEVKIMENFK 106
Db 54 CLSS--TTHQEVRLAIVFPPTVMGNRF-ASLTFNPSEBSYDERVIVLKKVYKILIST 110
Cc 107 SLEDCGNDLQRLVLDVVERLGIDRHPKKEIKTALDVV-NS---YNNKSGIGGREGSV 162
Cc 111 S-----DSVETVLTIDLCRLGVSYHENDIEBSLKFISQSDPLDEK-----E 155
Cc 163 TDLNSTALGLRTLLHGTVSSDVLNVFKDKNQGFSSSTANIQIBGEIRGVNLFRASLVA 222
Cc 156 CDLYTAAIVFRVFFQHGFKMSDVFSKFKOSDGKFKS----LNGDAAKMLSLFEASHLS 211
Cc 223 FPGKRVDEAFETSTYKYLEBALOKIPASSILSLERDVEYGMHNLPRLEANNMDFVQOH 281
Cc 212 VHGDDILEEAFKFDYQSSAVELFPN--LKHITTALEQPPHSGVRLKARFIDLY 268
Cc 282 GQHTKNNAEKLELAKLEFNIFHSLOERELKHVSWMKDSG--SPEMTFCRHHVVEYVA 340
Cc 269 EADIECRN--ETLEFALDNRVOLHQQELCOFSKMWKDLNLASDIPYARDMAELFF 326
Cc 341 LASCIAEPHSGFRLEFTKMSHLITVLDMMYDVGTVDELELFTATIKRMDPSAMECLP 400
Cc 327 WYVAMVFEPPDYAHRMIAKVVLLISLDDITDVAIMEETHILAEVARDMGCLEKLP 386
Cc 401 EYKGVMMYVHTVEMARVAEKAQGRD-TLNYARQAECPDSYMOEAKVIATGYLPEEYL 459
Cc 387 DYMKVIYKLLNLTNSFEFEKEL-TAEKGSYGVYGREAFQELVRSYVLEAVVRDEGKLP 445
Cc 460 EYVLENGKVSANHRPCALQPIITLDIRPPHI--LKE---VDFPSKINDLICILRLRQD 514
Cc 446 DDVLYNSGMT----GLPLVSTASFMGVQDETGLNEFQWLETNPKSYASGATIRLVND 500
Cc 515 TRCYKADRARGELHSSISCYMDNPGLTEDALNHNFMIRDAIRELWELKPDNSVPTS 574
Cc 501 LSHVTEQQRHVAASCDCTVNNQH-GVSKDEAVIILQKMAIDCKEINEECMR-QSQVSV 558
Cc 575 TSKKHAFDISRVHNGRYRDYGSFANVETKSLVMRTIEPVPL 618
Cc 559 GILMIRIVLARTIDVSXYKGDGYTDSQ-QLKQFVKGLEFVDPIS 601

RESULT 13
SEAS_TOBAC STANDARD; PRT; 548 AA.
ID SEAS_TOBAC STANDARD; PRT; 548 AA.
AC Q40577;
DT 15-JUL-1998 (Rel. 36, Created)
```

DT 15-JUN-1998 (Rel. 36, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE Aristolochene synthase (EC 4.2.3.9) (5-epi-aristolochene synthase)
DE (EAS).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
OC Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids;
OC Lamiales, Solanales, Solanaceae, Nicotiana.
OC NCBI_TaxID=4097;
OX [1]
RN SEQUENCE FROM N. A., AND SEQUENCE OF 56-73.
RP STRAIN=cv. NK326;
RC MEDLINE=93066390, PubMed=1438319;
RX Facchini P.J., Chappell J. ;
RA "Gene family for an elicitor-induced sesquiterpene cyclase in
RT tobacco." ;
RT Proc. Natl. Acad. Sci. U.S.A. 89:11088-11092 (1992).
RL [2]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS), AND REVISIONS.
RX MEDLINE=97442533; PubMed=9295271;
RA Starcks C.M., Back K., Chappell J., Noel J.P. ;
RT "Structural basis for cyclic terpene biosynthesis by tobacco 5-epi-
RT aristolochene synthase." ;
RL Science 277:1815-1820 (1997).
CC -I- FUNCTION: Catalyzes the cyclization of trans,trans-farnesyl
CC diprophosphate (FPP) to the bicyclic intermediate 5-epi-
CC aristolochene, initial step in the conversion of FPP to the
CC sesquiterpene antifungal phytoalexin capdidol.
CC -I- CATALYTIC ACTIVITY: Trans,trans-farnesyl diphosphate =
CC aristolochene + diphosphate.
CC -I- COFACTOR: Binds 3 magnesium ions per subunit.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- INDUCTION: By fungal elicitor.
CC -I- SIMILARITY: Belongs to the terpene synthase family.
CC -----
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CC -----
DR EMBL; L04680; AAA19216.1; -.
DR PIR; T03714; T03714.
DR PDB; SEAS; 15-OCT-97.
DR PDB; SEAT; 12-NOV-97.
DR PDB; SEAU; 08-APR-98.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C1.
KW Lyase; Magnesium; 3D-structure.
FT FT ACT_SITE 273 273 PROTON ACCEPTOR.
FT FT ACT_SITE 444 444
FT FT ACT_SITE 520 520
FT ACT_SITE 525 525
FT CONFLICT 42 42 Y -> Y1Y (IN REF. 1).
FT CONFLICT 44 44 K -> Q (IN REF. 1).
FT CONFLICT 55 55 N -> S (IN REF. 1).
FT CONFLICT 62 62 M -> R (IN REF. 1).
FT CONFLICT 73 73 T -> I (IN REF. 1).
FT CONFLICT 89 89 D -> E (IN REF. 1).
FT CONFLICT 388 388 T -> M (IN REF. 1).
FT HELIX 26 29
FT HELIX 36 57
FT HELIX 58 58
FT TURN 60 61
FT TURN 64 76
FT HELIX 77 78
FT TURN 77 78

[illegible]

QY 165 LNSTALGLRTLRHGYVSSDVNLVFPKDKNGQSPSTANIOIEGRVNLFRASIVAF 224
 DB 104 LCTSLALPRLRQGFNISPEIFSKFQDENKFKES-----LASVGLGLNLYASHVKT 159
 QY 225 GEKVMDEAFETSTKYLEALQKIPASSILSLERDVLEYGHTVLPRLAENYMDVGOH 284
 DB 160 ADOLLEALAFSTHLSAAPHL--KSPLRQGVTHALBQCLHAKVPRVETRFISITDK 217
 QY 285 TKNNAAEKLLEAKLEFNIFHSLQERELKIVSRMKD--SGSPMTFCRHRVHYVALAS 343
 DB 218 EOSKN--NVLRFKADFNILLQMLHKOELAQVSRMKDLDFVTLLPYARDRVCECYFAL 275
 QY 344 CIAPEPHSGFRGLFTKMSHLITVLDKMYDVFGVDELELTATIKRDPNACLPBYM 403
 DB 276 GYVFEPPYQARVNLVTISMSIVDDTFDPAFGVKELEATDAIQRDINEIDRLPYM 335
 QY 404 KGVYMMVYHTVEMARVAEKAQGRDTLVYARQAWBACFDSYMOBAKIATGYLPTFEBYL 463
 DB 336 KISKALDLKYDEKELSSAGSHYCHALEKKEVYRANVNESVTFIEGTYPEVSEYL 395
 QY 464 ENGRVSAHRCALQPLITLDIPPPDHILKEVDFP-----SKLNDLICITLRLRGDTRCY 518
 DB 396 SNALATTYYLATTSYLGW-----KSATQDFEMLSKNPKILEASVILCRVIDDTATY 449
 QY 519 KADARBEESISICVKNQDGLTEBDALNINIMDAIRELWELLKPNQSPITSK- 577
 DB 450 EVERSROQIATGIECCRDY--GISTKEAMAKFQNNAEATWMDINEGLLRP--TPVSTEF 505
 QY 578 -KHAFDISRVWHNGRYR--DGYSPANVETKSLMRTVIEPVL 618
 DB 506 LTPILNARIVEVYIYNLDGYTHPEKYLKPHIINLVDSIKI 548

RESULT 14

UBRL_KLUJA STANDARD; PRT; 1941 AA.
 ID UBRL_KLUJA
 AC 060014;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE N-end-recognition protein (Ubiquitin-protein ligase E3 component) (N-recognin).
 GN UBRL.
 OS Kluyveromyces fragilis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 CX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Waller P.R.H., Varchavsky A.;
 RL Submitted (A/R-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Recognition component of the N-end rule pathway. Binds
 to proteins bearing amino-terminal residues that are destabilizing
 according to the N-end rule, but does not bind to otherwise
 identical proteins bearing stabilizing amino-terminal residues.
 CC -1- SIMILARITY: Contains 1 UBRL-type zinc finger.
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 or send an email to license@ebi.ac.uk).
 CC EMBL; AF061554; AAC15841.1;
 DR PIR; T30554; T30554
 DR InterPro; IPR003126; Znf_NrecoGn1.
 DR InterPro; IPR001841; Znf_1ing.
 DR Pfam; PF02207; Znf-UBRL1; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00396; Znf_UBRL1; 1.
 DR SEQUENCE FROM N.A.

KW Ligase: Ub1 conjugation pathway.
 SQ SEQUENCE 1941 AA; 223682 MW; 37C2E1BCA0803268 CRC64;

Query Match 4.1%; Score 133; DB 1; Length 1941;
 Best Local Similarity 29.3%; Pred. No. 0.81;
 Matches; 141; Conservative 85; Mismatches 244; Indels 226; Gaps 34;

QY 104 NFKSLDEGG-----NDLQRL--LYD-----DYERLQID-----R 132
 DB 176 NCKAEDNGRLIEDYFDHDKISKMLSEVLELFDHITDVFNQNIETPTTQKPLAQLR 235
 QY 133 HFKE-----IKTALDVNSYMNKGIQCGRESVVDNLSTALGLRTL--RLHG 180
 DB 236 YFNPEREIEADLRLRLAARNQYMDDEESSNKHLSLSDPLSTLKQYALIVYDEPHNY 295
 QY 181 TVSSDVNLVFPKDKIGQPS-STANIQIEGRVNLFRASIVAFG----- 225
 DB 296 SQASAAIRQGGPDHKLIDLAKIDSEG--RSLLR-C-SADIASIMGHI FVSQNSGLSCTI 352
 QY 226 ---EKVMDAETSTKYLEALQKIPASSILS-----EI 257
 DB 353 TQWTEYLHQEACKTSIMWINDCL-NIPNSTQSLFRNAIGKVLCSKTEPFYQSIDMTSV 411
 QY 258 RDVLEYGHTVLPRLAENYMDVFGQHTKNNAAEKLLE-----LAKLEFNIFHS 307
 DB 412 RDVSDSYLSDPPLVYADH--SVLGEQVKIPLGRHKSIDPDIDSAISPLMKVIAEDHNE 469
 QY 308 LOERELKIV--SRMKD-----SGS-- 325
 DB 470 YTNRLQYVLEFLERMYKLRKIKIVQDLIPTLASSAVQKPMFTDQVLEIFPMTRRSQTFM 529
 QY 326 ---PEMTFCRHRHVEYVALASCIAPFPOHSGFRGLFTKMSHLITVLDKMYDVFGVDELE 382
 DB 530 DREPOLTSLSRESVQLFTCP--TAVSIFHS-----HFNLYMSVDIVDFESTMDGCT 582
 QY 383 LFTATIKRWDPS-----AMECL-----PEYM--KGVYMMVY--HTVEMAR 419
 DB 583 LVMQVRQNSPNSKYSISFKQGLAVAVETLSKIDPMLLKRGFIMLVTLCKLFNGMWK 642
 QY 420 VAEKAQGRDT-----LVYARQAW--ACDSTMOEAK-----WATGYLPTFEY 462
 DB 643 IKKRGEGSHVLEQOHFIPYLEYTSVYSIIQTDKVLQSKDHIDRLLGAINLDSF 702
 QY 463 LENGKVS-----SAHRCALQPLITLDIPPPDHILKEVDFP--SKLNDLIC 506
 DB 703 LGHNNLSYKLYKDEITIKFOISKQVSPFMDVHTLFCFLVQHVFLQVSIQVLSQSKYLV 762
 QY 507 II-LRLRGDTRCYKADRA---RGEBASISICVKNQDGL---TEBDALNINIMI--RD 556
 DB 763 ISDFALRSVLCQIDIGFWRNMGMSVLHQSAVYKNNPENSYSRDIQLNQLAFLEKND 822
 QY 557 AIRFL---NWILK--PDNSVPTSKKAFDISRV 586
 DB 823 FQVIVYMLDRWMLLDWFDGSPSTETVYDDKISSI 858

RESULT 15

BXAZ_CLOBO STANDARD; PRT; 1295 AA.
 ID BXAZ_CLOBO
 AC 045894; P77780;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Botulinum neurotoxin type A precursor (BC 3.4.24.69) (BoNT/A)
 DE (Botocyllysin A) (BOTCY) [Contains: Botulinum neurotoxin A, light-
 chain; Botulinum neurotoxin A, heavy-chain].
 GN BOTX OR BNA OR ATX.
 OS Clostridium botulinum.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Kyoto-F;
 RX MEDLINE=94143603; PubMed=8310180;
 RA Williams A., East A.K., Lawson P.A., Collins M.D.;
 RT "Sequence of the gene coding for the neurotoxin of Clostridium
 RT botulinum type A associated with infant botulism: comparison with
 RT other clostridial neurotoxins.";
 RL Res. Microbiol. 144:547-556 (1993).
 RN [2]
 RP SEQUENCE OF 1-65 FROM N.A.
 RC STRAIN=Kyoto-F;
 RX MEDLINE=97016817; PubMed=8863443;
 RA East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
 RT "Organization and phylogenetic interrelationships of genes encoding
 RT components of the botulinum toxin complex in proteolytic Clostridium
 RT botulinum types A, B, and F: evidence of chimeric sequences in the
 RT gene encoding the nontoxic nonhemagglutinin component.";
 RL Int. J. Syst. Bacteriol. 46:1105-1112 (1996).
 CC -1- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
 CC binds with high affinity to peripheral neuronal presynaptic
 CC membrane, is then internalized by receptor-mediated endocytosis.
 CC The C-terminus of the heavy chain (H) is responsible for the
 CC adherence of the toxin to the cell surface while the N-terminus
 CC mediates transport of the light chain from the endocytic vesicle
 CC to the cytosol. After translocation, the light chain (L)
 CC hydrolyzes the 197-Gln-Arg-198 bond in SNAP-25, thereby blocking
 CC neurotransmitter release. Inhibition of acetylcholine release
 CC results in flaccid paralysis, with frequent heart or respiratory
 CC failure (by similarity).
 CC -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
 CC detected action on small molecule substrates.
 CC -1- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H) (by similarity).
 CC -1- STRUCTURAL LOCATION: Secreted.
 CC -1- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -1- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 CC -----
 DR EMBL: X73423; CA651824.1; -;
 DR EMBL: X87974; CA61234.1; -;
 DR PIR: I40645; I40645.
 DR HSSP: P10845; 3BTA.
 DR MEROPS: M27.002; -;
 DR InterPro: IPR006985; ConA like lec_g1.
 DR InterPro: IPR002160; Kunitz legume.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR000395; Peptidase_M27.
 DR Pfam: PF01742; Peptidase_M27; 1.
 DR PRINTS: PR00760; BONTOXILYSIN.
 DR PRODOM: PD001963; Bontoxilysin; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; FALSE NEG.
 DR Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 KW INIT_MET 0
 FT CHAIN 1 447
 FT CHAIN 448 1295 BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
 FT METAL 222 222 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 223 223 BY SIMILARITY.
 FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 429 453 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 1234 1279 BY SIMILARITY.
 FT TRANSMEM 626 646 POTENTIAL.
 FT TRANSMEM 655 675 POTENTIAL.
 SQ SEQUENCE 1295 AA; 149279 MW; 5DA04A13D98D6372 CRC64;

Query Match 3.8% Score 125; DB 1; Length 1295;

Best Local Similarity 19.0%; Pred. No. 1.6;
 Matches 138; Conservative 102; Mismatches 247; Indels 238; Gaps 32;
 QY 3 LLSITP---LVSRSSCLASSSSHEIKALRR-----TIPTIGI 33
 DB 150 LVIIIGPADIIQECSSFGHDVLANLTNGSGTOYIIFSPDPTFGFESSELEVDINPLIGA 209
 QY 34 CR---PGKSVASHINCLTSVASTDSVORVGNVHSLM-----D 70
 DB 210 GKFPATPAVTLAHLIAHRLVGIAlNPNRVFPKVNNAVYEMSGLEVSFEELATFGCHD 269
 QY 71 DDFIQSILSTPYGAPDYREPAD--RLIGEYKDIWFNFKSLJEDGNDLLQRLLVLD--- 124
 DB 270 AKFDSIQEHBFRLLYYNKKFQDVASTLNKAKSIIGTASIQYMKGVKFKELISEDSGK 329
 QY 125 --VERLIDHFRK--KEIKTALDVN-----SYVN-EKIGCGRESVYTDNLTALG 171
 DB 330 FSVKLFKDKYIKMLTIYEDNFFKVIINRKYTNFPAV--PRINVPDENYTIKD 387
 QY 172 LRTLRHGYTVSSDVLNVFKDKNGQSPSTANIQIEGIRGVNLFRASLV--APFGKVM 229
 DB 388 --GPNLKGANLSTN---FNGQNEINSRNFTRLK-NFTGLFEFYKLCVRGIIP----- 435
 QY 230 DEAFETSTKYLREALQKI-----PASSIISLEIRDVLYEGWHTNLRLE 273
 DB 436 ----FTKSIDEGYNKALNDLCIKVNMWDLFFSPSDNFTNLDKVEIYADTNIEAAE 490
 QY 274 ARNVMDFVGOH-----TKKNAAEKLE--LAKLE-----FNIF 305
 DB 491 ENISLIDLQOYLYTFPDNDEPENISINLSDDIIGLEPENIRFPNGKKYELDKTTF 550
 QY 306 HSLQERELKH-VSRKWKDSGSP-----MFCRRHVEYYALA-SCIAFEPQHSGR 355
 DB 551 HYLAQGFEGHDSRIILTNSAEELKPNVAYTFSSKYVKINKAVEAFMLWABEVL 610
 QY 356 LGFTKSHLITVLDMDVDF-----GVVDELELTATIKRNDPSAME 397
 DB 611 YDFDETFNEVYTMKIDITIIYVYIGPALNIGMLSKGEVEAIIPTGVV-----AMLE 665
 QY 398 CLPEYMGVMMVYHTVENARVAEKAQGRDLNVA---ROAEACFDSYMGAKWIAT 453
 DB 666 FIFETVY---LVPVGTALVSIYINKKLVYQTINNAISKNEKNDVY-----KTVY 714
 QY 454 GYLPTPEEYLENGKVSASHPCALQPIITLIDPPDHILKEVDPSPKLANDLICILRLRG 513
 DB 715 NWL-----AKVNTQIDIRE--- 729
 QY 514 DTRCYKADRRARGEASSISCMKDNPGLTREDAINHNINPMIRDAIRLNNELKPDNSVP 573
 DB 730 --KKKKALENQAEYTKAIIINYQVQ--YTEBEK-NNINFINIDLSKLNESI---NSAM 780
 QY 574 ITSCK 578
 DB 781 ININK 785

Search completed: July 23, 2004, 09:02:52
 Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 08:59:52 ; Search time 42 Seconds

(without alignments)
4642.625 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251

Sequence: 1 MALSLTPVLSRSLSSSHR.....FANVETSLVMRTYIEPVPL 618

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3251	100.0	618	10	Q94820
2	2416	74.3	618	10	Q94820
3	2385	71.6	629	10	Q94820
4	2265	69.7	627	10	Q94820
5	2264	69.6	630	10	Q94820
6	2237	68.8	634	10	Q94820
7	2205	67.8	633	10	Q94820
8	2163	66.5	627	10	Q94820
9	2151	66.2	628	10	Q94820
10	2137	65.7	630	10	Q94820
11	2084	64.1	637	10	Q94820
12	2041	62.8	637	10	Q94820
13	1985	61.1	615	10	Q94820
14	1909	58.7	574	10	Q94820
15	1295	39.8	581	10	Q94820
16	1242	38.2	579	10	Q94820

17	1240	38.1	577	10	Q94820
18	1231	37.9	593	10	Q94820
19	1187	36.5	782	10	Q94820
20	1187	36.5	817	10	Q94820
21	1178	36.3	816	10	Q94820
22	1131	34.8	873	10	Q94820
23	1055	32.5	853	10	Q94820
24	1052	32.4	861	10	Q94820
25	836	25.7	603	10	Q94820
26	824	25.3	606	10	Q94820
27	821	25.3	605	10	Q94820
28	812	25.0	597	10	Q94820
29	796	24.5	595	10	Q94820
30	794	24.4	595	10	Q94820
31	765	23.5	606	10	Q94820
32	757	23.3	576	10	Q94820
33	749	23.1	582	10	Q94820
34	747	23.0	607	10	Q94820
35	744	22.9	613	10	Q94820
36	742	22.8	583	10	Q94820
37	736	22.7	598	10	Q94820
38	732	22.5	583	10	Q94820
39	728	22.4	567	10	Q94820
40	727	22.4	620	10	Q94820
41	724	22.3	599	10	Q94820
42	721	22.2	597	10	Q94820
43	717	22.1	599	10	Q94820
44	710	21.9	551	10	Q94820
45	710	21.9	603	10	Q94820

ALIGNMENTS

RESULT 1

Q94820 PRELIMINARY; PRT; 618 AA.

AC Q94820.

DT 01-DEC-2001 (TRENBLER, 19, Created)

DT 01-DEC-2001 (TRENBLER, 19, Last sequence update)

DT 01-OCT-2003 (TRENBLER, 25, Last annotation update)

DE (-)-camphene synthase

GN AG6.5.

OS Abies grandis (Grand fir).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.

OX NCBI_TaxID=4611;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97413772; PubMed=9268308;

RA Bohlmann J., Steele C.L., Croteau R.;

RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";

RT J. Biol. Chem. 272:21784-21792 (1997).

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99373092; PubMed=1041373;

RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;

RT "cDNA cloning, characterization, and functional expression of four new monoterpene synthase members of the Trsd gene family from grand fir (Abies grandis).";

RT Arch. Biochem. Biophys. 368:232-243 (1999).

RL EMBL; U87910; AB0707.1; -

DR GO; GO:0016829; F:lyase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR005630; Terpene synth C.

DR InterPro; IPR008949; Terpenoid synth.

DR InterPro; IPR008930; Terp_cyc_Teroid.

DR InterPro; IPR01906; Terp_synth-like.

DR Pfam; PF03936; Terpene synth C; 1.

DR SEQUENCE 618 AA; 70749 MW; B07B518SC5C4CE1 CRC64;

Query Match 100.0%; Score 3251; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 9e-232;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MALISTIPVLSRSCSSSHKIKALRTTPTLGIICRPGKSVASHINMCLTSVASTDSVQRV 60
    |||
DB 1 MALISTIPVLSRSCSSSHKIKALRTTPTLGIICRPGKSVASHINMCLTSVASTDSVQRV 60
QY 61 VGNVSHNLMDDDPFIQSILSTPYGAPDYRERADRLIGEYKDIWFNFKSLSDGNDLRL 120
    |||
DB 61 VGNVSHNLMDDDPFIQSILSTPYGAPDYRERADRLIGEYKDIWFNFKSLSDGNDLRL 120
QY 121 LVDDVERLIGIDRHFKKEIKTALDVVNSYMNKGIICGREGSVTDLNSTALGLRTLRHG 180
    |||
DB 121 LVDDVERLIGIDRHFKKEIKTALDVVNSYMNKGIICGREGSVTDLNSTALGLRTLRHG 180
QY 181 TVSSDLNVFEDKXNGQFSSSTANIQIEGIRGVNLFRASLVAFPGKVMDEAEFTSTKY 240
    |||
DB 181 TVSSDLNVFEDKXNGQFSSSTANIQIEGIRGVNLFRASLVAFPGKVMDEAEFTSTKY 240
QY 241 REAŁQKTPASSISLSLEIRDVLEYGMHTNLPRLERANVMDFGQHTKKNAAEKLELAK 300
    |||
DB 241 REAŁQKTPASSISLSLEIRDVLEYGMHTNLPRLERANVMDFGQHTKKNAAEKLELAK 300
QY 301 EFNIFHSLQERELKGVSRMWDKSGSPENTFCRHRHVEYYALASCIAPESQHSFRLGFTK 360
    |||
DB 301 EFNIFHSLQERELKGVSRMWDKSGSPENTFCRHRHVEYYALASCIAPESQHSFRLGFTK 360
QY 361 MSHLITVLDMDYDFGVDELFTATIKRMDPSAMECLPEYMGVYMYVHTVENARV 420
    |||
DB 361 MSHLITVLDMDYDFGVDELFTATIKRMDPSAMECLPEYMGVYMYVHTVENARV 420
QY 421 AEKQAGDNTLVYAAQAWACPDSYMOKWATATGYLPPREXYLNGKVSASHRCAŁPI 480
    |||
DB 421 AEKQAGDNTLVYAAQAWACPDSYMOKWATATGYLPPREXYLNGKVSASHRCAŁPI 480
QY 481 LTLDDIPPPDHILKEVDPPSKLNDLCIILRLRGDTRCYKADRRAGEASISCYMKONG 540
    |||
DB 481 LTLDDIPPPDHILKEVDPPSKLNDLCIILRLRGDTRCYKADRRAGEASISCYMKONG 540
QY 541 LTEBDALNHINFMIRDAIRBELNELLKPDNSVPTTSKKHAFDISRWVHHGYRYSFA 600
    |||
DB 541 LTEBDALNHINFMIRDAIRBELNELLKPDNSVPTTSKKHAFDISRWVHHGYRYSFA 600
QY 601 NVEKSLVMRTVIEPVPL 618
    |||
DB 601 NVEKSLVMRTVIEPVPL 618
```

RESULT 2

```
Q94FWO PRELIMINARY; PRT; 623 AA.
AC Q94FWO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pinene synthase (Fragment).
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21297238; PubMed=11404343;
RA Trapp S.C., Croteau R.B.;
RT "Genomic organization of plant terpene synthases and molecular
RL evolutionary implications.";
RL Genetetics 158:811-832(2001).
RL EMBL: AF326517; AAK83564.1;
DR GO: GO:0016829; F: lyase activity; IEA.
DR GO: GO:0008152; P: metabolism; IEA.
DR InterPro; IPR005630; Terpene_synth_C.
```

DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp. cyc. toroid.
DR InterPro; IPR001906; Terp. synth.-like.
DR Pfam; PF01397; Terpene synth. 1.
DR Pfam; PF03936; Terpene synth. C; 1.
FT NON TER 1
SQ SEQUENCE 623 AA; 70948 MW; 823B82B38113467B CRC64;

Query Match 74.3%; Score 2416; DB 10; Length 623;
Best Local Similarity 74.8%; Pred. No. 5.2e-170;
Matches 467; Conservative 59; Mismatches 82; Indels 16; Gaps 6;

```
QY 8 PLVSRCL-----SSSHKIKALRTTPTLGIICRPGKSVASHINMCLTSVASTDSVQRV 62
    |||
DB 3 PLASKSCLHRSLSSTHELKALSTRTIPALGMSRGRKSIPTSISSSTVTVDDGVRBMG 62
QY 63 NYSHNLMDDDPFIQSILSTPYGAPDYRERADRLIGEYKDIWFNFKSLSDGNDLRL 117
    |||
DB 63 DFNHNLMDDDVIOSL-PTAYEKSYLERAKLIGEYEN-MENSNLSDEGLMSPLNDLIQ 120
QY 118 RLILVDDVERLIGIDRHFKKEIKTALDVVNSYMNKGIICGREGSVTDLNSTALGLRTLR 177
    |||
DB 121 RLIVDSLGRLGHRHFKDEIKSHLDVYISYMGENGICGREGSVTDLNSTALGLRTLR 180
QY 178 HGYTVSSDLNVFEDKXNGQFSSSTANIQIEGIRGVNLFRASLVAFPGKVMDEAEFTST 237
    |||
DB 181 HGYTVSSDLNVFEDKXNGQFSSSTANIQIEGIRGVNLFRASLVAFPGKVMDEAEFTST 240
QY 238 KYLREALQKTPASSISLSLEIRDVLEYGMHTNLPRLERANVMDFGQHTKKNAAEKLELAK 294
    |||
DB 241 KYLREALQKTPASSISLSLEIRDVLEYGMHTNLPRLERANVMDFGQHTKKNAAEKLELAK 299
QY 295 LELAKLEFNIFHSLQERELKGVSRMWDKSGSPENTFCRHRHVEYYALASCIAPESQHSF 354
    |||
DB 300 LELAKLEFNIFHSLQERELKGVSRMWDKSGSPENTFCRHRHVEYYALASCIAPESQHSF 359
QY 360 RLGFATKCHLITVLDMDYDFGVDELFTATIKRMDPSAMECLPEYMGVYMYVHTV 419
    |||
DB 415 NEMARVAKAQAGDNTLVYAAQAWACPDSYMOKWATATGYLPPREXYLNGKVSASHR 474
    |||
DB 420 NEMARVAKAQAGDNTLVYAAQAWACPDSYMOKWATATGYLPPREXYLNGKVSASHR 479
QY 475 CALOPITLDDIPPPDHILKEVDPPSKLNDLCIILRLRGDTRCYKADRRAGEASISCY 534
    |||
DB 480 SALOPITLDDIPPPDHILKEVDPPSKLNDLCIILRLRGDTRCYKADRRAGEASISCY 539
QY 535 MKDNPGLTBEDALNHINFMIRDAIRBELNELLKPDNSVPTTSKKHAFDISRWVHHGYR 594
    |||
DB 540 MKDNPGVSEBDALDHINAMISDVYKGLNELLKPDINVPISAKGHAFDIARAFHYGYR 599
QY 595 DGYSFANVETKSLVMRTVIEPVPL 618
    |||
DB 600 DGYSFANVETKSLVMRTVIEPVPL 623
```

RESULT 3

```
Q84KL6 PRELIMINARY; PRT; 629 AA.
AC Q84KL6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pinus taeda (loblolly pine).
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
```

RT "cDNA isolation, functional expression, and characterization of (+)-
alpha-pi-ene synthase and (-)-alpha-pi-ene synthase from loblolly pine
RT (Pinus taeda): Stereococontrol in pine biosynthesis."

DR EMBL: AF543527; AAO61225.1; -
DR GO: 0016829; F: lyase activity; IEA.
DR GO: 0008152; P: metabolism; IEA.
DR InterPro: IPR005630; Terpenoid synthase.
DR InterPro: IPR008949; Terpenoid synthase.
DR InterPro: IPR008930; Terp. cyc. coroid.
DR InterPro: IPR001906; Terp. synth-like.
DR Pfam: PF01397; Terpene synthase; 1.
DR Pfam: PF03936; Terpene synthase; 1.
DR SEQUENCE 629 AA; 71807 MW; 39DDCC936BCB1791 CRC64;

Query Match 71.6%; Score 2328.5; DB 10; Length 629;
Best Local Similarity 72.0%; Pred. No. 1.6e-165;
Matches 456; Conservative 67; Mismatches 91; Indels 19; Gaps 8;

1 MALISTIPVSRGCLSS-----HEIKALRTITPTLIGCPKGSVAH-SINMCLTSVAS 53
1 MSPSVISLPSDCLPTSFIDRSGRELIPHTIPNVMRRQGLMTRASNMNLRATV 60
54 TDSVORVGNVHSLMPDDFIQSLISTPYGAPDYERADRLIGKQIMPFKSLDDG- 112
61 DDVIRRGDPHSLMDDDLQSL-SFYGEPSTREARERLIGVKN-SFMSNEDGES 118
113 ---NDLLQRLVDDVERLIGIDRHFKKEIKTALDYVNSYNEKIGCGRESVTDLNST 168
119 ITPDLDLQRLMVDYERLIGIDRHFKKEIKSALDYVNSYNEKIGCGRESVTDLNST 178
169 ALGRTIRLHGTYSSDVLANFKDNGQFSSSTANIQTIGELRGVNLPRALVAFPGKV 228
179 ALGRTIRLHGTYSSDVLANFKDNGQFSSSTANIQTIGELRGVNLPRALVAFPGKV 237
229 MDEAFSTKYLRALOKIPASSILSLIRDVLEYGHTNLPRLERARYMDFGQHTKN 288
238 MDEAFSTKYLRALOKIPASSILSLIRDVLEYGHTNLPRLERARYMDFGQHTKN 296
289 NA--AEKLELALKEFNIFHSLOERELKHVSRRWKDGSPEMTFCRRHVEYYALASCI 345
297 KSVKTEKLELALKEFNIFHSLOERELKHVSRRWKDGSPEMTFCRRHVEYYALASCI 356
346 AFEPOHSGFRIGFRKMSHLITVLDMDYDVGCTVDELEFTATTIKRWDPSAMECPETVYK 405
357 AFEPOHSGFRIGFRKMSHLITVLDMDYDVGCTVDELEFTATTIKRWDPSAMECPETVYK 416
406 VYVNVVHTVNMMAVNAEAKOGRDTLNTYARQWACFDSYMOEAKMIATGYLPTFEYEN 465
417 VYVNVVHTVNMMAVNAEAKOGRDTLNTYARQWACFDSYMOEAKMIATGYLPTFEYEN 476
466 GKVSARPCALQPIITLTDIPFPDHILKEVDPSKNDLICIILRLGRTCYADRRAG 525
477 GKVSARPCALQPIITLTDIPFPDHILKEVDPSKNDLICIILRLGRTCYADRRAG 536
526 BEASSISCTMKNGQLBEDALNINMIRAIKELWELLKPNDSVPTSKKAIFDLSR 585
537 BEASSISCTMKNGQLBEDALNINMIRAIKELWELLKPNDSVPTSKKAIFDLSR 596
586 VMHGYRVDGYSFANVETKSLVMRTVLEPVL 618
597 AFHGYKTRDGYSVSVETKSLVMRTVLEPVL 629

RESULT 4
084K14 PRELIMINARY; PRT; 627 AA.
AC 084K14; 084K14; 24, Created)
DT 01-JUN-2003 (Tremblrel, 24, last sequence update)
DT 01-OCT-2003 (Tremblrel, 25, last annotation update)
DE Alpha-terpinol synthase.
Pinus taeda (loblolly pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;

RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "cDNA isolation, functional expression, and characterization of (+)-
alpha-pi-ene synthase and (-)-alpha-pi-ene synthase from loblolly pine
RT (Pinus taeda): Stereococontrol in pine biosynthesis."

DR EMBL: AF543529; AAO61227.1; -
DR GO: 0016829; F: lyase activity; IEA.
DR GO: 0008152; P: metabolism; IEA.
DR InterPro: IPR005630; Terpenoid synthase.
DR InterPro: IPR008949; Terpenoid synthase.
DR InterPro: IPR008930; Terp. cyc. coroid.
DR InterPro: IPR001906; Terp. synth-like.
DR Pfam: PF01397; Terpene synthase; 1.
DR Pfam: PF03936; Terpene synthase; 1.
DR SEQUENCE 627 AA; 71883 MW; FACA215FA739B63 CRC64;

Query Match 69.7%; Score 2266.5; DB 10; Length 627;
Best Local Similarity 70.0%; Pred. No. 6e-159;
Matches 443; Conservative 78; Mismatches 91; Indels 21; Gaps 9;

1 MALISTIPVSRGCL-----SSHEIKALRTITPTLIGCPKGSVAH-SINMCLTSVAS 53
1 MDLISVLPSSAKSCVCLHKLPLSSSTHKLKPKCTIRILVMRRRPFAPPS--MELSTVAS 58
54 TDSVORVGNVHSLMPDDFIQSLISTPYGAPDYERADRLIGKQIMPFKSLDDG- 112
59 EDDIQRTGTYLSLMDNDVQ-FLSTPYGELAYREARERLIDVRI-PSSMLEDEEF 116
113 NDLLQRLVDDVERLIGIDRHFKKEIKTALDYVNSYNEKIGCGRESVTDLNSTALGL 172
117 SDLIQRLMVDYERLIGIDRHFKKEIKSALDYVNSYNEKIGCGRESVTDLNSTALGL 176
173 RTLRHGTYSSDVLANFKDNGQFSSSTANIQTIGELRGVNLPRALVAFPGKV 228
177 RTLRHGTYSSDVLANFKDNGQFSSSTANIQTIGELRGVNLPRALVAFPGKV 235
229 MDEAFSTKYLRALOKIPASSILSLIRDVLEYGHTNLPRLERARYMDFGQHTKN 287
236 MDEAFSTKYLRALOKIPASSILSLIRDVLEYGHTNLPRLERARYMDFGQHTKN 294
288 --KNAEKLALKEFNIFHSLOERELKHVSRRWKDGSPEMTFCRRHVEYYALASCI 345
295 EPNKTEKLELALKEFNIFHSLOERELKHVSRRWKDGSPEMTFCRRHVEYYALASCI 354
346 AFEPOHSGFRIGFRKMSHLITVLDMDYDVGCTVDELEFTATTIKRWDPSAMECPETVYK 405
355 AFEPOHSGFRIGFRKMSHLITVLDMDYDVGCTVDELEFTATTIKRWDPSAMECPETVYK 414
406 VYVNVVHTVNMMAVNAEAKOGRDTLNTYARQWACFDSYMOEAKMIATGYLPTFEYEN 465
415 VYVNVVHTVNMMAVNAEAKOGRDTLNTYARQWACFDSYMOEAKMIATGYLPTFEYEN 474
466 GKVSARPCALQPIITLTDIPFPDHILKEVDPSKNDLICIILRLGRTCYADRRAG 525
475 GKVSARPCALQPIITLTDIPFPDHILKEVDPSKNDLICIILRLGRTCYADRRAG 534
526 BEASSISCTMKNGQLBEDALNINMIRAIKELWELLKPNDSVPTSKKAIFDLSR 585
535 BEASSISCTMKNGQLBEDALNINMIRAIKELWELLKPNDSVPTSKKAIFDLSR 594
586 VMHGYRVDGYSFANVETKSLVMRTVLEPVL 618
595 AFHGYKTRDGYSVSVETKSLVMRTVLEPVL 627

RESULT 5
09M7D1

ID Q9M7D1 PRELIMINARY; PRT; 630 AA.
AC Q9M7D1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-phellandrene synthase.
GN AGC8.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Abies.
OC NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Stem;
RX MEDLINE=99373092; PubMed=10441373;
RA Bohlmann J., Phillips M., Ramchandiran V., Katoh S., Croteau R.,
RT "cDNA cloning, characterization, and functional expression of four new
RT monoterpene synthase members of the Trpd gene family from grand fir
RT (Abies grandis).";
RL Arch. Biochem. Biophys. 368:232-243 (1999).
DR EMBL: AF139205; AAF61453.1; -.
DR HSSP: QA0577; 5E4U.
DR GO: GO:0016829; P:lyase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR005630; Terpenoid synth. C.
DR InterPro: IPR008949; Terpenoid synth.
DR InterPro: IPR008930; Terp. cyc. toroid.
DR InterPro: IPR001906; Terp. synth-like.
DR Pfam: PF01397; Terpene_synth_C; 1.
DR Pfam: PF03936; Terpene_synth_C; 1.
DR SEQUENCE 630 AA; 72784 MW; B0E4374B262FF2D1 CRC64;
SQ

Query Match 69.6%; Score 2264; DB 10; Length 630;
Best Local Similarity 68.3%; Pred. No. 9.2e-159;

Matches 435; Conservative 76; Mismatches 98; Indels 26; Gaps 9;

QY 1 MALISTPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTVA54
DB 1 MALVSSAP---KSGLHSLRSTHHEIKPLRRTIPTLGICRGRKSPFMSVMSLTVA5D 57
QY 55 DSVQRVGNTHSNLWDDPFIOSLISTPYGADYRERADRLIGVYKDIMFNKSLSDG-- 112
DB 58 DGLQRRIGDTHSNLWDDPFIOSL-STPYGEPSTREAREKLGVEYK-MFNSMPSDESM 115
QY 113 ---NDLQRLLLVDVERLGIDRHFKEIKTALDYNSYWNKKGICGGRSVTDLNSTA 169
DB 116 SPLNDLIERLMMVDSVERLGIDRHFKEIKSALDYVSYWNKKGICGGRSDVFDVNSTA 175
QY 170 LGLATTLRHGYVSSDYLVNFKDNGQFSSSTANIQIEGIRGVNLFRASLVAEPGEKV 229
DB 176 SGFTTLRHGYSSSEVLKVPQDNGQFAPSPRK-ERDIRTVNLVRASPIAFPEGEKV 234
QY 230 DEAEFTSTKYRLAKQIPASSITLSLEIRDVLEFGHTNLRLRLAANYMDVFGQHT--- 285
DB 235 EEAEIFSSRYLKEAVQKIPVSS-LSOEIDYLEFGHTNMRLRLRYLDFGHPTSPWL 293
QY 286 KKNKA-----AEKLELAKLEFNI FSHLOERELKGVSRWMDSGSPMTFCRRHVEYYA 341
DB 294 KKKRTQYLDSEKLELAKLEFNI FSHLOERELKGVSRWMDSGSPMTFCRRHVEYYA 353
QY 342 ASCTIAEPQSGRGLFTKMSHLITVLDNMYDVEGVDELELFTATIKRMDPSAMECLPE 401
DB 354 SSCIAETPKSAFRLGFAKCHLITVLDNMYDVEGVDELELFTAEVARNMPSEKERLPE 413
QY 402 YMKGVMMVYHTVNEARVAEKAQGRDTLNTYARQAMEACFDSYMOAKWITATGILPTFE 461
DB 414 YMKELIYALYEALTDMAKEAEKQGRDTLNTYARQAMEVYLDSTYQBAKWLASGLPTFE 473
QY 462 YLENGKSSAHRPCALPILTLDPFPHILKEVDPEPSKLNDLICITLRLAGDRCYKAD 521
DB 474 YLENAKSSSGHRAALPLTLDPVLPEDVTKGIDFSPRFNDLASSFLRLAGDRCTKAD 533
QY 522 RARGEASSISCYMKDNPGLTEEDALNHINEMIRDAIRLAWELLKPDNSVPLTSKQIAF 581

DB 534 RDRGEASSISCYMKDNPGLTEEDALNHINEMIRDAIRLAWELLKPDNSVPLTSKQIAF 593
QY 582 DISRWMEHGYRNDGYSFANVETKSLVMRTVIEVPVL 618
DB 594 ELTRAFQLYKYRNDGYSFANVETKSLVMRTVIEVPVL 630

RESULT 6

Q9AKA5 PRELIMINARY; PRT; 634 AA.

ID Q9AKA5
AC Q9AKA5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-phellandrene synthase-like protein.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Picea.
OC NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.

RA Morency M.J., Nicole M.C., Seguin A.;
RT "Terpene synthase from Norway spruce, cDNA isolation and
RT characterization of beta-phellandrene synthase-like gene.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF369918; AAK39127.2; -.
DR GO: GO:0016829; P:lyase activity; IEA.

DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR005630; Terpenoid synth. C.
DR InterPro: IPR008949; Terpenoid synth.
DR InterPro: IPR008930; Terp. cyc. toroid.
DR InterPro: IPR001906; Terp. synth-like.
DR Pfam: PF01397; Terpene_synth_C; 1.
DR Pfam: PF03936; Terpene_synth_C; 1.
DR SEQUENCE 634 AA; 72768 MW; BE140A49C46B4404 CRC64;
SQ

Query Match 68.8%; Score 2237; DB 10; Length 634;
Best Local Similarity 68.0%; Pred. No. 9.2e-157;

Matches 434; Conservative 75; Mismatches 105; Indels 24; Gaps 10;

QY 1 MALISTPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLT-5V4S 53
DB 1 MSPSVVPLVAYKCLPSRLMSSSREYVPLHITIPNLQCMCRGKSMASAPSTSMILTA5VD 60
QY 54 TDSVQRVGNTHSNLWDDPFIOSLISTPYGADYRERADRLIGVYKDIMFNKSLSDG-- 112
DB 61 DSVQRVGNTHSNLWDDPFIOSL-STPYGEPSTREAREKLGVEYK-MFNSMPSDESM 115
QY 113 ---NDLQRLLLVDVERLGIDRHFKEIKTALDYNSYWNKKGICGGRSVTDLNSTA 168
DB 119 ITPLNDLQRLMMVDSVERLGIDRHFKEIKSALDYVSYWNKKGICGGRSDVFDVNSTA 178
QY 169 ALGRTLRHGYVSSDYLVNFKDNGQFSSSTANIQIEGIRGVNLFRASLVAEPGEKV 228
DB 179 ALGRTLRHGYVSSDYLVNFKDNGQFAPSPRK-ERDIRTVNLVRASPIAFPEGEKV 237
QY 229 MDEAEFTSTKYRLAKQIPASSITLSLEIRDVLEFGHTNLRLRLAANYMDVFGQHT--- 285
DB 238 MDEAEFTSSRYLKEAVQKIPVSS-LSOEIDYLEFGHTNMRLRLRYLDFGHPTSPWL 293
QY 286 --KKNKA-----AEKLELAKLEFNI FSHLOERELKGVSRWMDSGSPMTFCRRHVEYYA 340
DB 297 LKKKRTQYLDSEKLELAKLEFNI FSHLOERELKGVSRWMDSGSPMTFCRRHVEYYA 356
QY 341 LAGCTIAEPQSGRGLFTKMSHLITVLDNMYDVEGVDELELFTATIKRMDPSAMECLP 400
DB 357 LGSCTIADPKHRAFLGFTVCHLNTVLDNMYDVEGVDELELFTAEVARNMPSEKERLPE 416
QY 401 EYMGVMMVYHTVNEARVAEKAQGRDTLNTYARQAMEACFDSYMOAKWITATGILPTFE 460
DB 417 EYMGVMMVYHTVNEARVAEKAQGRDTLNTYARQAMEVYLDSTYQBAKWLASGLPTFE 476

Qy	461	LYLENGKXSSAHRPCALQPIETLFDIPEPHILIKENDPEBKLDLJCILRLREDTCYRA	520
Db	477	EYFENGKISSAARAALTPITLFDVLPPEYLKIGDIPFRFNDLASSFLRLREDTCYRA	536
Qy	521	DRARGEASISCYCKONPGLTPEEDALNNINFMIRDAIRELMWELKPNDSVPTSCKHA	580
Db	537	DRARGEASISCTCKMKNPGSTGEEDALNNINSMINEIILKELMWELRPSDNIIMPAKHA	596
Qy	581	FDISRVMHGGYRRDGYGFANETKSLWRITIEPVPL	618
Db	597	FDITRALHLYKYRDGFSVATETKTSLSVSRMTLEPVPL	634

RESULT 7

AD 094KA4; PRELIMINARY; PRT, 633 AA.
AC
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mycene synthase-like protein.
OS Picea abies (Norway spruce) [Picea excelsa].
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_taxonomy=3329;
RN [1]
RP SEQUENCE FROM N.A.
RA Morency M.J., Nicole M.C., Seguin A.;
RT "terpene synthase form Norway spruce, cDNA isolation and
RT characterization of mycene synthase-like gene by 5'- and 3'-RACE
RT amplification."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF369919; AYK9128.2; "-.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR InterPro; IPR008930; Terp_cyc_toicoid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
SQ SEQUENCE 633 AA; 72576 MW; b6c7c7ca895a7db1 CRC64;

Query Match	Score	DB	Length
67.8%	2205.5	10	633

Matches 430; Conservative 79; Mismatches 103; Indels 23; Gaps 9;

[illegible]

Db	357	ASCIATEPKHSAFRJGFGFANKCHLYLVLDVYDTFGCMDELBELFTAAVVKXMDLSETERLPE	416
Qy	402	YMKGYVMYVTHVTNEMARVAEKAQRDLTNARQWAECPDSYMOZAKAIATSYLPTFER	461
Db	417	YMKGYLVVLEFETVELAQEAETQORNTLNVRKMEAEAFDSYMKAEAMISTGYLPTFER	476
Qy	462	YLENGKVSASRARCLOPILTLTDIPEPHILEKVPSPSYLNDLICIILRLGDRCYKAD	521
Db	477	YXENGKVSARVALQPILTLDVQLPDLIGDIPSPSPFNDLASFLLRLGDRTCYKAD	536
Qy	522	RARGEASSISCYMDNPGLTBEDALNHINFMIRDAIRELNELLKPDNSVPTSKCAF	581
Db	537	RARGEASSISCYMDHPGSTEEDAVNHNIMAINIIEILANEFLEKPDNSNIPWARKAHF	596
Qy	582	DISRWHMHGARYRDGSPFANVETSLNWRVTEPV	616
Db	597	DITRLNHLIYYRDSFVASKETKQLVKEALAEAV	631

RESULT 8

ID	PRELIMINARY;	PRT;	627 AA.
084SM8;			
AC 084SM8;			
DT 01-JUN-2003	(TREMBLrel. 24,	Created)	
DT 01-JUN-2003	(TREMBLrel. 24,	Last sequence update)	
DT 01-OCT-2003	(TREMBLrel. 25,	Last annotation update)	
DE (+)-3-carene synthase.			
GN JF67.			
OS <i>Picea abies</i> (Norway spruce) (<i>Picea excelsa</i>).			
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta			
OC Spermatozoa; Coniferopsida; Coniferales; Pinaceae; Picea.			
OC NCBI_TaxId=3329;			

RP SEQUENCE FROM N.A.
RX MEDLINE=22490501; PubMed=12602896;
RA "Traumatic, resin defense in Norway spruce (*Picea abies*): methyl
RT jasmonic-ac, resin defense in Norway spruce (*Picea abies*): methyl
RT jasmonic-ac, resin defense in Norway spruce (*Picea abies*): methyl
RT and functional characterization of (+)-3-carene synthase.";
RL Plant Mol. Biol. 51:119,113(2003).
DR EMBL: AF461460; AAC73861.1; -
DR GO: GO:0016829; F:lyase;activity: IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR005630; Terpene_synth_C.
DR InterPro: IPR008949; Terpenoid_synth.
DR InterPro: IPR008930; Terp_cyc_cofold.
DR InterPro: IPR001906; Terp_synth-like.
DR Pfam: PF01397; Terpene_synth_C_1.
DR Pfam: PF03936; Terpene_synth_C_1.
QO SEQUENCE 627 AA; 71912 MW; B1B1AD15FC50F47 CRC64;

Query Match	66.5%	Score 2163.5	DB 10	Length 627
Best Local Similarity	66.4%	Pred. No. 2.5e-151		
Matches 419, Conservative	81	Mismatches 114	Indels 17	Gaps 7

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OY      1  FALISTIPVRSCT-----SSSHEIKLRRTIPLVIGICRCKSVAHJINMCLTSVASTD  55
Db      1  MSVSIILPLAKSCICYKSLMSSTHKLKCPRIATLGMCRCKRSWASXSTSLTAVSD  60
OY      56  SVORRVGNHNLWIDDFIOSLISTPYGAPDVRERADRILGEVKOIMENFKSLBEDG---  112
Db      61  GVORRIGHHNMLWIDNFIOSLSSPYGASSGEAERILGVEKELFNSLRTDDELVS  118
OY      113  --NNLLQBLILVDDVERLGIIDRHFKELIKTALDYNASYWNKEGICGGRSVYTDLNSTAL  170
Db      119  HVDDLQILSNWMDYNERGIDIRHFKTEIKVSLDYVYSYWKSEKGISGRDILVCTDLNTTAL  178
OY      171  GLRLRLHGYVSSDYLVNVEFKDXNQPSSTANIOIEGERIGULNPRSLVAPRGKXWD  230
Db      179  GFRILRLGIVFPDVEFHKDQMKRICSDN-ITERQSLSTLNLFRASLIAPFEKXVW  237
OY      231  EAEFTSTYKLEALCKIPASSILSLERDVLVEYGHNTNLPRLEARNYMDPQOHTKXKA  290

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238 EAEIFATYLKALQITPVSS-LSOEIQVLYQYRMSNLPRLBARTYIDILLOENTKQML 296
QY 291 ---ABKLELAKLEFNFHSLQRELBKHSRMMWKGSPBMTFCRRHVEYVALASCI 347
DB 297 DVNTKVLLEAKLEFNFHSLQRELBKHSRMMWKGSPBMTFCRRHVEYVALASCI 356
QY 348 EPOHSGFRLGFTKMSHLITVLDMYDFGVTVDELELEFTATIKRWDPSAMECLPEYMGV 407
DB 357 EPHGCFRLSEFVKCHLITVLDMYDFGVTVDELELEFTATIKRWDPSAMECLPEYMGV 416
QY 408 MMVYHTNEMARVAEAKQSGDITLVYARQAWBACDSTMOEAKVATGYLPTFEYLENG 467
DB 417 TVYETYNEMARVAEAKQSGDITLVYARQAWBACDSTMOEAKVATGYLPTFEYLENG 476
QY 468 VSSAHRPCALOPTLTDIPPPHILKEVDPPSKNDLICTILRLRGDTRCYKADRRAGE 527
DB 477 VSSGHRATLPTLTDIPPPHILKEVDPPSKNDLICTILRLRGDTRCYKADRRAGE 536
QY 528 ASSISCYMKDNPGLTEBDALNHINFMIRDAIRELWELLKPDNSVPTSKKAFDISRV 587
DB 537 ASSISCYMKDNPGLTEBDALNHINFMIRDAIRELWELLKPDNSVPTSKKAFDISRV 596
QY 588 HNGYRFDGYSFANVETKSLVMTVIEPVPL 618
DB 597 HNGYRFDGYSFANVETKSLVMTVIEPVPL 627

RESULT 9

084KL3 PRELIMINARY; PRT; 628 AA.
ID 084KL3
AC 084KL3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE (+)-alpha-pine synthase.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "CDNA isolation, functional expression, and characterization of (+)-
alpha-pine synthase and (-)-alpha-pine synthase from loblolly pine
Pinus taeda: Stereoccontrol in pine biosynthesis.";
RT Arch. Biochem. Biophys. 411:267-276(2003).
RU Arch. Biochem. Biophys. 411:267-276(2003).
DR EMBL; AF543530; A061228.1; -;
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_Teroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth; 1.
SQ SEQUENCE 628 AA; 71495 MW; 420822261256837 CRC64;

Query Match 66.2%; Score 2151; DB 10; Length 628;
Best Local Similarity 65.8%; Pred. No. 2.1e-150;
Matches 416; Conservative 92; Mismatches 106; Indels 18; Gaps 8;
QY 1 MALSTIPLVSRCL-----SSHEIKALRTTPTLGLCRGKSVASINM-CLTSVAST 54
DB 1 MALVSANPLNSKLCIRTLRFSGHSLRAHSTVNLGCRGKSIAPBSMSSTTSVSN 60
QY 55 DSVQVRGVNHSNIMDDPFIQSLISTPYGADYERADRLIGEVKDIMENFKSLIEDG 112
DB 61 DGVRRIAGHSHNIMDDSIASL-STSYEAPSYRKADKILGEVANI-FDIMSVEDEVFT 118
QY 113 ---NDLQRLLDVDERLGTDRHFKKEIKALDVYNSYNNKEKIGCRRESVVDLNSTA 169
DB 119 SPLSDLHRRIMWDSVERLGIIDRHFKEINSLDHLVYSYWKTEKIGRGRESGVTDLN 178

QY 170 LGRTRLHGVTSSDVLANVFKDNGQFSSTANIOIEGIRGVNLFRASLVAFPEKVM 229
DB 179 LGRTRLHGVTSSDVLANVFKDNGQFSSTANIOIEGIRGVNLFRASLVAFPEKVM 237
QY 230 DEAFSTKTLREALOKIPASSILSLERIVLEYGHTNLPRLBARTYIDILLOENTK 289
DB 238 EAEIFATYLKALQITPVSS-LSOEIQVLYQYRMSNLPRLBARTYIDILLOENTK 296
QY 290 ---ABKLELAKLEFNFHSLQRELBKHSRMMWKGSPBMTFCRRHVEYVALASCI 346
DB 297 DVNTKVLLEAKLEFNFHSLQRELBKHSRMMWKGSPBMTFCRRHVEYVALASCI 356
QY 347 EPOHSGFRLGFTKMSHLITVLDMYDFGVTVDELELEFTATIKRWDPSAMECLPEYMGV 406
DB 357 EPHGCFRLSEFVKCHLITVLDMYDFGVTVDELELEFTATIKRWDPSAMECLPEYMGV 416
QY 407 MMVYHTNEMARVAEAKQSGDITLVYARQAWBACDSTMOEAKVATGYLPTFEYLENG 466
DB 417 TVYETYNEMARVAEAKQSGDITLVYARQAWBACDSTMOEAKVATGYLPTFEYLENG 476
QY 467 VSSAHRPCALOPTLTDIPPPHILKEVDPPSKNDLICTILRLRGDTRCYKADRRAGE 526
DB 477 VSSGHRATLPTLTDIPPPHILKEVDPPSKNDLICTILRLRGDTRCYKADRRAGE 536
QY 527 ASSISCYMKDNPGLTEBDALNHINFMIRDAIRELWELLKPDNSVPTSKKAFDISRV 586
DB 537 ASSISCYMKDNPGLTEBDALNHINFMIRDAIRELWELLKPDNSVPTSKKAFDISRV 596
QY 587 HNGYRFDGYSFANVETKSLVMTVIEPVPL 618
DB 597 HNGYRFDGYSFANVETKSLVMTVIEPVPL 628

RESULT 10

09M7D0 PRELIMINARY; PRT; 630 AA.
ID 09M7D0
AC 09M7D0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Terpinolene synthase.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373092; PubMed=10441373;
RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;
RT "cDNA cloning, characterization, and functional expression of four new
monoterpene synthase members of the Tpsd gene family from grand fir
Abies grandis.";
RT Arch. Biochem. Biophys. 368:232-243(1999).
RU Arch. Biochem. Biophys. 368:232-243(1999).
DR EMBL; AF139206; AAF6154.1; -;
DR HSSP; Q40577; SEAU.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_Teroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth; 1.
SQ SEQUENCE 630 AA; 72508 MW; 452437887F203DBA CRC64;

Query Match 67.7%; Score 2137; DB 10; Length 630;
Best Local Similarity 67.4%; Pred. No. 2.3e-149;
Matches 427; Conservative 73; Mismatches 114; Indels 20; Gaps 9;
QY 1 MALSTIPLVSRCL-----SSHEIKALRTTPTLGLCRGKSVASINM-CLTSVAST 55


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DB 1 MALVSIPLSKSVLHSMWIVSTYEHKAIKSTIINLGIKRGKSVTHSLRSLSTAVSD 60
QY 56 -SVORGVNTHSNIMDDDFIOSLSTPYGADYERADRLIGEVKDMFNKSLDGG-- 112
DB 61 HGVORRIVEFNSIMDDFIQSL-STPYGADYERADRLIVEVGI-FTSISADGELI 118
QY 113 ---NDLORLLVNDVRLGIDRHFKKEIKTALDVYNSYNNKGGICGGRSVVDINSTA 169
DB 119 TPLNDLQRLMNVNVERLIGIDRHFKKEIKTALDVYNSYNNKGGICGGRSVVDINSTA 178
QY 170 LGLRTTLHGTVSSDVLNVPK--KNGQFSTANIQIEGEIRGVNLFRAVLAFPEEK 227
DB 179 LGRFLLHGVSSDVLNHPKKEKQFVCSA-IGREBKIVNLFRAVLAFPEEK 237
QY 228 VMDAEFTSTKYREALOKIPASSILSLRIDVLEYGHTNLPRLEARNYMDVFGQHTN 287
DB 238 VMEBAEFKSKYLKEALQNIIVSS-LSREIEVLEDDGQTMPLRETNITDVGENDR 296
QY 288 KNA---AEKLELAKLEFNIHSLQERELKHSRWKSGSPENTFCRRHVEYALASC 344
DB 297 ETLVNNKLELAKLEFNIHSLQERELKHSRWKSGSPSHLTFSSHRRVEYALASC 356
QY 345 IAFEPQSGFRLGFTKMSHLITVLDMDYVFGTDELELFTATIKRMDPSAMECLPEYMK 404
DB 357 IETDKKSGFRLGFTKMSHLITVLDMDYVFGTDELELFTATIKRMDPSAMECLPEYMK 416
QY 405 GYVMVYVTVNEMARVAEKAQGRDTLVNARQAMECFDSYNOEAKMTATGYLPTFEYLE 464
DB 417 GLVNVVETVNEIAREADKSGRETLNDARAMEYLDYSYKAEAWISSGYLPTFEYLE 476
QY 465 NGKVVSAHRPCALOPILTDIPFPDHILKEVDPSKNDLCIILRLRGDRCTKADAR 524
DB 477 TSRSVFRYRFPALOPILTDIPFPDHILKEVDPSKNDLCIILRLRGDRCTKADAR 536
QY 525 GEEASSISCVKDPGRLTEEDALNHNFMIRDAIRELMWELLKPDNSVITSKGAFFIS 584
DB 537 GEEASSISCVKDPGRLTEEDALNHNFMIRDAIRELMWELLKPDNSVITSKGAFFIS 596
QY 585 RVMHGVRDGVSAFANVETKSLVRYTIEPVL 618
DB 597 KGLHGYKVRDGVSAFANVETKSLVRYTIEPVL 630

RESULT 11
Q9M7C9 PRELIMINARY; PRT; 637 AA.
AC Q9M7C9;
DT 01-OCT-2000 (Tremblrel. 15. Created)
DT 01-OCT-2000 (Tremblrel. 15. Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
DE (-)-limonene/(-)-alpha-pinene synthase.
GN AGC11.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=4611;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99373092; PubMed=10441373;
RA Bohmann J., Phillips M., Ramchandiran V., Katoh S., Croteau R.,
RT "cDNA cloning, characterization, and functional expression of four new
RT monoterpen synthase members of the Trpd gene family from Grand fir
RT (Abies grandis).";
RL Arch. Biochem. Biophys. 368:232-243 (1999).
DR HSPB: AF139207; AAF61455.1; -.
DR HSPB: Q40577; S5AS.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR005630; Terpene_synth_C.
DR InterPro: IPR008949; Terpenoid_synth.
DR InterPro: IPR008930; Terp_cyc_toroid.

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DR InterPro: IPR001906; Terp_synth-like.
DR Pfam: PF01397; Terpene_synth_1.
DR Pfam: PF03936; Terpene_synth_C_1.
SQ SEQUENCE 637 AA; 73273 MW; 83574986FEC96C6B CRC64;
Query Match 64 1%; Score 2084.5; DB 10; Length 637;
Best Local Similarity 64.9%; Pred. No. 1.86-145;
Matches 417; Conservative 80; Mismatches 115; Indels 31; Gaps 13;

QY 1 MALISTPL-VSRSC-----LSSHEIKAL--RTIPTLIGICRPGKVAHSINMCTISVA 52
DB 1 MALISTPLVQPKSCGKSLSSSNVQALCISTAVPLFRRRKQALV--INMKTIVS 58
QY 53 STDS-----VORRGVTHSNIMDDDFIOSLSTPYGADYERADRLIGEVKDMFNK-- 105
DB 59 HRDNGGCVLQRRADHPNIMEDDFIOSL-SPEYGGSSYERAVTVVEEYK-MFNIP 116
QY 106 --KSLDQGNLQRLVNDVRLGIDRHFKKEIKTALDVYNSYNNK-GICGGRSVV 162
DB 117 NNRELFGSNDLRLIMVDSIERLGIDRHFKKEIKTALDVYNSYNNKGGICGRDSTF 176
QY 163 TDINSTALGLRTTLHGTVSSDVLNVPKNGQFSTANIQIEGEIRGVNLFRAVL 221
DB 177 PDINSTALAKRTTLHGTVSSDVLNVPKNGQFSTANIQIEGEIRGVNLFRAVL 235
QY 222 AFPEKVMDEMETSTKYREALOKIPASSILSLRIDVLEYGHTNLPRLEARNYMDV 281
DB 236 AFPEKVMDEMETSTKYREALOKIPASSILSLRIDVLEYGHTNLPRLEARNYMDV 294
QY 282 GQHTKNNK-----AEKLELAKLEFNIHSLQERELKHSRWKSGSPENTFCRRH 335
DB 295 GQHTKNNK-----AEKLELAKLEFNIHSLQERELKHSRWKSGSPENTFCRRH 354
QY 336 VEYTMASCIAMEBKHAFLRGFKTCHILTVLDMDYVFGTDELELFTATIKRMDPSA 395
DB 355 VEYTMASCIAMEBKHAFLRGFKTCHILTVLDMDYVFGTDELELFTATIKRMDPSA 414
QY 396 MECLPEYMKGYVMVYVTVNEMARVAEKAQGRDTLVNARQAMECFDSYNOEAKMTATGY 455
DB 415 MECLPEYMKGYVMVYVTVNEMARVAEKAQGRDTLVNARQAMECFDSYNOEAKMTATGY 474
QY 456 LPTFEYLENGKVSASRRPCALOPILTDIPFPDHILKEVDPSKNDLCIILRLRGDR 515
DB 475 LPTFEYLENGKVSASRRPCALOPILTDIPFPDHILKEVDPSKNDLCIILRLRGDR 534
QY 516 RCYKADRRAGEASSISCVKDPGRLTEEDALNHNFMIRDAIRELMWELLKPDNSVIT 575
DB 535 RCYKADRRAGEASSISCVKDPGRLTEEDALNHNFMIRDAIRELMWELLKPDNSVIT 594
QY 576 SKKAFDISRVMHGVRDGVSAFANVETKSLVRYTIEPVL 618
DB 595 SKKAFDISRVMHGVRDGVSAFANVETKSLVRYTIEPVL 637

RESULT 12
Q94FV9 PRELIMINARY; PRT; 637 AA.
AC Q94FV9;
DT 01-DEC-2001 (Tremblrel. 19. Created)
DT 01-DEC-2001 (Tremblrel. 19. Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25. Last annotation update)
DE (-)-4S-limonene synthase.
GN Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=4611;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21297238; PubMed=11404343;
RA Tripp S.C., Croteau R.B.,
RT "Genomic organization of plant terpene synthases and molecular
RT evolutionary implications.";
RL Genetics 158:811-832 (2001).

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DR EMBL; AF326518; AAK83565.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
DR SEQUENCE 637 AA; 73535 MW; 2D86B2E14866F378 CRC64;

Query Match 62.8%; Score 2041.5; DB 10; Length 637;
Best Local Similarity 63.8%; Pred. No. 2.7e-142;
Matches 410; Conservative 84; Mismatches 118; Indels 31; Gaps 14;

QY 1 MALISTPL-VSRSG-----LSSSHEIKAL--RRTPTLIGICRGKGVASHINMCLTSA 52
DB 1 MALISTVSLQPKSCGOKSLISSNVOKALCISTAVPTLRKRKOKALV--INMKLTIVS 58
QY 53 STDS-----YORRVGNHSLMDDDFIQSLISTPYGAPDYERADRLIGEVKDIMFNF-- 105
DB 59 HRDNDGCVLQRRADHHPNLMEDDFIQSL--SSPYGSSYSERAETLVEBVK--MFRSIP 116
QY 106 --KSLEDGNDLQRLLLVDVERLIGIDRFKKEIKTALDYNSYNNEK-GICGGRSVV 162
DB 117 NNHELFGSQNDLRLTMVVDISERLIGIDRFQNEIRVALDYVSYMKKEGICGGRDSTF 176
QY 163 TDINSTALGRTLRHGYTSSDVLNFKDKNGQFSSSTANIQIEGET--RGVLANFRASIV 221
DB 177 PDLNSTALAKRTLRHGYNSSDVLEYFKDKNGHACPA--LTLEGQTRSVLANFRASIV 235
QY 222 AFPEKYMDEAETPSTYLRREALOKIPASSILSLERIDVLEYGWHNLPRLEARNYMDVF 281
DB 236 AFPEKMEBEAEIFSAYLKEVLOKIPVN--LSGEIYVLEYGWHNLPRLEARNYIEVY 294
QY 282 ---GQHTKKNKA--AEKLFLALERNIFHSLOERELKAVSRWKSGSPGEMTFCRRH 335
DB 295 EOSGYEELNENPYNMKKLQLAKLEFNIFHSLOERELKAVSRWKSGSQLTFTTRRH 354
QY 336 VEYVALASCTAFEPHSGFRIGFTKMSHLITVLDMDVFGTVDELELFTATIKRMPBSA 395
DB 355 VEYITMASCISMESKSAFRMEFYKCHLVLDITDITFTMELQLFTDAIKRMDIST 414
QY 396 MECLPEYMKGVYMYHTVNMARVAEKAQGRDITLNTARQAMEACFDSYMOEAKMIATGY 455
DB 415 TRMLPEYMKGVYMDLYCINEMVEEAOQKGRDMLNTIYQNGWEALPFTFQEAKMISSEY 474
QY 456 LPTEBEYLENGKVSARPCALQPIILTDIPFPHILKEVDPESKANDLICITIRLGGDT 515
DB 475 LPTEBEYLKNAKAVSSGSRITATLQPIILTDVLPDIYIQLQEIIDYPSRFNELASSILRLGDT 534
QY 516 RCYKADARGBEASISCYMKDNGPLTEBDALNHINFIRDAIRELMWELLKPPNSVPT 575
DB 535 RCYKADARGBEASISCYMKDNGHGSTBEDALNHINMISDAIRELMWELLKPPNSKBPIS 594
QY 576 SKGIAFDISRVMHGYYRDGYSFANVETKSLVNRVYIEPVPL 618
DB 595 SKGIAFDITRAFHHVYKRDGYTAVSNNETKNLVNKTVLEPVL 637

RESULT 13
Q84KL2 PRELIMINARY; PRT; 615 AA.

AC 084KL2; 084KL2; 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Monoterpen synthase-like protein.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_taxid=3352;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "cDNA isolation, functional expression, and characterization of (+)-
RT alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine
RT (Pinus taeda): Stereocontrol in pinene biosynthesis.";
RL Arch. Biochem. Biophys. 411:267-276(2003).

DR EMBL; AF543511; AAO61229.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
DR SEQUENCE 615 AA; 70574 MW; B6F5F453A052AEC6 CRC64;

Query Match 61.1%; Score 1985.5; DB 10; Length 615;
Best Local Similarity 63.1%; Pred. No. 3.5e-138;
Matches 397; Conservative 82; Mismatches 123; Indels 27; Gaps 10;

QY 1 MALISTPLVS--RSCSSHEIKALRRTIPTIGICRGKGVASHINMCLT-SVASTDSV 57
DB 3 LALVSAPLVSMKRSLSFSSPELKSIDKTIPLNVCCKRSGRPSIVSSTASVNDGV 62
QY 58 QRRVGNHSLMDDDFIQSLISTPYGAPDYERADRLIGEVKDIMFNFKSLEDG----- 112
DB 63 RRRVGDYRNMHMBEDLIDSL-ATSYEAPSYLKADTLVEATKQ--RFSMWGVDQGRMSPL 120
QY 113 NDILQRLLVDDVERLIGIDRFKKEIKTALDYNSYNNEKIGICGGRSVTTDLNSTALGL 172
DB 121 TDLYQRLMMDVSVERLIGIDRFQNEIRKALDYVSYMKKEGICGGRSAVTDLNSTALGL 180
QY 173 RTLRHGYTSSDVLNFKDKNGQFSSSTANIQIEGETRGVLANFRASIVAPGSKMDEA 232
DB 181 RTLRHGYTPVSSDVLNFKDKNGQF--TCSGIGTBEIRGVLANFRASIVAPGSKMDEA 239
QY 233 ETPSTKYLRREALOKIPASSILSLERIDVLEYGWHNLPRLEARNYMDVFGQHTKKNAAE 292
DB 240 EIPSTYVLKHALQKIAVSS--LSGEIYVLEYGWHNLPRLEARNYMEVFPQDTIYE--Q 295
QY 293 KLEFLALERNIFHSLOERELKAVSRWKSGSPGEMTFCRRHVEYALASCTAFEPHGS 352
DB 296 KLVELAVERNIFHSLOERELKAVSRWKSGSPGEMTFCRRHVEYALASCTAFEPHGS 355
QY 353 GFRIGFTKMSHLITVLDMDVFGTVDELELFTATIKRMPBSAMECLPEYMKGVYMYHT 412
DB 356 AFRIGFAMKSYFTVLDITDITFTMELBLFTAIKRPBPSVVDCLPEYMKGVYMYHT 415
QY 413 TVNEMARVAEKAQGRDITLNTARQAMEACFDSYMOEAKMIATGYLPTEBEYLENGKVSAAH 472
DB 416 TVNEMARVAEKAQGRDITLNTARQAMEACFDSYMOEAKMIATGYLPTEBEYLENGKVSAAH 475
QY 473 RPCALQPIILTDIPFPHILKEVDPESKANDLICITIRLGGDTTCYKADARG---EAS 529
DB 476 RITLQPIILTLGELSHEILOEIDPSAKFNDLSVILRLG-----GQGSVVEAS 526
QY 530 SISCYMKDNGPLTEBDALNHINFIRDAIRELMWELLKPPNSVPTSKGIAFDISRVMH 589
DB 527 SVSCYMKDNGPLTEBDALNHINFIRDAIRELMWELLKPPNSVPTSKGIAFDISRVMH 586

RESULT 14
Q84KL5 PRELIMINARY; PRT; 574 AA.

AC 084KL5; 084KL5; 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Alpha-farnesene synthase.
 OS Pinus taeda (loblolly pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22510022; PubMed=12623076;
 RA Phillips M.A., Wilding M.R., Williams D.C., Hyatt D.C., Croteau R.;
 RT "cDNA isolation, functional expression, and characterization of (+)-
 alpha-pinenene synthase and (-)-alpha-pinenene synthase from loblolly pine
 (Pinus taeda): Stereoccontrol in pinene biosynthesis.";
 RL Arch. Biochem. Biophys. 411:267-276(2003).
 DR EMBL, AF543528; AAC61226.1;
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR005630; Terpene synth C.
 DR InterPro; IPR008930; Terpenoid synth.
 DR InterPro; IPR001906; Terp_cyc foroid.
 DR Pfam; PF03936; Terpene synth; 1.
 DR Pfam; PF03936; Terpene synth; 1.
 SQ SEQUENCE 574 AA; 65941 MW; 26746BAE32ACF19A CRC64;

Query Match 58.7%; Score 1909; DB 10; Length 574;
 Best Local Similarity 63.3%; Pred. No. 1.5e-1102;
 Matches 366; Conservative 88; Mismatches 132; Indels 14; Gaps 8;

QY 50 SVASTDSVQRVGNHNSLMDDDFIOSLSTPYGAPDYRERADRLIGEVKIDMFNFSLK 109
 DB 2 SSLAVDDAKRVGDHPLMDALISL-STPYGASPRDVAKEIKERKE-MFASISIE 59
 QY 110 DGGNDL---LQRLLLVDDVERLIGIDRHFKEIKTALDYVNS-YNNEKIGIGRESVYTDL 165
 DB 60 DGDDEICVFLQRLMWDNVERLGISRHFENEIKAMEDYVSRHMSDKGACGRHSVADL 119
 QY 166 NSTLGLRTLLHGTSSDVLVNPKDKNGQSSSTANQIBEGICVNLPRASIVAPRG 225
 DB 120 NSTLALFTLLRHGVSVDVFKITQDQGEFACAD-QTEBEGIGILNRLASLAPRG 178
 QY 226 EKVMDEAFSTFKYLREALOKIPASSISLEIRDLVLEYGMHTNLPRLBARNYMDVFGQ- 284
 DB 179 ERIIOENAFITTYLKEALPKIQSR-LSQIEEYLVLEGMWLTDLRLTRNYIEVLAEI 237
 QY 285 ----TKNNAAEKLELAEFNIFHSIOERELKIVSRWMDGSGPEMTFCHRHVEYIA 340
 DB 238 TPYFKKPCMAVEKILAKIEFNHLSIQETELKLSRWMDSGPAQLFTFHRHVEFY 297
 QY 341 LASCIAPEHSGFRIGFTKSHLITVLDMDYDVGYTDELEFPAITKRWDPSAMECLP 400
 DB 298 LASCIAPEHSGFRIGFTKSHLITVLDMDYDVGYTDELEFPAITKRWDPSAMECLP 357
 QY 401 EYMGVYVNVHTVENARVAEKAQGRDLYNARQAECPDSYQOAKMIATGYLPTFE 460
 DB 358 EYMGVYVNVHTVENARVAEKAQGRDLYNARQAECPDSYQOAKMIATGYLPTFE 417
 QY 461 EYMGVYVNVHTVENARVAEKAQGRDLYNARQAECPDSYQOAKMIATGYLPTFE 520
 DB 418 KYLDNGKVSFGVRAATLQPIITLIDIPPLHILQIETIDPSSFNDLASITLRAGDIGYOA 477
 QY 521 DRAGEEASSTSCYKNDPGLTEBDALNHINFMIDARLNMWELKPDNSVPITSKGA 580
 DB 478 ERSRGEASSTSCYKNDPGLTEBDALNHINFMIDARLNMWELKPDNSVPITSKGA 536
 QY 581 FDISRVHNGYRYDGYSPAVNETKSLVMRTVEVPVL 618
 DB 537 FDLIRAFYHLKYRNGFSIAKETKCLVMRTVLDVPM 574

RESULT 15
 ID 064404 PRELIMINARY; PRT; 581 AA.

AC 064404;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE D-selinene synthase.
 OS Abies grandis (Grand fir).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
 NCBI_TaxID=46611;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98113169; PubMed=9442047;
 RA Steele C.L., Crook J., Bohlmann J.;
 RT "Sesquiterpene synthases from grand fir (Abies grandis). Comparison of
 constitutive and wound-induced activities, and cDNA isolation,
 RT characterization, and bacterial expression of delta-selinene synthase
 RT and gamma-humulene synthase.";
 RL J. Biol. Chem. 273:2078-2089(1998).
 DR EMBL, U92266; AAC05727.1;
 DR HSSP; 040577; SEAU.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR005630; Terpene synth C.
 DR InterPro; IPR008930; Terpenoid synth.
 DR InterPro; IPR001906; Terp_cyc foroid.
 DR Pfam; PF03936; Terpene synth; 1.
 DR Pfam; PF03936; Terpene synth; 1.
 SQ SEQUENCE 581 AA; 67967 MW; 864622AB8BC32C8 CRC64;

Query Match 39.8%; Score 1295.5; DB 10; Length 581;
 Best Local Similarity 44.1%; Pred. No. 3.5e-87;
 Matches 255; Conservative 118; Mismatches 190; Indels 15; Gaps 8;

QY 53 STDVSQREVGNYHNSLMDDDFIOSLSTPYGAPDYRERADRLIGEVKIDMFNFSLK 112
 DB 5 SSSIIPRTGNHNGVMDDDLHSL-NSPYGAPVYELLQKILHILITEMMDGDD 63
 QY 113 NDLLORLLVDDVERLIGIDRHFKEIKT-ALDYNSYNNEKIGIGG-RESVYTDLNSL 170
 DB 64 HDLKRQIIVDTLCLGIDRHFHEHIOPLADYVYRWNNKIGIGGSDSSKDLNATL 123
 QY 171 GLRTLRHGTVSSDVLVNPKDKNGQSSSTANQIBEGICVNLPRASIVAPRG 226
 DB 124 GFRALRLRNVSSGVLNFKDENGKFCNFTGE-EGGDKOVMSMLSLRASEISFGE 182
 QY 227 KVMDEAFSTFKYLREAL---OKIPASSISLEIRDLVLEYGMHTNLPRLBARNYMDVFG 282
 DB 183 KVMDEAFSTFKYLREAL---OKIPASSISLEIRDLVLEYGMHTNLPRLBARNYMDVFG 242
 QY 283 QHTK--NKNAAEKLELAEFNIFHSIOERELKIVSRWMDGSGPEMTFCHRHVEYIA 340
 DB 243 HNSHMLKSNINQKMLKALYDENILQCKGHEKIEQFITWMDSDSGISQINFRKRVVEYS 302
 QY 341 LASCIAPEHSGFRIGFTKSHLITVLDMDYDVGYTDELEFPAITKRWDPSAMECLP 400
 DB 303 WVMVICFEPESESRIAPAKTALICTVLDYDTHALHETKIMTEGVRRWDLSTLDDP 362
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 QY 461 EYMGVYVNVHTVENARVAEKAQGRDLYNARQAECPDSYQOAKMIATGYLPTFE 520
 DB 423 EYIRGNMASSGMCILNIPLLIDKLIPDNILQIHSKSLIDLELGRADLKDDED 482
 QY 521 DRAGEEASSTSCYKNDPGLTEBDALNHINFMIDARLNMWELKPDNSVPITSKGA 580
 DB 483 EKERGEASSTSCYKNDPGLTEBDALNHINFMIDARLNMWELKPDNSVPITSKGA 541
 QY 581 FDISRVHNGYRYDGYSPAVNETKSLVMRTVEVPVL 618
 DB 542 FNIGRGLQFIYKRDGLYISDKEVDDQIFKILVHQPVM 579

Search completed: July 23, 2004, 09:03:45
Job time : 45 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 17:02:17 ; Search time 128 Seconds
(without alignments)
2679.372 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALLSTRIPVSRCLSSSHSHE.....FANVETSLVWRTYIEPVPL 618

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdl
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA:

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6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3251	100.0	2013	4	US-09-360-545-64 Sequence 64, Appl
2	2453	75.5	2018	4	US-09-360-545-3 Sequence 3, Appl
3	2453	75.5	2018	4	US-09-360-545-19 Sequence 19, Appl
4	2453	75.5	2018	4	US-09-360-545-19 Sequence 19, Appl
5	2453	75.5	2018	4	US-09-887-586A-19 Sequence 19, Appl
6	2453	75.5	2018	4	US-09-887-586A-19 Sequence 19, Appl
7	2453	75.5	2018	4	US-09-900-012B-19 Sequence 19, Appl
8	2264	69.6	2186	4	US-09-360-545-66 Sequence 66, Appl
9	2200.5	67.7	2196	4	US-09-360-545-1 Sequence 1, Appl
10	2200.5	67.7	2196	4	US-09-360-545-1 Sequence 1, Appl
11	2200.5	67.7	2196	4	US-09-887-586A-29 Sequence 29, Appl
12	2200.5	67.7	2196	4	US-09-887-586A-29 Sequence 29, Appl

13	2200.5	67.7	2196	4	US-09-903-012B-29 Sequence 29, Appl
14	2200.5	67.7	2196	4	US-09-900-797-29 Sequence 29, Appl
15	2197.5	67.6	2205	4	US-09-360-545-11 Sequence 31, Appl
16	2137	65.7	1890	4	US-09-360-545-77 Sequence 77, Appl
17	2084.5	64.1	2425	4	US-09-360-545-68 Sequence 68, Appl
18	2031.5	62.5	2085	4	US-09-360-545-5 Sequence 5, Appl
19	2031.5	62.5	2085	4	US-09-360-545-5 Sequence 5, Appl
20	2031.5	62.5	2085	4	US-09-360-545-5 Sequence 5, Appl
21	2031.5	62.5	2085	4	US-09-887-586A-57 Sequence 57, Appl
22	2031.5	62.5	2085	4	US-09-887-586A-57 Sequence 57, Appl
23	2031.5	62.5	2085	4	US-09-903-012B-57 Sequence 57, Appl
24	1295.5	39.8	1865	4	US-09-900-797-57 Sequence 57, Appl
25	1295.5	39.8	1865	4	US-09-398-395A-47 Sequence 47, Appl
26	1295.5	39.8	1865	4	US-09-887-586A-47 Sequence 47, Appl
27	1295.5	39.8	1865	4	US-09-895-752-47 Sequence 47, Appl
28	1295.5	39.8	1865	4	US-09-903-012B-47 Sequence 47, Appl
29	1295.5	39.8	1885	3	US-09-900-797-47 Sequence 47, Appl
30	1295.5	39.8	1885	3	US-09-234-393-45 Sequence 45, Appl
31	1295.5	39.8	1885	3	US-09-234-393-47 Sequence 47, Appl
32	1295.5	39.8	1885	4	US-09-865-171-45 Sequence 45, Appl
33	1295.5	39.8	1885	4	US-09-865-171-47 Sequence 47, Appl
34	1295.5	39.8	1888	3	US-09-234-393-19 Sequence 19, Appl
35	1295.5	39.8	1888	4	US-09-865-171-19 Sequence 19, Appl
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37	1250.5	38.5	1967	3	US-09-865-171-43 Sequence 43, Appl
38	1250.5	38.5	1967	4	US-09-360-545-17 Sequence 17, Appl
39	1250.5	38.5	1967	4	US-09-865-171-14 Sequence 14, Appl
40	1240.5	38.2	2700	3	US-09-315-861-14 Sequence 14, Appl
41	1240.5	38.2	2700	4	US-09-398-395A-43 Sequence 43, Appl
42	1240.5	38.2	2700	4	US-09-887-586A-43 Sequence 43, Appl
43	1240.5	38.2	2700	4	US-09-895-752-43 Sequence 43, Appl
44	1240.5	38.2	2700	4	US-09-903-012B-43 Sequence 43, Appl
45	1240.5	38.2	2700	4	US-09-593-253-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-360-545-64 Application US/09360545
Sequence 64, Appl
Patent No. 6429014
GENERAL INFORMATION:
APPLICANT: Croceau, Rodney B
APPLICANT: Bohlmann, Joerg
APPLICANT: Steele, Christopher L
APPLICANT: Phillips, Michael A
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REFERENCE: waur13885
CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
EARLIER FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 2013
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (36)..(1889)
US-09-360-545-64

Alignment Scores:

Pred. No.: 0
Score: 3251.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 2013
Matches: 618
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-025-145a-65 (1-618) x US-09-360-545-64 (1-2013)

QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeuSerSerHisGlu 20
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QY 21 IleValAlaLeuArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal 40
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QY 41 AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60
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QY 61 ValGlyAsnThrHisSerAsnLeuThrAspAspPheIleGlnSerIleIleSerThr 80
DB GTGGGCAACATATCATTCACACCTGTGGGACGATATTTATACAGTCTGTATCTCAACG 275
QY 81 ProTyrGlyAlaProAspTyrArgGlyValArgAlaAspArgLeuIleGlyGluValLysAsp 100
DB CCTATGAGAGACCTGATTAACGGGAAACGTCTGACACACTTATTTGGGAAAGTAAAGAT 335
QY 101 IleMetPheAsnPheLysSerLeuGlnAspGlyGlyAsnAspLeuGlnArgLeu 120
DB ATATGTTCAATTCATTAAGTCGCTGAAAGATGAGGCAATGATCTCTTCAACGACTTTTG 395
QY 121 LeuValAspAspValGlyValArgLeuGlyIleAspArgHisPheLysGlyIleLysThr 140
DB CTGGATCGATGACGTTGAAAGCTTTGGAAATCGACAGCGCTTTCAAAAGAAATAAAAACG 455
QY 141 AlaLeuAspTyrValAlaSerSerTyrTrpAsnGlnLysGlyIleGlyCysGlyArgGlyLys 160
DB GCACTCGATTAATGTTACAGTTATTTGGAACGAAAAAGCATTTGATGTGGAGGGAAGAT 515
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180
DB GTTGTGCTGCTCACTCAACCTCAACCGCTTGGGCGCTTCGACCTCCGACTCAGCGATAC 575
QY 181 ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr 200
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QY 201 AlaAsnIleGlnIleGlyGlyIleArgGlyValLeuAsnLeuPheArgAlaSerLeu 220
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QY 241 ArgGlnAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGlnIleArgAspVal 260
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QY 261 LeuGlyTyrGlyTyrPheIleThrAsnLeuProArgLeuGlnAlaArgAsnTyrMetAspVal 280
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QY 281 PheGlyGlnHisThrLysAsnLysAsnAlaAlaGlyLysLeuGlnLysAlaLysLeu 300
DB TTTTGAGACGACACATTAATAAATAGAACCCCGCAGAAACTTTTAAAGACTTGCAAAATG 935
QY 301 GluPheAsnIlePheHisSerLeuGlnGlyArgGlyLeuLysHisValSerArgTyrTrp 320
DB GAATTCATATATTTCACTCTTACAGAGAGAGAGATTAAACATGTTTCCCGATGGTGG 995
QY 321 LysAspSerGlySerProGlyMetThrPheCysArgHisArgHisValGlyTyrTyrAla 340
DB AAAGACTCGGGTCTCTCGAGATGACCTTCTGTGACATCTGCACGAGTAATACGACT 1055
QY 341 LeuAlaSerCysIleAlaPheGlyProGlnHisSerGlyPheArgLeuGlyPheThrLys 360
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DB CTGGAACTCTTACAGCGACAAATTAAGATGGATCCGTCGCGAGGAATGCTTCCA 1235
QY 401 GluTyrMetLysGlyValLysTyrMetMetValTyrHisThrValAsnGlyMetAlaArgVal 420
DB GAATATATGAAAGAGATGATCATGATGTTTATCACACCTTAATGAAATGCGAGTG 1295
QY 421 AlaGlyLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaATPGLuAlaCys 440
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QY 441 PheAspSerTyrMetGlnGlyAlaLysTyrIleAlaThrGlyTyrLeuProThrPheGlu 460
DB TTTGATTCGTATATGACAGAAACAAAGTGAATGCGCACTGGTATCTGCCACGTTGAG 1415
QY 461 GluTyrLeuGlnAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
DB GAGTACTTGGAGAAACGGGAAAGTTAGCTGTGCTGATGCCATGCGCATGCAACCATTT 1475
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DB CTGACGTTGACATCCCTCTTCTGATCACATCTTCAAGGAAGTTGACTTCCATGAG 1535
QY 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla 520
DB CTCAATACCTTGATATGATATCATCTTTCGATTAAGAGTATACACCGCTGTCMAAGCA 1595
QY 521 AspArgAlaArgGlyGlyGlnAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540
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DB AACGTTAAACAAAGATTTGGTATGATGAACCGTCACTTGAACCTGTGGCTTGG 1889

RESULT 2
US-09-360-545-3
; Sequence 3, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wu013885
; CURRENT APPLICATION NUMBER: US/09/360,545
; EARLIER FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentm Ver. 2.0
; SEQ ID NO 3

LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6) ... (1892)
OTHER INFORMATION: Clone AG3.18 encoding pinene synthase
US-09-360-545-3

Alignment Scores:

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Percent Similarity:	84.63%	Conservative:	59
Best Local Similarity:	75.28%	Mismatches:	81
Query Match:	75.45%	Indels:	16
DB:	4	Gaps:	6

US-10-025-145A-65 (1-618) X US-09-360-545-3 (1-2018)

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QY 56 SerValGlnArgValGlyAsnTyrlHisSerAsnLeuThrAspAspPheIleGln 75
DB 186 GGTGTAGCAACACCGATGGGCGATTTCATTCCAACTCTGGAGAGATGTCATTACAG 245
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DB 246 TCTTTA---CCAAAGGCTTATGAGGAAATATCTTACCTGAGAGCGTCTGAGAAATGATC 302
QY 96 GlyIleValIleValAspIleMetPheAsnPheLeuSerLeuGluAspGlyIle----- 112
DB 303 GGGGAGTAAAGAAC--ATGTTCAATTGCATGTATTAGAAAGATGAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATTCATTCAACCGCTTGTGATGTCAGACGCTTGAAAGTTGGGATC 419
QY 131 AspArgHisPheLeuValGluIleValSerThrAlaLeuAspTyrlValAsnSerTyrlTrpAsn 150
DB 420 CATGACATTTTCAAAGATGAGATTAATATCGGCGCTTGATTTATGTTTACAGTTATGGGCG 479
QY 151 GluIleValGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATAGGCATCGGATGCGGAGGAGAGTGTGTGTACTGATCTGAATCTCAATCGCGTGG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrlThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTGGAACTTACGACTACAGGATACCGGCTTGTCAAGTGTTCMAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB 600 AAAGGCCAAATGGGCGAGTTTCTCGCTCGTCAAAATATTCAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIleValIleMetAsp 230
DB 660 GGCCTTCTGAAATTTATTCGGGCGCTCTCTCATTTGCTTTCAGGGGGAATAATATGAGAT 719
QY 231 GluIleArgIleThrPheSerThrIleTyrlLeuArgGluIleGluIleValIleProAlaSer 250
DB 720 GAGGCTGAATCTTCTTACCAAAATATTTAAAGAACGCTGCAGAAATTCGGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrlGlyTrpHisThrAsnLeuPro 270

DB 780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGACACATATTTGGCG 836
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QY 348 GluProGlnHisAspArgPheArgLeuGlyPheThrIleYsMetSerHisLeuIleThrVal 367
DB 1077 GAGCTTCAACATTTGATGATGAGCTCGCTTTCGCAAGACGTGATCTTATACAGGAT 1136
QY 368 LeuAspAspMetTyrlAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB 1137 CTGACGATATGTACGACACTTGGGACAGTACAGAGCTGGAACCTTTCACAGCGACA 1196
QY 388 IleYsArgTrpAspProSerAlaMetGluCysLeuProGluTyrlMetIleGlyValTyrl 407
DB 1197 ATGAAGAGATGGATTCGCTCTCATAGATTCCTTCAGAAATATGAAAGAGTGTAC 1256
QY 408 MetMetValTyrlHisThrIleAsnGluMetAlaArgValAlaGluIleValGluIleValArg 427
DB 1257 ATAGCGTTTACGACCGTAAATGAAATGAGCTGAGAGGAGAGAGGCTTCAAGCGCA 1316
QY 428 AspThrLeuAsnTyrlAlaArgGlnAlaTrpGluIleCysPheAspSerTyrlMetGlnIle 447
DB 1317 GATAGCGTCAATATGCTCGGGAAGCTTGGAGGCTTATATGATTGATTATGCAAGAA 1376
QY 448 AlaYsTrpIleAlaThrGlyTyrlLeuProThrPheGluGluTyrlLeuGluAsnGlyIle 467
DB 1377 GCAAGGTGATCGACACTGCTTACCTCGCTTGTGATGTCCTTACGAAATGGGAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB 1437 GTTACCTGTGCTATTCGATATCCGATTCGACCACTTCTTGACAAATGGAATCCCTTT 1496
QY 488 ProAspHisIleLeuValGluValAspPheProSerIleValLeuAsnAspLeuIleCysIle 507
DB 1497 CTTGATCATATCTCAAGGAATGATGATCCCATCAAAAGCTTAAAGCACTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrlValAlaAspArgAlaArgGlyGluIle 527
DB 1557 ATCTTCGATTACAGAGTATACCGGCTGTACAGGCGGACAGGCGCTCGGAGAAAGA 1616
QY 528 AlaSerSerIleSerCysTyrlMetIleAspAsnProGlyLeuThrGluIleAspAlaLeu 547
DB 1617 GCTTCCTTATATGATGTTATATGAAGACATCTGAGATATGAGAAAGAGATGCTTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuIleVal 567
DB 1677 GATCATATCAAGGCAATGATGATGAGATGATCAAGATTAATTTGGAACTTCTCAA 1736
QY 568 ProAspAsnSerValProIleThrSerIleValHisAlaPheAspIleSerArgValTrp 587
DB 1737 CCAGACATCAATGTTCCATCTCGCGAAGAAATCTTTTTCATCGCAGAGCTTC 1796
QY 588 HisHisGlyTyrlArgTyrlArgAspGlyTyrlSerPheHisAlaAsnValGluThrIleSerIle 607
DB 1797 CATTAAGCTTCAATATCCGAGAGCTTACAGCTTGCATGTTGAACGAAGATTTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
DB 1857 GTACAGAGAACCTCTTGAATCTGTGCTTTG 1889

RESULT 3
US-09-398-395A-19
; Sequence 19, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappel1, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney R.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; PRIORITY FILING DATE: 1999-09-17
; PRIORITY FILING DATE: 1998-09-18
; PRIORITY FILING DATE: 1999-04-22
; PRIORITY FILING DATE: 1999-08-23
; PRIORITY FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-398-395A-19

Alignment Scores:
Pred. No.: 3.98e-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
Gaps: 6

US-10-025-145a-65 (1-618) x US-09-398-395A-19 (1-2018)

QY 1 MetAlaLeuSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 15
DB 6 ATGCTCTAGTTTCTACCGCACCGTTGGCTTCCAATATGCTGCACAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB 66 AGTTCCTACCCATGAGCTTAAAGCTCTCTAGAACAAATTCAGAGCTTGAAGATGATAGG 125
QY 36 ProGlyLeuSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 126 CGAAGGAATTTATCATCTCTCCATCCAGCATGAGCTTACCACTGTTGTAAACGATAT 185
QY 56 SerValGlnArgArgValGlyAsnIleHisSerAsnLeuTrpAspAspAspPheIleGln 75
DB 186 GGTGTACGAAGACGATGGCGGATTTCCATTCCAACCTCGGACGATGATGCTATACAG 245
QY 76 SerIleLeuSerThrProTyrGlyAlaProAspTyrArgGluValGlnAlaAspArgLeuIle 95
DB 246 TCTTTA---CCAAAGGCTTATGAGAAATAATCGTACCTGAGCGGTGAGAAACTGATC 302
QY 96 GlyValIleValAspAlaMetPheAsnPheLeuSerIleGluAspGlyIle----- 112
DB 303 GGGGAAGTAAAGAAC---ATGTTCAATTGCATGTCATTAGAAAGATGAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCATATGATTCATTCACAACGCTTGGATTGTGCGACGACGCTTGAACGTTGGGAGATC 419
QY 131 AspArgHisPheLeuValGluIleValAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 420 CATGACATTTTCAAGATGAGATAAAATCGCGCTTGTATGTATTACAGTTATTGGGCGC 479

QY 151 GluIleGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATATGCATTCGATCCGGGAGGAGAGAGTGTATTCTGATCTGAATCAATCGCGTTG 539
QY 171 GlyLeuArgThrLeuValGluHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTGAACCCCTACACATACACGATACCGGATGCCGTTCTCAGATGTTTCCAAAGCTTCC 599
QY 191 LysAspLysAsnGlyIlePheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
DB 600 AAAGGCCAAATGGCGAGTTTCTGCTGAAATATATCAGACGATGAAAGATACAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
DB 660 GGGCTTGAATTTATTCGGGGCTCCCTCATTTGCTTCCAGGGAGGAAATATATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGluIleProAlaSer 250
DB 720 GAGGCTGAATCTTCTACCAATATTTAAAGAACCCCTGCAGAAAGATTCGCGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrTrpHisThrAsnLeuPro 270
DB 780 AGT---CTTTCGCGAGATCGGGAGCTTTGAAATATGATGGGACACATATTTCCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
DB 837 CGATTGAGACGAAGATTCATCATCAAGTCTTGGACAGACACTGAGAACAGACAGATGCA 896
QY 291 -----AlaGluLysLeuLeuGluIleValLysLeuGluPheAsnIlePheHisSer 307
DB 897 TATGTGAAGAGCAAAAACTTTTGAACCTGCAGAAATGGAGTTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysValSerArgTrpTrpLysAspSerGlySerProGlu 327
DB 957 TTACAAAGAGGGAGTTAGAAAGTCTGTGATGATGGAGAAAGATCGGTTTCTCGAG 1016
QY 328 MetThrPheCysArgHisValGluIleValLysLeuGluPheThrLysMetSerHisLeuVal 347
DB 1017 ATGACCTTTCGCGACATCGTCACTGGAATACATCACTTGGCTTCGATTCGCGTTC 1076
QY 348 GluProGlnHisSerGlyPheValGluGlyPheThrLysMetSerHisLeuVal 367
DB 1077 GAGCCTCAACATTCGATTCAGACTCGCGCTTGGCCAAAGCGTGCATCTTATACCGGT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
DB 1137 CTGACGATATGATGACACACTTGGCACAGTACAGACCTGGAACCTTTCACAGCGACA 1196
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
DB 1197 ATGAAGAGATGGATCCGCTCGATGATGATGCTTCCAGAAATATGAAAGAGTGTAC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
DB 1257 ATACCGGTTTACGACACCGTAAATGAATGCTTCGAGGCGAGGAGCGCTCAAGGCGGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnIle 447
DB 1317 GATACGCTCATATGCTCCGGAAGCTTGGAGGCTTATATGATTGTTGATATACAAAGA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
DB 1377 GCAAGGTGATCGCATCGGTATCTCCCTCTTATGATGATGATGATGATGATGATGATGAT 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB 1437 GTTGGCTGTGTCTATCCATATCCGATTCGACATCCATTCGACAAAGGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB 1497 CCGATCATATCTCCAAAGAGATGTTGACTTCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556

QY 508 ILeuauRgLeuAArgIYArpThrArgCySerYrlysaAlaAaPArgAlaArgIYGlulgu 527
DB 1557 ATCTTGGATTACAGAGGTGATACCGGCTGCTACAGAGGCGAGGCTCGTGAGAGAA 1616
QY 528 AlaSerIleSerCySerYrMetLySaPaAnProGlyLeuThGluGluAaPaAlaLeu 547
DB 1617 GCTTCTCATATCATGTATATATGAAGACATCTGGAGATATAGAGAGAAATGCTCTC 1676
QY 548 AaHhIglLeaAnPheMetIlaArgPaAlaIleArgGluLeuAaPTrpGluLeuLys 567
DB 1677 GATCATATCAACGGCATGATGATGATCAAGATTAATGGAACCTTCTCAA 1736
QY 568 ProKaPaAnSerValProIleThrSerLySaHsAlaPheAaPleSerArgValTrp 587
DB 1737 CCAACATCAATGTTCCATCTCCGCGAAGAAACATGCTTTGACATCGCAGACCTTTC 1796
QY 588 HIsHsGlyYrArgYrArgAaPQlyYrSerPheAlaAaValGluThrLySerLeu 607
DB 1797 CATACGGCTCAAAATACCGAGCGCTACAGCGTTGCCAAAGTTGAACGAAGATTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
DB 1857 GTCAGAGAACCTCTTGAATCTGCTTGG 1889
RESULT 4
US-09-887-586A-19
Sequence 19, Application US/09887586A
Patent No. 6495354
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph P.
APPLICANT: No. 64953541, Joseph P.
APPLICANT: Stark, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
PRIORITY FILING DATE: 2001-06-22
PRIORITY APPLICATION NUMBER: 09/398,395
PRIORITY FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: 60/130,628
PRIORITY FILING DATE: 1999-04-22
PRIORITY APPLICATION NUMBER: 60/150,262
PRIORITY FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(1889)
OTHER INFORMATION: pinene synthase
US-09-887-586A-19
Alignment Scores:
Pred. No.: 3,98e-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 4 Gaps: 6
US-10-025-145A-65 (1-618) x US-09-887-586A-19 (1-2018)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCyLeu----- 15
DB 6 ATGCTCTAGATTCTACCGCACCGTGGCTTCCAATCATGCTGTCACAAATCGTTATC 65
QY 16 SerSerSerHsIgluIleLyAlaLeuArgTrpIleProThrLeuGlyIleCyArg 35
DB 66 AGTTCTACCATGAGCTTAAGGCTCTCTAGAACAAATTCAGAGCTTAGAATGAGTAGG 125

QY 36 ProGlyLySerValAlaHsSerIleAaMetCyLeuThrSerValAlaSerThrAsp 55
DB 126 CGAGGAAATATATACCTCTCCATGACGATAGCTGTACACCGTTGTAAACGATAT 185
QY 56 SerValGlnArgArgValGlyAsnTrpHisSerAnLeuTrpAaPAsPheIleGln 75
DB 186 GGTGTACGAAGACCATGCGGATTCATTCACAACTCTGGAGCATGATGATCATACAG 245
QY 76 SerLeuIleSerThrProTrpGlyAlaProAspTrpArgGluAaPaArgIleLeu 95
DB 246 TCTTTT---CCAAAGCTTATGAGAAATAATGATCGAGCGGTGAGAAACTGATC 302
QY 96 GlyGluValLySaPleMetPheAaPheLySerLeuGluAaPQlyGly----- 112
DB 303 GGGGAAGTAAAGAC---ATGTTCAATTCAGATGATTAAGATGAGAGATTATGAT 359
QY 113 -----AaAaPleLeuGlnArgLeuLeuValAaPaPValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATCTCATCAACGCTTGTGATGTCAGACGCTTGAACGTTGGGATC 419
QY 131 AaPArgHsPheLeuLyGluIleLyThrAlaLeuAspTrpValAsnSerTrpAsn 150
DB 420 CATGACATTTCAAGATGATTAATCGCGCTGTATATGTTTACATTAATTTGGCGC 479
QY 151 GluLySerGlyIleGlyCySerGlyArgGluSerValValThrAaPLeuAsnSerThrAlaLeu 170
DB 480 GAAATGCGATCGATGCGGAGGAGAGGTGTTTACTGATCTGAACTCACTCGCTG 539
QY 171 GlyLeuArgThrIleLyArgLeuHsIglYrThrValSerSerAaPValLeuAsnValPhe 190
DB 540 GGGCTTCAACCCATACGATACGATACCGGCTGTGATGATGTTTCAAAAGCTTTC 599
QY 191 LySaPlySaAnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluIleArg 210
DB 600 AAAGGCCAAATGGCAGTTTCTGCTGAAATATTCAGACAGTAAGAGATGACGA 659
QY 211 GlyValLeuAaPLeuPheArgAlaSerLeuValAlaPheProGlyGluLyValMetAsp 230
DB 660 GCGCTTCAATTTATTCGCGGCTCTCCATGCTTCCAGGGGAAATATTTGAT 719
QY 221 GluAlaGluTrpPheSerThrLyArgIleuArgGluAlaLeuGlnLyIleProAlaSer 250
DB 720 GAGGTGAATCTCTCTCAAAATATTAAAGAACGCTGCAAAAGATCCGGCTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTrpGlyTrpHisIleThrAsnLeuPro 270
DB 780 AGT---CTTTGCGAGAGATCGGGGACGTTTGGAAATGATGTCACACATATTTCGCG 836
QY 271 ArgLeuGluAlaIleAsnTrpMetAspValPheGlyGlnHsThrLySaPLeuAsnAla 290
DB 837 CGATTGAGCAAGGAATTTACATCAAGTCTTTGGACAGACACTGAGAAACAGAGATCA 896
QY 291 -----AlaGlyLyLeuLeuGluIleuAlaLyLeuGluPheAsnIlePheHsSer 307
DB 897 TATGGAAGACGCAAAACTTTTGAACCTCGCAAAATGAGATTCATCATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLyHsValSerArgTrpTrpLySaPAsPheIleSerProGlu 327
DB 957 TTACAAAAGAGAGTGAAGAGTGTGTCAGATGCTGGAAGAAATCGGGTTTCTTAG 1016
QY 328 MetThrPheCySaHsArgHsValGluTrpTrpAlaLeuAlaSerCyIleAlaPhe 347
DB 1017 ATGACCTTCTCCGACATCGTCACGTGAAATACACACTTTGGCTTCTGCAATTCGCTTC 1076
QY 348 GluProGlnHsSerGlyPheArgLeuGlyPheThrLySaMetSerHsIleuIleThrVal 367
DB 1077 GAGCTCAACATTCGATTCAGACTCGGCTTGCAGAAAGTGCATCATTCACGCGTT 1136
QY 368 LeuAaPAsPheTrpAaPValPheGlyThrValAspGluLeuGluPheThrAlaPhe 387
DB 1137 CTTAGCATATGTCGACACCTTTCGCGCACGTAGACGAGCTTCAACGCGGCA 1196
QY 388 ILeuLyArgTrpAaPProSerAlaMetGluCyLeuProGluTrpMetLyGlyValTrp 407

Db	1197	ATGAGAGATGGATCCGTCCTCCATGATGTCCTTCCAGATATATGAAAGGTGAC	1256
Qy	408	MeMeetValTYrhistrhValaBsnGluMeLaahrgValaIagIuYsaIagInglYarg	427
Db	1257	ATACGGGTTTACGACCCGTTAAATGAAATGCTCGAGAGCGAGAGAGGCTCAAGCCCA	1316
Qy	428	AspThrhLeuBentYrYalabrgInAlATrpgIuaIaCyBphleApsSerTYrMeGInglu	447
Db	1317	GATCGCTCATATATGCTCGGGAAAGCTTGGAGGCTTATATATGATTCGTATATCAAGA	1376
Qy	448	AlaIasrTrpIleAlaThrhGlyTYrLleuBproThrhPheGIngluTYrLleuGlaAsnGlyAs	467
Db	1377	GCAAGGGTGAATGCCACTGCTTACTGCCCTCTTGTATGAGTCTACGAGAAATGGGAA	1436
Qy	468	ValSerSerAlaHisArgProCysAlaIleuGInProIleuThrhLeuAspIleProPhe	487
Db	1437	GTTAGCTGTGTCATCCGATATCCGCAATGGAAACCAATTCGACAAATGGAATCCCTTT	1496
Qy	488	ProAspHisIleLeuYsgIuValaAspPheProSerIysLeuAsnAspLeuIleCysIle	507
Db	1497	CCTGATCATATCCCTCAAGAAAGTTGACTTCCCATCAAAAGCTTAAACGACTTGCAATGTGCC	1556
Qy	508	IleLeuArgLeuArgIYAspThrhArgCysEtyrIysAlaAspArgAlaArgGlyGInglu	527
Db	1557	ATCCTTCGATTACAGCGATGATACCGGTGCTTACAGAGCGGACAGGCTCGTGGAGAAAGAA	1616
Qy	528	AlaSerSerIleSerCysTYrMeCylsAspAsnProGlyLeuThrhGluGluAspAlaIleu	547
Db	1617	GCTTCCTCTATATCATGTATATATGAAACAATCTCGAAGTATCAGAGAAAGATGCTCTC	1676
Qy	548	AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuIleYs	567
Db	1677	GATCATATCAACGCCATGATCAGTACGATATCAAAAGGATTAATATGGGAATCTCTCAA	1736
Qy	568	ProAspAsnSerValProIleThrSerIysIysHisAlaPheAspIleSerArgValTrp	587
Db	1737	CCAAACATCATATGTCCTCCATCTCGGCGGAAAGAAACATGCTTTTGACATCGCAAGCTTTC	1796
Qy	588	HisIleGlyTYrArgTYrArgAspGlyTYrSerPheAlaAsnValaGluThrIysSerIeu	607
Db	1797	CATTACGGCTTCAAAATACCGAGCGGCTACAGCGCTTGCCAAAGTTGAACAAAGATTTG	1856
Qy	608	ValMetArgThrhValIleGluProValProIeu	618
Db	1857	GTCAAGAAACCTTCCTGTAATCTGTGCTTTG	1889
RESULT 5			
US-09-895-752-19			
Sequence 19, Application US/09895752			
Patent No. 6559297			
GENERAL INFORMATION:			
APPLICANT: Chappell, Joseph			
APPLICANT: No. 6559297, Joseph P.			
APPLICANT: Starks, Courtney M.			
APPLICANT: Manna, Kathleen R.			
TITLE OF INVENTION: SYNTASES			
FILE REFERENCE: 07678-025001			
CURRENT APPLICATION NUMBER: US/09/895,752			
CURRENT FILING DATE: 2001-06-29			
PRIOR APPLICATION NUMBER: 09/398,395			
PRIOR FILING DATE: 1999-09-17			
PRIOR APPLICATION NUMBER: 60/100,993			
PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: 60/130,628			
PRIOR FILING DATE: 1999-04-22			
PRIOR APPLICATION NUMBER: 60/150,262			
PRIOR FILING DATE: 1999-08-23			
NUMBER OF SEQ ID NOS: 58			
SOFTWARE: PastedSeq for Windows Version 3.0			
SEQ ID NO 19			
LENGTH: 2018			
TYPE: DNA			

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; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-895-752-19
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Alignment Scores:

Pred. No.:	3,986-288	Length:	201
Score:	2453.00	Matches:	475
Percent Similarity:	84.63%	Conservative:	59
Best Local Similarity:	75.28%	Mismatches:	81
Query Match:	75.45%	Indels:	16
DB:	4	Gaps:	6

US-10-025-145A-65 (1-618) x US-09-895-752-19 (1-2018)

Qy	1	MetAlaLeuLeuSerLlethProLeuValSerPysSerCysLeu-----	15
Db	6	AlNGCCTCAAGTTTCTACCGCACCGCTGGCTTCCAAATCAATGCTCGACAAATCGTTGATC	65
Qy	16	SerSerSerHisGluLlelyValaLeuArgTrgThrLleProThrLeuGlyLeCysArg	35
Db	66	AGTTTACCACTAGAGTTTAAAGGCTCTCTCTGAACAATTCAGCTCTAGAAATAGTAAAGG	125
Qy	36	ProGlyLysSerValAlaHisSerLleAsnMetCysLeuThrSerValAlaSerThrAsp	55
Db	126	CGAGGAAATCATCACTCTTCCTCAATGCAATGAGCTTCTACACCGTTGTATACCGATAT	185
Qy	56	SerValGlnArgArgValGlyAsnTyrrHisSerAsnLeuTrpAspAspPheIleGln	75
Db	186	GGGTTCGAAAGACGATGGCGCATTTCCATTCCAACTCTGGACGATGATGTCATACAG	245
Qy	76	SerLeuLleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuLle	95
Db	246	TCTTTA---CCAACGGCTTATAGGAAATAATCGTACCTGGAGCGCTGCGTGAATCGATC	302
Qy	96	GlyGluValLysAspLleIleMetPheAsnLysSerLeuGlnAspGlyGly-----	112
Db	303	GGGGAAAGTAAAGAC--ATGTTCAATTCGATGTCATTAGAAAGTGAAGACTTAATAGT	355
Qy	113	-----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyLle	130
Db	360	CGGCTCAATGATCTCATTTCAAGCCTTTGATGTGCGACAGCCTTGAACGTTTGGGGATC	419
Qy	131	AspArgHisPheLysLysGluLlelySerThrAlaLeuAspTyrValaAsnSerTyrTrpAsn	150
Db	420	CATAGCAATTTCAAAGATGAGTAAATACGGCGCTGTATATGTTTACAGTTTATGGGCG	479
Qy	151	GluLysGlyLleGlyCysGlyArgGlySerValValThrAspLeuAsnSerThrAlaLeu	170
Db	480	GAATAATGGCATCGGATCGGAGGGAGAGTGTGTACTGATCTGAACCTCAACGCGCTTG	539
Qy	171	GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe	190
Db	540	GGGCTTCGAACCTCACTACGACTACACGGATACCCGGGTGCTTCAGATGTTTCAAAGCTTTC	599
Qy	191	LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluLeArg	210
Db	600	AAAGGGCAAAATGGGCAAGTTTCTCGCTGTAATAATATTCAGACAGATGAAGAGATCAGA	659
Qy	211	GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValaMetAsp	230
Db	660	GGGCTTCTGAATTTATTCGGGCTCCTCTCATTCCTTTCCAGGGAGGAAATATTAGAT	719
Qy	231	GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysLleProAlaSer	250
Db	720	GAAGCGTGAATCTCTCTACCAAAATATTTAAAGAGCCCTGCAAAAGATTTCCGCTCC	779
Qy	251	SerLleLeuSerLeuGlnLleArgAspValLeuGluTyrGlyTyrTPH.smtAsnLeuPro	270
Db	780	AGT---CTTTCGAGAGATCGGGGACGTTTGGAAATGTGTTGGACACATATTTGCGG	836

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Qy 271 ArgLeuGluAlaArgAspThrMetAspValPheGlyGlnHisThrLeuAsnLysAsnAla 290
Db CGATTGGAGGAGGAAATTTACATCCAACTCTTGGACAGACACTGAGAACACGAAATGCA 896
Qy 291 -----AAGTCTGLeuLeuGluLeuAlaLysLeuGluPheAsn11ephHisSer 307
Db TATGGAAAGACAAAACCTTTAGACCTCGGAAAATTGGATTCAATCTTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTPTPTPLysAspSerGlySerProGlu 327
Db TTACAAAAGAGGGAGTTGAAAAGTCTGTCAGATGTTGAAAAGAAATCCGGTTTCTTAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysSerIleAlaPhe 347
Db ATGACCTTCTCCGACATGTCACGCGAATATCACTTGGCTTCTGCAATGCGTTT 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db GAGCTCAACATTTGCGATTGAGTTCAGACTCGGCTTTCGCAAGACGTTCATCTTACAGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db CTTCAGATATATGTCAGACACCTTCGCGACAGTACGAGCTGGAACCTTTCACACGCA 1196
Qy 388 IleLysArgTTPAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db ATGAAAGATGGAGATCCGCTCCGATAGATGCTTCCGAAATATATGAAAGAGATGAC 1256
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnTyrArg 427
Db ATAGCGGTTTACGACACCGCTAAATGAAATGCTCGACAGAGCGACGAGGCTCAAGCGCA 1316
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTPTGluAlaCysPheAspSerTyrMetGlnGlu 447
Db GATACGCTCAATATGCTCGGGAAGCTTGGAGCTTATATGATTCCTAATATGCAAGAA 1376
Qy 448 AlaLysTPTIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db GCAGAGTGGATCGCCACTGTTACTGCTCTTGTATGATGACTTACGAGATGGGAAA 1436
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAsp11eProPhe 487
Db GTTAGCTGTGTCATCGCATATCGCATTTGCAACCATTTGACAAATGAGACATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db CCTGATCATATCCCAAGAGAGTTGACTTCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db ATCTTCATTAACGAGTGATACGGGTGCTACAGGCGAGAGGGCTCGTGAGAGAGAA 1616
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db GCTTCCTCATATCATGTTATATGAAAGACATCTGAGATATACAGAGAAAGATGCTCTTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTPTGluLeuLys 567
Db GATCATATCAACGCGCATATCAGTACGTAATCAAAAGATTAATAATGGAACTTCTCAA 1736
Qy 568 ProAspAsnSerValProIleThrSerLysHisAlaPheAsp11eSerArgValTyrP 587
Db CCAAGCATCAATGTTCCATCTCGCGAAGAAACATGCTTTTGACATGCGCAAGCTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db CATTAACGCTCAACATACCGAGACGGCTACAGCGCTTGCACAGCTTGAACAGAGGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db GTCAAGAGAACCCCTCTTGAATCTGTGCTTTG 1889

```

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US-09-903-012B-19
; Sequence 19 Application US/09903012B
; Patent No. 6569566
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
; US-09-903-012B-19

Alignment Scores:
Pred. No.: 3,986-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 4 Gaps: 6

US-10-025-145a-65 (1-618) X US-09-903-012B-19 (1-2018)
Qy 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTAGTTTCTACCGGACCGTGGCTTCCAAATCATGCTCGCAAAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyTyleArg 35
Db 66 AGTTCTACCCATGAGCTTAAGCTTCTCTTAAGCAATTCAGCTTACGATGATGAG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGAAATATATCACTCTTCCATCGATGAGCTTACCAACCGTTGTAACGATAT 185
Qy 56 SerValGlnArgValGlyAsnTyrHisSerAsnLeuTTPAspAspPheIleGln 75
Db 186 GGTGAGACAAAGCCATGCGGATTCATTCACACCTCGGAGAGATGATATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAGCGCTTATGAGAAAATCGTACCTGAGCGCTGAGAAAACGTGATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyLys----- 112
Db 303 GGGAGAGTAAAGAAC---ATGTTCAATTCAGTGCATTTAGAAAGATGAGAGATTAAATGAT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyTle 130
Db 360 CCGCTCATATGATTCATTTCAACGCGCTTGTGATGTCGACACCTGAAACGTTGCGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrTyrValAsnSerTyrTTPAsn 150
Db 420 CATGACATTTTCAAGATGAGATTAATAATCGCGCTTATATGTTTACAGTTATTTGGGCG 479
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170

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Db 126 CGAGGAAATCTATCACTCTTCCATGACATGAGCTCTACACCGTTGTAACGATAT 185
 Qy 56 SerValGlnArgValGlyAsnTyrHisSerLeuLeuTrrPhePheAspPheIleGln 75
 Db 186 GGTGTAGAGAGACCATGGGCGATTTCCATTCACACTCTGGAGAGAGATGTCATAAG 245
 Qy 76 SerLeuLeuSerTrrProTyrGlyValAspAspTyrArgGluArgAlaAspArgLeuIle 95
 Db 246 TCTTTA---CCAGCGCTTATGAGGAAAAATCGTACCTGGAGCGTGTGAGAAATGATC 302
 Qy 96 GlyGluValIlyAspIleMetPheAsnPhelYsSerLeuGluAspGlyGly----- 112
 Db 303 GGGAGAGTAAAGAAC---ATGTTCAATTCGATGTCATTAGAAGATGAGAGTTAATAGT 359
 Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
 Db 360 CCGCTCATATGTCATTCATCAACGCTTTGATGTCAGACGCTTGAAAGTTTGGGGATC 419
 Qy 131 AspArgHisPheIlySylGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
 Db 420 CATGACATTTCAAGATGAGATGAAATCGGCGCTTGATGTTATGTTACAGTTATTGGGCG 479
 Qy 151 GlyIlySylIleGlyCySylArgGluSerValIlyThrAspLeuAsnSerThrAlaLeu 170
 Db 480 GAAATGCGATCGATGCGGAGGAGAGTGTGTTATCGATCTGAATCAACTCGCGTTG 539
 Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
 Db 540 GGGCTTGACACCTACGACATACAGGATACCGGCTGCTTCAGATGTTTCMAAGCTTTC 599
 Qy 191 LysAspIlyAsnGlyIlyPheSerSerThrAlaAsnIleGlnIleGlyIlyIleArg 210
 Db 600 AAAGGCCAAATGGGCGACTTTCTCGCTCGTAAATATTCAGACAGATGAAGATCGA 659
 Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIlyValMetAsp 230
 Db 660 GCGCTTCGATTTATTCGCGGCTCCCTCATTCGCTTCCAGGGGAGAAATATGAT 719
 Qy 231 GlnAlaGluThrPheSerThrIlyTyrLeuArgGluAlaLeuGlnIlyIleProAlaSer 250
 Db 720 GAGGCTAAATCTTCTCAACAAATATTTAAAGAACGCTGCAAAATTCGCTTCC 779
 Qy 251 SerIleuSerLeuGluIleArgAspValLeuGluTyrGlyTrrPheIleAsnLeuPro 270
 Db 780 AGT---CTTTCGAGAGATCGGGACGTTTGGAAATGGTGGCACACATATTGGCG 836
 Qy 271 ArgLeuGlnAlaArgAsnTyrMetAspValPheGlyGlnIleHisThrIlyAsnIlyAsnAla 290
 Db 837 CGATTGAGAGCAAGATTATCATCAAGTCTTTGGACAGACACTGAGAACACGAGTCA 896
 Qy 291 -----AlaGluIlyLeuLeuGluLeuAlaIlyLeuGluPheAsnIlePheHisSer 307
 Db 897 TATGTGAAGCAAAAACTTTAGAACTCCCAAAATGGAGTTCAACATCTTTCAATCC 956
 Qy 308 LeuGlnIlyArgGluLeuLeuHisValIleSerArgTrrPrrIlyAspSerGlySerProGlu 327
 Db 957 TTTAAAGAGAGGAGTTAGAAAGTGTGTCAATGGTGGAAAGATCCGGGTTTCTTGAG 1016
 Qy 328 MetThrPheCySylArgHisValGlnIlyTyrAlaLeuAlaSerCyIleAlaPhe 347
 Db 1017 ATGACCTTTCGCGACATCGTCACTGGAATATACATTTGGCTTCTCGATTCGCTTC 1076
 Qy 348 GluProGlnHisSerGlyPheArgLeuGlyIlyPheThrIlyMetSerHisLeuIleThrVal 367
 Db 1077 GAGGCTCAACATTTGATTCAGACTCGCTTGGCAGAGCGTGCATCTTATCAGCGTT 1136
 Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
 Db 1137 CTTAACATATATGACACACTTCGGCACAGTACAGAGCTGGAACCTTTACAGCGACA 1196
 Qy 388 IleLysArgTrrAspProSerAlaMetGluCyLeuProGluTyrMetIlyGlyValIly 407
 Db 1197 ATGAAGAGATGGATCGCTCTCGATGATGCTTCCAGAAATATATGAAGAGATGTA 1256

Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluIlyAlaGlnIlyArg 427
 Db 1257 ATACCGGTTTACGACACCGTAAATGAAATGCTTCGAGAGGACAGAGGCTCAAGCGCGA 1316
 Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrrPgluAlaCySylPheAspSerTyrMetGlnGlu 447
 Db 1117 GATACGCTCATATGCTCGGGAAGCTTGGAGGCTTATATGATGTTGCTATATGCAAGAA 1376
 Qy 448 AlaIlyTrrIleAlaIlyThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyIly 467
 Db 1377 GCAAGTGTGATCGCACGTGTTACCTCCCTCTTGTATGATGATCTACGAAATGGGAAA 1436
 Qy 468 ValSerSerAlaHisArgProCyAlaLeuGlnProIleuThrLeuAspIleProPhe 487
 Db 1437 GTTAGCTGTGTATCGCATATCCGATGTCACATCCATCTTGACAAATGGATCCCTTT 1496
 Qy 488 ProAspHisIleLeuIlySylGluValAspPheProSerIlySylLeuAsnAspLeuIleCyIle 507
 Db 1497 CTTGATCATATCCCAAGAGATGATGATCCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556
 Qy 508 IleLeuArgLeuAlaGlyAspThrArgCySylTyrIlyAlaAspAlaArgGlyGluGlu 527
 Db 1557 ATCTTCGATTTACGAGGTGATACCGGCTGCTACAAAGCGGACAGGCGCTCGGAGAGAA 1616
 Qy 528 AlaSerSerIleSerCySylMetIlyAspAsnProGlyLeuThrGluIlyAspAlaLeu 547
 Db 1617 GCTTCCTCTATATCATGTTATATGAAGACATCTTGAGATGATCAAGAGAGATGCTTC 1676
 Qy 548 AsnHisIleAsnFleMetIleArgAspAlaIleArgGluLeuAsnTrrPgluLeuIlySyl 567
 Db 1677 GATCATATCAAGCGCATGATGATGATGATCAAGATTAATTTGGAACTTCTCAA 1726
 Qy 568 ProAspAsnSerValProIleThrSerIlySylHisAlaPheAspIleSerArgValTrr 587
 Db 1737 CCAGACATCAATATCTCCATCTCGCGAAGAAACATGCTTTTGACATCGCAGAGCTTTC 1796
 Qy 588 HisHisGlyTyrGlyTyrArgAspGlyTyrSerPheHisAsnValGluThrIlySerLeu 607
 Db 1797 CATTAAGCTTACAAATACCGAGCGCTACAGCGCTTGCAACGTTGAACAGAGATTTG 1856
 Qy 608 ValMetArgThrValIleGluProValProLeu 618
 Db 1857 GTCAAGAGAACCTCTGTAATCTGTGCTTTG 1889

RESULT 8
 US-09-360-545-66
 ; Sequence 66, Application US/09360545
 ; Patent No. 6429014
 ; GENERAL INFORMATION:
 ; APPLICANT: Croceau, Rodney B
 ; APPLICANT: Bohmann, Jörg
 ; APPLICANT: Steele, Christopher L
 ; APPLICANT: Phillips, Michael A
 ; TITLE OF INVENTION: MONOMERENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
 ; FILE REFERENCE: wu013685
 ; CURRENT APPLICATION NUMBER: US/09/360,545
 ; CURRENT FILING DATE: 1999-07-26
 ; EARLIER APPLICATION NUMBER: 60/052,249
 ; EARLIER FILING DATE: 1997-11-07
 ; EARLIER APPLICATION NUMBER: PCT/US98/14528
 ; EARLIER FILING DATE: 1998-07-10
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 66
 ; LENGTH: 2186
 ; TYPE: DNA
 ; ORGANISM: Abies grandis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (34)..(1923)
 US-09-360-545-66

Qy 448 AAlaSerTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGGATCTCTAATGTTATCTGCCAATGTTTGAAGATACCATGAGATGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGATATCGCGTGAACAACATTCGACACCATCTTGAATGCAATGGCTT 1556
Qy 488 ProAspHisIleLeuValAspGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTATATACATCTTGAAAGGAAATGATTTTCATCCATGCAATGATTTGGCAATCGTCC 1616
Qy 508 IleLeuArgLeuAspGluValAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 1617 TTCTTCGGCTACGAGGAGACACGCTGCTACAGGCCGATGGGATCGTGGTGAAGA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAACAACATCTGATCAACGGAAGATGCTCTC 1736
Qy 548 AsnHisIleAsnProMetIleArgAspAlaIleatGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGTCATCATCAATCAAAAGATTAATTTGGAACTTCTAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysHisIleAspIleSerArgValTrp 587
Db 1797 TCCACACGCAATATTCATATCTGCGCAAGAAACATGCTTTGACATACAGAGCTCTC 1856
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGCTTTAGTGTGTCACCAAGAAACAAAATTTG 1916
Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTATGGAAACATCTCTGAA 1937

RESULT 11

US-09-887-586A-29
Sequence 29, Application US/09887586A
Patent No. 6495354
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 64953541, Joseph P.
APPLICANT: Stark, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-02501
CURRENT APPLICATION NUMBER: US/09/887,586A
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69)...(1949)
OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Alignment Scores:

Pred. No.: 2,59e-257 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17

DB: 4 Gaps: 7
US-10-025-145A-65 (1-618) x US-09-887-586A-29 (1-2196)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTGTTTCATCTCATCTCAACCGTGGCTTCGAATCTTCGCTCGCAAGCTTGATC 128
Qy 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTCATGACATACATACCTCCCTATGAAACAAATCCAAATCTTGAAATGGTGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGAAATCTGCACGCCCTTCATGACATCGCTTTGGCCACCGCTGCACCTGATAT 248
Qy 56 SerValGlnArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGACAAAGACCATATGATGATACCATTCATATCTGGAGATGATTTCTATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA---TCAAGGCTTATGGGGAACCTCTTACCAAGAAACGCTGAGAGATTAAT 365
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyLys----- 112
Db 366 GTGGAGTAAAGAGATG---TTCATTCATATGATCTGATGATGAGATTAATGAT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCTTTATATGATCTCATATGCAACGCTTGCATATGATGATGATGATGATGATGATGAT 482
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTCACAGACAGATTAACATCACTCTGATTTATGTTTCCGTACTCGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACCGCATTTGATGATGGAGACAGATGTTTACTGATCTCACTCACTCACTGCTG 602
Qy 171 GlyLeuArgThrIleLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTGCACTCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
Qy 191 LysAspLysAsnGlyLysPheSerSerThrAlaAsnIleGlnIleGluGlyLysArg 210
Db 663 CAAGATCAAAATGACAGATTTGTATGCTCCCGCT---CAGACAGAGGGTGAATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyLysValMetAsp 230
Db 720 AGCGTTCTTACATATATCGGCTTCCCTCATCTGCTTCCCTGATGACAAAGTTATGAA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTCTCCACAAAGATTTGAAAGAGCTTCAAAAGATTCAGCTGCC 839
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIsthAsnLeuPro 270
Db 840 GCT---CTTTCACAAAGATTAAGTTGTTATGGAATATGCTGCGCACAAATTTTGCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnIsthLys-----Asn 287
Db 897 AGATTGGAAGCAAAATTTACATGACACACTTGAGAAAGACACAGCTGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGAGAGAGAGCTTTAGAACTTGCAAAATTTGAGTTCAATATTTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAAACAAAGAAATTAACATATCTTTGAGATGGGGAAGAGGATGCTGATTCCTTAA 1076
Qy 328 MetThrPheCysArgHisValGlnValGluTyrAlaLeuAlaSerCysIleAlaPhe 347

QY 211 G1YValIeuAenLeuPheArGAlaSerIeuValAlaPheProG1YgluLyValMetAsp 230
DB 720 AGCGTCTTAACCTATATATCGGCGTTCCTCAATGCTTCCTGGTGAAGAACTATGGA 779
QY 231 G1uAlaIuThrPheSerThrIleuArgIuAlaIeuG1uValIleProAlaSer 250
DB 780 GAACCTGAATCTCTCCACAAGATATTGAAGAAGCTTCACAAGATTCAGCTCC 839
QY 251 SerIleuSerIeuG1uIleArgPheValIeuG1uYrG1YrPheIleAsnLeuPro 270
DB 840 GCT---CTTTCACAAGATATAAGTTGTGTATGAAATGCTGCAACAATTTGCCA 896
QY 271 ArgIeuG1uAlaArgAenTYrMetAspValPheG1YrInHleThrIle-----Asn 287
DB 897 AGATTGGAAGCAAGAAATTACATAGACACCTTGAAAGAACACCATGCTCAT 956
QY 288 LysAsnAlaAlaIuLyLeuIeuG1uLeuAlaLyLeuG1uPheAsnIlePheHisSer 307
DB 957 AAAAATCTGGGAAGAGACCTTTGAACCTTCGAAATTCGAGTTCAATATTTAACTCC 1016
QY 308 LeuG1uIuArgIuLeuLyLeuValSerArgTrpIlyAspSerG1YSerProG1u 327
DB 1017 TTACAACAAAAGAAATTCATATCTTTGAGATGCTGAAAGAGTCCGATTTGCCATA 1076
QY 328 MetThrPheCySarGHIleArgHleValG1uYrTYrAlaIeuAlaSerCyAlaIlePhe 347
DB 1077 TTGACATTGCTCGCATCGTCATGTGAATTCACCTTGGCTCTTGATTTGCCATT 1136
QY 348 GluProG1uInHleSerG1YPheArgLeuG1YrPheThrIlyMetSerHleuIleThrVal 367
DB 1137 GACCCAAAACATTTGCTGATTCAGACTGAGCTTCGCAAAATGTGTCATCTGTCAAGTT 1196
QY 368 LeuAspPheMetTYrAspValPheG1YrValAspG1uLeuPheThrAlaThr 387
DB 1197 TTGACGATATTTCAGACACTTTTGAACGATTCGAGCTTGAACCTTCATCACTTCA 1256
QY 388 IleIysArgTrpAspProSerAlaMetG1uCyLeuProG1YrMetIyG1YValTYr 407
DB 1257 ATTAAAGATGAATTCATCAGAGATGAGACCTTCGAAATATATGAATGTGTGAC 1316
QY 408 MetMetValTYrHleSThrValAsnG1uMetAlaArgValAlaG1uLyValG1uYr 427
DB 1317 ATGCTCGTGTGAAACCTGTAATGAACAGACAGAGGCGGAGAAACCTCAAGGAGAA 1376
QY 428 AspThrLeuAenTYrAlaArgG1uAlaTrpG1uAlaCySarPheAspSerTYrMetG1u 447
DB 1377 AACACTCTCACTATGTTGCAAGGCTTGAGAGCTTATTTGATTCATATATGAGAA 1436
QY 448 AlaIysTrpIleAlaThrG1YrTYrLeuProThrPheG1uG1uYrTYrLeuG1uAsnG1Y 467
DB 1437 GCAAAATGATCTCTAATGTTATCTGCAATGTTGAAGATGCATGAGAAATGGGAAA 1496
QY 468 ValSerSerAlaHleSarProCyAlaIleAlaIeuG1uProIleuThrLeuAspIleProPhe 487
DB 1497 GTGAGCTCTGATATCGGTAGCAACATTCGAAACCATCTTCATTTGAATGATGCTT 1556
QY 488 ProAspHisIleLeuLyLeuValAspPheProSerIlyLeuAsnAspLeuIleCysIle 507
DB 1557 CCTGATTAACATCTGAAGGAGAAATGATTTTCATTCAGCTTCATGATTTGGCATCTGCC 1616
QY 508 IleLeuArgLeuArgIyAspThrArgCyTrpIlyValAlaAspArgAlaArgG1uG1u 527
DB 1617 TTCTTCGCTGACAGAGTGAACACGCTGCTACAAAGCCGATAGGATCGTGGAGAA 1676
QY 528 AlaSerSerIleSerCyTYrMetIyAspAspProG1YLeuThnG1uG1uAspAlaIeu 547
DB 1677 GCTTCGTATATCATGTTATATGAAGACATCTGATCAACGGAAGAAAGATGCCCTTC 1736
QY 548 AsnHisIleAsnPheMetIleArgPheAlaIleArgG1uLeuAsnTrpG1uLeuLy 567
DB 1737 AATCATATCAATGCTATGCTCAATGATCAATCAAAAGATTAATTTGGAACTTCTAGA 1796
QY 568 ProAspAsnSerValProIleThrSerIyLyShIleAlaPheAspIleSerArgValTrp 587

DB 1797 TCACAAGCAATATTCGAATGCTGCCAAGAAACATGCTTTTGAATACAAAGAGCTCTC 1856
QY 588 HisIleG1YrTYrArgAspG1YrSerPheAlaAsnValG1uThrIlySerIeu 607
DB 1857 CACCATCTCTCAATATTCGAGATGCGCTTATGTTGCCAACAAGAAACAAAAATTG 1916
QY 608 ValMetArgThrValIleG1u 614
DB 1917 GTTATGAAACATCTCTTGA 1937
RESULT 13
US-09-903-012B-29
Sequence 29, Application US/09903012B
Patent No. 6569656
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. 6569656, Joseph P.
APPLICANT: Starke, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: STRIPASERS
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/903,012B
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURES:
NAME/KEY: CDS
LOCATION: (69)...(1949)
OTHER INFORMATION: myrcene synthase
US-09-903-012B-29
Alignment Scores:
Pred. No.: 2,598-257 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
Gaps: 7
US-10-025-145A-65 (1-618) x US-09-903-012B-29 (1-2196)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 69 ATGCTCGTGTATCTATCTACCGTTGCGTTGCAAACTTGCCTGCCCAAGTCGTTGATC 128
QY 16 SerSerSerHisG1uIleLyAlaLeuArgTrpIleProThrLeuG1YIleCysArg 35
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Db 423 TCCCTTATGATGTCATGCAACGCGCTTTGAGTACGATGCGTTGAAAGCTTTGGAGATA 482
Qy 131 AspArgHisPheIysGlyLeuIleIysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
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Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
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RESULT 14
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; Sequence 29, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No.6645762L, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-900-797-29

Alignment Scores:
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Best Local Similarity: 68.10% Mismatches: 106
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; Sequence 31, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohmann, Jörg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wu913885
; CURRENT APPLICATION NUMBER: US/09/360,545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528

Tue Jul 27 08:32:48 2004

us-10-025-145a-65.rn1

Page 19

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Search completed: July 26, 2004, 20:38:40
Job time : 180 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 19:38:30 ; Search time 684 Seconds

(without alignments)
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Title: US-10-025-145A-65

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Searched: 3216467 seqs, 244419694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2453	75.5	2018	9	US-09-903-012-19	Sequence 19, Appl
4	2453	75.5	2018	10	US-09-900-797-19	Sequence 19, Appl
5	2453	75.5	2018	13	US-09-893-820-19	Sequence 19, Appl
6	2453	75.5	2018	14	US-10-041-007-21	Sequence 21, Appl
7	2453	75.5	2018	15	US-10-025-145A-3	Sequence 3, Appl
8	2264	69.6	2186	15	US-10-025-145A-66	Sequence 66, Appl
9	2200.5	67.7	2196	9	US-09-887-586A-29	Sequence 29, Appl
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12	2200.5	67.7	2196	13	US-09-900-797-29	Sequence 29, Appl
13	2200.5	67.7	2196	14	US-10-041-007-25	Sequence 25, Appl
14	2200.5	67.7	2196	15	US-10-025-145A-1	Sequence 1, Appl
15	2197.5	67.6	2205	15	US-10-025-145A-31	Sequence 31, Appl
16	2137	65.7	1890	15	US-10-025-145A-77	Sequence 77, Appl
17	2084.5	64.1	2429	14	US-10-041-007-27	Sequence 27, Appl
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19	2031.5	62.5	2089	9	US-09-887-586A-57	Sequence 57, Appl
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21	2031.5	62.5	2089	10	US-09-900-797-57	Sequence 57, Appl
22	2031.5	62.5	2089	13	US-09-893-820-57	Sequence 57, Appl
23	2031.5	62.5	2089	14	US-10-041-007-23	Sequence 23, Appl
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27	1295.5	39.8	1865	10	US-09-900-797-47	Sequence 47, Appl
28	1295.5	39.8	1865	13	US-09-893-820-47	Sequence 47, Appl
29	1295.5	39.8	1865	14	US-10-041-007-17	Sequence 17, Appl
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34	1240.5	38.2	2700	12	US-10-041-018-363	Sequence 363, Appl
35	1240.5	38.2	2700	13	US-09-893-820-43	Sequence 43, Appl
36	1231	37.9	1795	9	US-09-887-586A-49	Sequence 49, Appl
37	1231	37.9	1795	9	US-09-903-012-49	Sequence 49, Appl
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39	1231	37.9	1795	13	US-09-893-820-49	Sequence 49, Appl
40	1231	37.9	1795	14	US-10-041-007-19	Sequence 19, Appl
41	1187	36.5	2424	9	US-09-887-586A-45	Sequence 45, Appl
42	1187	36.5	2424	9	US-09-903-012-45	Sequence 45, Appl
43	1187	36.5	2424	10	US-09-900-797-45	Sequence 45, Appl
44	1187	36.5	2424	13	US-09-893-820-45	Sequence 45, Appl
45	1187	36.5	2424	14	US-10-041-007-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-025-145A-64
Sequence 64, Application US/10025145A
Publication No. US20030175861A1
GENERAL INFORMATION:
APPLICANT: Croceau, Rodney B.
APPLICANT: Bohlmann, Joerg
APPLICANT: Steele, Christopher L.
APPLICANT: Phillips, Michael A.
TITLE OF INVENTION: Monoclonal Synthesases from Grand Fir (Abies Grandis)
FILE REFERENCE: MSUR118414
CURRENT APPLICATION NUMBER: US/10/025, 145A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 09/360, 545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052, 249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 64
LENGTH: 2013

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; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(1889)
; OTHER INFORMATION:
US-10-025-145a-64

Alignment Scores:
Pred. No.: 0 Length: 2013
Score: 3251.00 Matches: 618
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Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-025-145a-65 (1-618) x US-10-025-145a-64 (1-2013)

QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeuSerSerHisGlu 20
DB ATGGCTCTTCTTCTAATTACTCCGCTGGTTTCCAGTGTGCTCCTCAGTTCTTCATGAG 95
QY 21 IleValAlaLeuAgaGThIleProThIleuGlyIleCysArgProGlyIlySerVal 40
DB ATTAAGCTCTCCGTAGAACAACTCCAACTCTGGAACTGCAGGCCGGGAAATCCGTC 155
QY 41 AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60
DB GCGCATTCCTAATACATGTGTGTTGACAAAGCTCCGATCTTACTGATCTGTACAGAGCG 215
QY 61 ValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIleGlnSerIleSerThr 80
DB GTGGGCAACTATCATCTCCAACTGTGGGACGATGATTCATACAGTCTGTATCTCAACG 275
QY 81 ProGlyGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyIleValIlyAsp 100
DB CTTATGAGACACTGATTTACCGGAAAGTGTCTGACACATTAATGGGAAAGTAAGGAT 335
QY 101 IleMetPheAsnPheIlySerLeuGlnAspGlyIlyAsnAspLeuLeuGlnArgLeuLeu 120
DB ATATGTTTCATTTCAAGTCCCTGGAAAGTGGAGCAATGATCTCTTCACAGACTTTTG 395
QY 121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheIlyIlySerGluIleIlySerThr 140
DB CTGCTGCATGACGTGTGAACGTTGGGAATCGACAGGCAATTTCAAAAAAGATTAAGACG 455
QY 141 AlaLeuAspTyrValAsnSerTyrTyrAsnGluIlySerGlyIleGlyCysGlyArgGluSer 160
DB GCACTCGATTATGTTAACAATTATTTGAACGAAAAAGGCATTTGATGGAGGAGAGGT 515
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180
DB GTTGTGACTGACCTCAACTCAACCGCTTGGGCTTCGAACTCTCCAGCTACAGAGATAC 575
QY 181 ThrValSerSerAspValLeuAsnValPheIlyAspIlyAsnGlyIlyInPheSerSerThr 200
DB ACTGTGCTTCAGATGTTTGAACGTTTAAAGACAAAAATGGGCAATTTTCTCCACT 635
QY 201 AlaAsnIleGlnIleGluGlyIleArgGlyValLeuAsnLeuPheArgAlaSerIleu 220
DB GCCAATATTCAGATAGAGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTC 695
QY 221 ValAlaPheProGlyGlyIlyValIleMetAspGlyAlaGluThrPheSerThrIlySerIleu 240
DB GTCCCTTTCCTCCGGCGAGAAAGTTATGATGAGCTGAAACATCTCTACAAAAATATTTA 755
QY 241 ArgGluAlaLeuGlnIlyIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal 260
DB AGAAGAGCCCTGCAAAAGATTCGCGCATCCAGTACTTACTTACTTACAGATACGGGACGCT 815
QY 261 LeuGluIlyArgIlyTyrPheIleThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal 280
DB CTGGAAATATGATGGACACCAAAATTTGGCAGCTTGGAGAGAGAAATTAACATGAGCGTC 875
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QY 281 PheGlyGlnHisThrIlyAsnIlyAsnAlaAlaGlyIlyLeuLeuGluLeuAlaIlyLeu 300
DB TTTCGACAGCACACTAAAAATTAAGAACGCCCGGAGAACTTTTGAACATTCGCAAAATTG 935
QY 301 GluPheAsnIlePheHisSerLeuGlnGluArgIlyLeuIlySerHisValSerArgTyrTrp 320
DB GAATTCATATATATTTCACTCCTTACAGAGAGAGATTAACATGTGTTCCCGATGTGTGG 995
QY 321 LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla 340
DB AAGACCTCGGTTCTCTTGAGATGACCTTCTGTGCAATGTGCACGTCGGAATACTAGCT 1055
QY 341 LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrIly 360
DB TTGGCTTCCTGATATGGTTGAGCTTCACCATTCCTGATTCAGACTCGGCTTTACCAAG 1115
QY 361 MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu 380
DB ATGTCTCATCTTATCACAGGTTCTTGACACATGACACGCTTCGACACAGTAGACAG 1175
QY 381 LeuGluLeuPheThrAlaThrIleIlyAspArgTyrAspProSerAlaMetGluCysLeuPro 400
DB CTGGAACCTTTCACAGCGACAAATTAAGAGATGGATCGCTCCGAGTGAATGCCCTTCCA 1235
QY 401 GluTyrMetIlySerIlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420
DB GAATATATGAAGAGGTATCATATGATGTTTATCACACCGTAATATGGCTCGAGTG 1295
QY 421 AlaGluIlyValArgIlyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCys 440
DB GCAAGAGAGCTCAAGGCCGAGACACCGCTCAACATTCACAAAGACAGCGCTTGGAGAGCGTGT 1355
QY 441 PheAspSerTyrMetGlnGluAlaIlySerIleAlaThrGlyTyrLeuProThrPheGlu 460
DB TTTGATTCGTTATGACGAGAAAGTGGATGCCACTGGTTTATCTGCCACGTTTGAG 1415
QY 461 GluTyrLeuGluIlyAsnGlyIlyValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
DB GAGTACTTGGAGAAACGGAAAGTTAGCTGTGCTCATGCGCCATCGCATGCAACCATTT 1475
QY 1416 GAGTACTTGGAGAAACGGAAAGTTAGCTGTGCTCATGCGCCATCGCATGCAACCATTT 1475
DB 481 LeuThrIleuAspIleProPheProAspHisIleIleuIlySerGluValAspPheProSerIly 500
DB 1476 CTGACGTGTGAACATCCCTTCTCGATCACATCTCAAGAAAGTTGACTTCCCATCGAAG 1535
QY 501 LeuAspAspLeuIleCysIleIleLeuArgLeuArgIlyAspThrArgCysTyrIlyAla 520
DB 1536 CTCAATGACTGATATGATATCATCTTCGATTAAGAGTATACACCGCTGTACAAAGCA 1595
QY 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetIlyAspAspProGly 540
DB 1596 GACAGGCGCGGTGGAGAAAGCTTCGCTATATCATGTTATGAAAGCAAACTCTGGA 1655
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560
DB 1656 TTAAACGAGAAAGATGTCTGAAATCATATCAACTTCATGATCAGGAGCGCAATAGAGAA 1715
QY 561 LeuAsnTyrGluLeuLeuIlyProAspAspSerValProIleThrSerIlySerHisAla 580
DB 1716 TTAAATTTGGAGCTTCTTAAGCCGACACACAGTCTTCCATCTTCAAGAAACAGCA 1775
QY 581 PheAspIleSerArgValTyrPheHisIleGlyTyrArgTyrArgAspGlyTyrSerPheAla 600
DB 1776 TTTCACATTAAGACAGAGTTTGACATCAAGTTTACAGATACGAGATGCTACAGCTTTGCC 1835
QY 601 AsnValGluThrIlySerSerLeuValMetArgThrValIleGluProValProLeu 618
DB 1836 AACGTTGAACCAAAAGATTTGGTATGAGAACCGTCACTTAACCTGTGCTTTG 1889
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RESULT 2
US-09-887-586A-19
; Sequence 19, Application US/09887586A
; Patent No. US20020094556A1

GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US200209456A11, Joseph P.
APPLICANT: Stark, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASE
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6)...(1889)
OTHER INFORMATION: pinene synthase
US-09-887-586A-19

Alignment Scores:
Pred. No.: 8,17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.45% Mismatches: 81
Query Match: 9 Indels: 16
Gaps: 6

US-10-025-145A-65 (1-618) x US-09-887-586A-19 (1-2018)

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QY      1 MetAlaLeuLeuSerLethrProLeuValSerArgSerCylou----- 15
DB      6 ATGGCTCTAGATTTTACCGCACCGCTTGCCTCAATATGCTCGACAAATCGTTGATC 65
QY      16 SerSerSerHisGluLeuLeuValAlaLeuArgTrpThrIleProThrLeuGlyIleCysArg 35
DB      66 AGTTCTACCCCTGAGCTTAAAGCTCTCTCTAGAACATTTCCAGCTCTAGAAATGATGAG 125
QY      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB      126 CGAGGGAATCTATCATCTCTCCATCAGCATGAGCTCTACACCGCTGTAAACGATGAT 185
QY      56 SerValGlnArgValGlyAsnTrpHisSerAsnLeuTrpAspAspPheIleGln 75
DB      186 GGTATGAGAACACCATGGGCGGATTTCCATTCACCTCTGGAGCATGATGTCATACAG 245
QY      76 SerLeuIleSerThrProTrpGlyValAlaProAspTrpArgGluArgAlaAspArgLeuIle 95
DB      246 TCTTTA---CCAAAGCGCTTATGAGGAAATATCGTACCTGAGCGGTCTGAGAAATGATC 302
QY      96 GlyValValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
DB      303 GGGGAGTAAAGAAC---ATGTTCAATTCATGTCATTAAGAAGATGAGAGTAAATGAGT 359
QY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAlaAspValGluArgLeuGlyIle 130
DB      360 CCGCTCATATGTCATTCATCAACCGCTTGTGATGTCGACACCTTGAAAGTTTGGGAGTC 419
QY      131 AspArgHisPheLysGlyValLeuThrAlaLeuAspTrpValAsnSerTrpAsn 150
DB      420 CATGACATTTTCAAAAGATGATATAATTCGCGCTTGTATGTTTACAGTTATTTGGGCG 479
QY      151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB      480 GAAATGCGCATCGATCGGAGGAGGAGGTGTTTACTGATCTGAATCTCAACTGCGTGT 539
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QY      171 GlyLeuArgThrLeuArgLeuHisGlyTrpThrValSerSerAspValLeuAsnValPhe 190
DB      540 GGGCTTGAAACCTTACACATCTACAGGATACCGGCTGCTTACAGTGTTTTCAACCTTTC 599
QY      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluLeuArg 210
DB      600 AAAGCCAAATGGACAGTTTCTCGCTCGTCAAAATATTCAGACAGAGAGATCAGAC 659
QY      211 GlyValLeuAsnLeuPheAsnArgAlaSerLeuValAlaPheProGlyGluValMetAsp 230
DB      660 GGCCTTCTGAAATTTATTCGCGGCTCCCTCTCAATTCCTTCCAGGCGGAGAAATATGAT 719
QY      231 GluAlaGluThrPheSerThrLysTrpLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB      720 GAGCTGAAATCTTCTTACCAAAATTTTAAAGAGCCCTGCAAAAGATTCGGCTCC 779
QY      251 SerIleLeuSerLeuGluLeuArgAspValLeuGluTrpGlyTrpHisThrAsnLeuPro 270
DB      780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGAAATGAGTTGGCACATATTTGCGG 836
QY      271 ArgLeuGluAlaIleAsnTrpMetAspValPheGlyGlnHisThrLysAsnLysAla 290
DB      837 CGATTGGAAAGCAAAATTCATCATCAAGCTTTTGACAGACACTGGAACACAGAACTCA 896
QY      291 -----AlaGlyLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB      897 TATGTGAAGACAAAAATCTTTTGAACCTCCCAAAATTTGAGTTCCACATCTTTCAATCC 956
QY      308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
DB      957 TTACAAAGAGAGGATTAGAAAGTCTGGTCAGATGTCGAAAGATCGGTTTCTCTGAG 1016
QY      328 MetThrPheCysArgHisArgHisValGluTrpTrpAlaLeuAlaSerCysIleAlaPhe 347
DB      1017 ATGACCTTCTCCGACATCGTCAGCTGGAATATCACTTTGCGCTTCCTGATTCGCTTC 1076
QY      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB      1077 GAGCTTCAACATTTCTGATTTACAGCTCGGCTTTGCCAAGAGCTGTCATCTTATCACGTT 1136
QY      368 LeuAspAspMetTrpAspValPheGlyThrValAspGluLeuPheThrAlaThr 387
DB      1137 CTTCAGCATATGTCAGACACCTTCGCGACAGTAGACAGCTGGAATCTTTCACAGCGACA 1196
QY      388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTrpMetLysGlyValLys 407
DB      1197 ATGAAGAGATGGATCGCTCTCGATAGATTTGCTTCAGAAATATTAAGAGAGTGTAC 1256
QY      408 MetMetValTrpHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnLysArg 427
DB      1257 ATAGCGGTTTACACACCGCTTAATGAAATGAGCTCGAAGGCGAGAGAGCTCAAGGCCGA 1316
QY      428 AspThrLeuAsnTrpAlaArgGlnAlaTrpGluAlaCysPheAspSerTrpMetGlnGlu 447
DB      1317 GATAGCGTCACATATGCTCGGAGAGCTTGGAGGCTTATATGATTGATTCATATATCAAGA 1376
QY      448 AlaLysTrpIleAlaThrGlyTrpLeuProThrPheGluGluTrpLeuGluAsnGlyLys 467
DB      1377 GCAAGGTGATGCGCACGCTGTACCTCGCTCTTGTGATGAGTCTACGAAATGGGAAA 1436
QY      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB      1437 GTTACGCTGGGTATTCGATATCCGATATCCGATTCACACCATTTCTGACATATGACATCCC 1496
QY      488 ProAspHisIleLeuLysGluValAlaAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB      1497 CCTGATATATCTTCAAGAGATGATGACTTCCATCAAGCTTAAACGACTTGCGATGTC 1556
QY      508 IleLeuArgLeuAlaArgTrpThrArgCysTrpTrpValAlaAspArgAlaArgGlyGluGlu 527
DB      1557 ATCTTTGATTTACAGATGATACGCGGTGCTTACAGGCGGACAGGCTCTGCGAAGAAA 1616
QY      528 AlaSerSerIleSerCysTrpMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
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Db 1617 GCTTCCTTATATCATGTTATATGAAAGACATCTGGAGATGACGAGGAAGATGCTTC 1676
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Qy 548 AsnHisIleAsnPhenMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
|||
Db 1677 GATCATATCAACGGCATGATGAGTACGTAATCAAGATTAAATGGAACTTCTCAAA 1736
|||
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
|||
Db 1737 CCAACATCATATGTTCCATCTCCGCGAAGAAACATGTTTGACATGCGACAGCTTTC 1796
|||
Qy 588 HisHisGlyTrpArgTrpArgAspGlyTrpSerPheAlaAsnValGluThrLysSerLeu 607
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Db 1797 CATTAACGGCTCAAAATACCGAGACGGCTACAGCGTTGCCAAGTTGAACGAAGTTTG 1856
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Qy 608 ValMetArgThrValIleGluProValProLeu 618
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Db 1857 GTCAAGAAACCTTCCTTGAATCTGTGCTTTG 1889
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RESULT 3

US-09-903-012-19
Sequence 19, Application US/09903012
Patent No. US20020094557A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094557A1, Joseph P.
APPLICANT: Starke, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT FILING DATE: 2001-07-11
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/100,993
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 2018
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (6) ... (1889)
OTHER INFORMATION: pinene synthase
US-09-903-012-19

Alignment Scores:

Pred. No.: 8.17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 9 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-903-012-19 (1-2018)

Qy 1 MetaLeuLeuSerIleThrProLeuValSerAspSerCysLeu----- 15
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Db 6 ATGGCTCTAGTTTCTTACCGCACCGTTGGCTTCCAATATAGCTGACAAATCGTTATC 65
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Qy 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
|||
Db 66 AGTTCTACCATGAGCTTAAGGCTCTCTAGAACAAATTTCCAGGCTTGAATGAGTAGG 125
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Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
|||
Db 126 CGAGGAAATCTATCATCTCTTCATCAGCATGAGCTTCAACCGTTGTAAACGATGAT 185
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Qy 56 SerValGlnArgArgValGlyAsnTrpHisSerAsnLeuTrpAspAspPheIleGln 75
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Db 186 GGTATGAGAGACCCATGCGGATTTTCATTTCCAACTCTGGACAGATGATGTCATACAG 245
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Qy 76 SerLeuIleSerThrProTrpGlyAlaProAspTrpArgGluArgAlaAspArgLeuIle 95
|||
Db 246 TCTTTA---CCAAACGGCTTATGAGAAATAATCGTACCTGGAGCGCTGCGTGAACATGATC 302
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Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
|||
Db 303 GGGGAAATGAAAGAAC---ATGTTCAATTCCATGATCATTAAGAAAGTGAAGCTTAATGAGT 359
|||
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
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Db 360 CCGCTCATATGATTCATTCATCAACGCTTTGATGATTCACAGCCTTGAACGTTGGGATC 419
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Qy 131 AspArgHisPheLysGlyIleLysThrAlaLeuAspTrpValAsnSerTrpAsn 150
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Db 420 CATAGACATTTCAAAAGATGAGATTAATCGCGCTGATTAATGTTACATTAATTTGGGCGC 479
|||
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
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Db 480 GAAATGCGCATCGATCGGAGGAGAGAGTGTGTACTGATTCGAACCTCAACTGCGCTG 539
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Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTrpThrValSerSerAspValLeuAsnValPhe 190
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Db 540 GGGCTTGAACCCCTACACATACAGCATACCGGTCCTTCAGATGTTTCAAGCTTTC 599
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Qy 191 LysAspLysAsnGlyIlePheSerSerThrAlaAsnIleGluGlyGluIleArg 210
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Db 600 AAAGCCAAATGCGCGAGTTTCTCGCTGAATATTCAGACAGATGAAGATCAGA 659
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Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
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Db 660 GCGCTTGAATTAATTCGCGGCTCTCCATATGCTTTCAGGAGGAGAAATTAATGAT 719
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Qy 231 GluAlaGluThrPheSerThrLysTrpLeuArgGluAlaLeuGlnLysIleProAlaSer 250
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Db 720 GAGGCTGAATCTTCTTCAACAAATATTAAABAAGCCCGCAAAAGATTCCGGTCTCC 779
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Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTrpGlyTrpHisAsnLeuPro 270
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Db 780 AGT---CTTTCGACAGAGATCGGGAGCGTTTGGAAATATGTTGGCACACATATTTCCG 836
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Qy 271 ArgLeuGluAlaArgAsnTrpMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
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Db 837 CGATTGAGACGAAAGATTAACATCAAGTCTTTGACAGACACTGAGAACAGCAAGTCA 896
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Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
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Db 897 TATGTGAAGAGCAAAATCTTTTGAACCTGCAAAATTTGAGTTCAACATCTTCAATCC 956
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Qy 308 LeuGlnGluArgGluLeuLysValSerArgTrpTrpLysAspSerGlySerProGlu 327
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Db 957 TTACAAAGAGGGGAGTTAGAAAGTCTGTGACAGATGGTGAAGAAAGATGGGTTTTCGAG 1016
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Qy 328 MetThrPheCysArgHisArgHisValGluTrpTrpAlaLeuAlaSerCysIleAlaPhe 347
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Db 1017 ATGACCTTCTGCGACATCGTACGTTGAADACTTACCTTGGCTTCTGCAATTCGCTTC 1076
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Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
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Db 1077 GAGCTCAACATCTTGATTCAGACTCGGCTTGGCCAAAGCTGATCATCTTATACCGGTT 1136
|||
Qy 368 LeuAspAspMetTrpAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
|||
Db 1137 CTTACACATATATGTCGACACCTTCGACAGTACACAGCTGGAACCTTTCACAGCGCA 1196
|||
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTrpMetLysGlyValTrp 407
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Db 1197 ATGAAAGATGAGGATCGCTCTCGATAGATTTGCTTCAAGATATATGAAAGAGTGTAC 1256
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Qy 408 MetcValTyrHisThrValAsnGluMetAlaArgValAlaGluValAsnGluValArg 427
Db 1257 ATACGGTTTACGACACCGTAAATGAGTCTCAGAGGCGACGAGAGCTTCAAGCCGA 1316
Qy 428 AspThrLeuAenTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGGCTACATATGCTCGGGAAGCTTGGAGGCTTATATGATATGATATGCAATA 1376
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATGCGCACCTGTTACTGCTCCCTTGTATGATGACTACAGAGATGGGAAA 1436
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTGCAACCATTCGACATGACATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCTCAAGAGAGTTGACTTCCCATCAAGCTTAAAGACTTGGCATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 1557 ATCTTCGATTACGAGTGATACGCGGTGCTAACAGCGGACAGGGCTCGTGAGAGAAA 1616
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCCTTAATCATGCTTAATATGAAAGACATCTGAGATCATCAGAGAGATGCTCTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCATATCATGATGACGTATCAAGATTAATATGGAGACTTCTCAA 1736
Qy 568 ProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCACACATCATATGCTCCATCTCGCGGAGAAACATGCTTTGATGATGCCAGACTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATACGGCTACAAATACCGAGACGCGCTACAGCGTTGCAACGTTGAACGAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCAAGAGAACCTCCTTGAATCTGTGCTTTG 1889

RESULT 4
US-09-900-797-19
; Sequence 19, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A11, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6) ... (1889)
; OTHER INFORMATION: pinene synthase
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US-09-900-797-19
Alignment Scores:
Pred. No.: 8,176-279 Length: 2018
Score: 2453/100 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 10 Gaps: 6
US-10-025-145a-65 (1-618) x US-09-900-797-19 (1-2018)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTTAGTTTTCACCGGCACCGTTGCTTCAATATATGCTTGCACAAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyTyrLeuArg 35
Db 66 AGTTCTACCATGAGCTTAAGGCTCTCTTAAGAAATTCAGCTCTGAGTATGATGAGG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATACCTCTTCATGACATGAGCTTACACCGCTTGTAAACGATAT 185
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 CGTGACAGAGACCGATGGGCAATTCATTCACACTTGGAGCATGATGTCTACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAAAGGCTTATGAGAGAAATCGATACCGAGCGGTGAGAACTGATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyLys----- 112
Db 303 GGGGAGAGTAAAGAAC--ATGTTCAATTCAGATGATTAAGAAATGAGAGTTAATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgGlyLys 130
Db 360 CCGCTCAATGATCTCATTCACACGCTTTGGATGTGACACGCTTGAACGTTTGGGAGTC 419
Qy 131 AspArgHisPheLysGlyLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCTAAAGATGAGATAAATCGCGCTGTATATGTTACATTAATATGCGGC 479
Qy 151 GlyLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGCGATCGATGCGGAGGAGAGGTGTGTACTGATCGAATCAACTGCGCTTG 539
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAAACCTTACGACTACGAGATACCGGTGTCTTCAAGATGTTTCAAGCTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLysArg 210
Db 600 AAAGGCCAAATGCGAGTTTCTCGCTCGTGAATATATTCAGACAGATGAAGATGACAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GCGCTTCGAAATTTATTCGCGGCTCTCCCTCATTCCTTCCAGAGGAGAAAATTAATGAT 719
Qy 231 GlnAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTTACCAATATTTAAAGAGCCCTGCAAGAGATTCGGTCTCC 779
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270
Db 780 AGT---CTTCCGAGAGATCGGGAGCGTTTGAATGATGTGGACACATATTTGCGG 836
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGAGAGAGAGAAATTAATCAAGCTTTTGGACGAGCACTGAGAACACGAGATGCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
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Db	897	TATGTGAAGACAAAACTTTTGAATCCGAAATTTGGAGTTCAACATCTTTCATATCC	956
Qy	308	LeuGlnGluArgGluLeuLeuYHisValSerArgTrpTrpLysAspSerGlySerProGlu	327
Db	957	TTACAAAAAGAGGAGTTAGAAAGTCGTGTCAAGATCGTGGAAAAAGATCGGGTTTCTCTAG	1016
Qy	328	MetThrPheCysValArgHisArgHisValGluTrpTrpAlaLeuAlaSerCysIleAlaPhe	347
Db	1017	ATGACCTTCTCCGACATCGTCAAGTGGAAATACACTTGTGGCTTCTGTCAATGCGTTC	1076
Qy	348	GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal	367
Db	1077	GAGCCTCAACATCTCGATTCAGACTCGGCTTTGGCAAGCGTGCATCTTATCAACGGTT	1136
Qy	368	LeuAspAspMetCysTrpAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr	387
Db	1137	CTTACACGATATAGTACGACACCTTCGGCACATGACGAGCTGGAACTCTTCAACGCCGA	1196
Qy	388	IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTrpMetLysGlyValTrp	407
Db	1197	ATGAGAGATGGGATCCGTCTCTCGATAGATTGCTTCCAGATATATAGAAAGAGCTATC	1256
Qy	408	MetMetValTrpHisThrValAsnGluMetAlaArgValAlaGluValGlnGlyArg	427
Db	1257	ATATCGGTTTACGACACCGTAAATGAATGGCTCGAGAGGACGAGGACGCTTCAAGGCCGA	1316
Qy	428	AspThrLeuAsnTrpAlaArgGlnAlaTrpGluLacysPheAspSerTrpMetGlnGlu	447
Db	1317	GATACGCTCACATATGCTCGGGAAAGCTGGGAGGCTTATATTGATTCGATATAGCAAA	1376
Qy	448	AlaLysTrpIleAlaThrGlyTrpLeuProThrPheGluGluTrpLeuGluAsnGlyLys	467
Db	1377	GCAAGTGATCGCACACTGTTACTCGCCCTCTTGAATGAGTACTACAGAAATGGCAAA	1436
Qy	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleuThrLeuAspIleProPhe	487
Db	1437	GTATGCTGTGGTCAATCGGATATCCGCATTTGCAACCATTTGACATGACATGATCCCTTT	1496
Qy	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
Db	1497	CCTGATCATATCTTCAGAAAGTTGACTTCCCATCAAGCTTAAACGACTTGGCATGTGCC	1556
Qy	508	IleLeuArgLeuArgGlyAspThrArgCysTrpLysValAspArgAlaArgGlyGluGlu	527
Db	1557	ATCTTCATATTAACGAGTGATACGGGGTCTACAAAGGGGACAGGGCTCTGGAGAAACA	1616
Qy	528	AlaSerSerIleSerCysTrpMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu	547
Db	1617	GCTTCCTCATATATCATGTTATATGAAACAACTCTGAGAGTATCAGAGAAAGATCTCTC	1676
Qy	548	AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys	567
Db	1677	GATCATATCAACGGCATGATCAGTGAAGCTTAATCAAAAGATTAAATTTGGAACTTCCAAA	1736
Qy	568	ProAspAsnSerValProIleThrSerLysValHisAlaPheAspIleSerArgValTrp	587
Db	1737	CGAGCATCAATATGTTCCATCTCGGCGGAAAGAACTGCTTTTGAATGCGCCAGACCTTTC	1796
Qy	588	HisHisGlyTrpArgTrpArgAspGlyTrpSerPheAlaAsnValGluThrLysSerLeu	607
Db	1797	CATTACGGCTCAAAATATACCGAGCGGCTACAGCGTTGCCAAGCTTGAACGAAAGGTTTG	1856
Qy	608	ValMetArgThrValIleGluProValProLeu	618
Db	1857	GTCAAGAAACCCCTCTTGAATCTGTGCTTTTG	1889

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RESULT 5
US-09-893-820-19
; Sequence 19, Application US/09893820
; Publication No. US20040053366A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph

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1  APPLICANT:  NO. US20040005386m11, Joseph P
2  APPLICANT:  Sparks, Courtney M.
3  APPLICANT:  Manna, Khatheer R.
4  TITLE OF INVENTION:  SYNTHASES
5  FILE REFERENCE:  07678-025001
6  CURRENT APPLICATION NUMBER:  US/09/893,820
7  CURRENT FILING DATE:  2001-06-28
8  PRIOR APPLICATION NUMBER:  US/09/398,395A
9  PRIOR FILING DATE:  1999-09-17
10 PRIOR APPLICATION NUMBER:  60/100,993
11 PRIOR FILING DATE:  1998-09-18
12 PRIOR APPLICATION NUMBER:  60/130,628
13 PRIOR FILING DATE:  1999-04-22
14 PRIOR APPLICATION NUMBER:  60/150,262
15 PRIOR FILING DATE:  1999-08-23
16 NUMBER OF SEQ. ID NOS.:  58
17 SOFTWARE:  FASTSEQ for Windows Version 3.0
18 SEQ. ID NO 19
19 LENGTH:  2018
20 TYPE:  DNA
21 ORGANISM:  Abies grandis
22 FEATURE:
23 NAME/KEY:  CDS
24 LOCATION:  (6)...(1889)
25 OTHER INFORMATION:  pinene synthase
26 US-09-893-820-19

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Alignment Scores:	
Pred. No.:	8, 176-279
Score:	2453.00
Percent Similarity:	84.63%
Best Local Similarity:	75.28%
Query Match:	75.45%
DB:	13
Gaps:	6
Length:	2018
Matches:	475
Conservative:	59
Mismatches:	81
Indels:	16

US-10-025-145A-65 (1-618) x US-09-893-820-19 (1-2018)

QY MetAlaIleuLeuSerIleThrProLeuValSerAspSerGly----- 15
 Db 6 ATGGCTCTGATTCTTCAAGCACCGCTTGGCTTCCAAATATATGCTGCACCAATCGTTGATC 65
 QY 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
 Db 66 AGTTTCAACCATGACGCTTAAAGCTCTCTCTGAAACAAATCCAGCTTAGAAGATAGTAGG 129
 QY 36 ProGlyIleSerValAlaHisSerIleAlanMetCysLeuThrSerValAlaSerThrAsp 55
 Db 126 CGAGGGAATCTTACCTCTCTTCATTCAGCATAGACTTACCAACCGCTTGTACACCGAT 185
 QY 56 SerValGluArgArgValGlyAsnTyrHisSerAlanLeuTyrPaspAspPheIleGln 75
 Db 186 GGTGTACGAAGACGCTAGGGCGCATTTCCATTCACCACTCTGGAGCGATGATGTCATCAG 245
 QY 76 SerLeuIleSerThrProGlyIleAlaProAspTyrArgGluAlaArgAlaAspArgIle 95
 Db 246 TCTTTA---CCAGCGCTTATAGAGAAAATCTGTAACCTGGAGCGCTGCTGAGAAAATCATC 302
 QY 96 GlyGluValIleAspIleMetPheAsnPheIleYsserLeuGluAspGlyIle----- 112
 Db 303 GGGGAAGTAAAGAAC---ATGTTCAATTGCATGTGCATTAGGAAGATGAGAGATTATAGT 359
 QY 113 -----AspAspLeuGlnPargLeuLeuValAspAspValGluArgLeuGlyIle 130
 Db 360 CCGCTCAATGATCTCAATTACAGCCTTTGGATGTGCGACAGCCTTGAACGTTTGGGATC 419
 QY 131 AspArgHisPheIleValGluIleValSerThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
 Db 420 CATAGACATTTCAAAAGATGAGATAAATCCGGCGCTGATTATGTTTACATTATTGGGGC 475
 QY 151 GluIleGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
 Db 480 GAAATATGGATCGAGTCGGAGGAGAGATGTTGTACTGATCTGAACTCAACTGCGGTG 538

171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
540 GGGCTTGACACCTTACGACCTACGACGATACCCGGTGTCTTCAAGATCTTTCAAAAGCTTTC 599
191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIleArg 210
600 AAAGGCCAAATGGGAGCTTTTCCGCTCGTGAATAATATTCAGACAGATGAAGAGATGACA 659
211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyValMetAsp 230
660 GGGCTTTCGAATTAATTCGGGGCCCTCCCTCATTCGCTTCCAGGGGAAATAATATGAT 719
231 GluAlaGluThrPheSerThrLeuTyrLeuArgGluAlaLeuGlnIleProAlaSer 250
720 GAGGTGAATCTTCTTACCAAAATATTAAGAGCCCTGCAAAAGATTCGGCTTCC 779
251 SerIleuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
780 AGT---CTTTCGGGAGATCGGGGAGCTTTTGGAAATGTGGTGGCACAATATTGGCG 836
271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
837 CGATTGGAAAGCAAGAAATTAATCAAGCTTTTGGACAGACACTGAGAAACAGAAAGTCA 896
291 -----AlaGluLysLeuLeuGluLeuAlaLysIleLeuGluPheAsnIlePheHisSer 307
897 TATGTGAAGACCAAAACCTTTAGAACTTCGAAATATGGAGTTCAACATCTTTCATTC 956
308 LeuGlnGluArgGluLeuLysHisIleValSerArgTyrTyrLysAspSerGlySerProGlu 327
957 TTACAAAGAGGAGATTGAAGAGTGTGTGATGATGTGGAAAGATCGGGTTTCTGAG 1016
328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
1017 ATGACCTTCTCCGACATCGTACGCTGGAATATCACTTTGGCTTCCGATTCGCTTC 1076
348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
1077 GAGCCTCAACATTCGTGATTCAGACTCGGCTTTGCCAAGAGCTGTCACTTATACGGGTT 1136
368 LeuAspAspMetTyrAspValPheGlyTyrValAspGluLeuGluPheThrAlaThr 387
1137 CTTACGATATGTACGACACCTTCGGGACAGTACGAGCGTGAACCTTTCACAGCGACA 1196
388 IleLysArgTyrPheProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
1197 ATGAAGAGATGGATCCGCTCTCGATGATTCCTTCAGAAATATATGAAGAGATGTAC 1256
408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
1257 ATACCGGTTTACGACACCGTAAATGAATGGCTCGAAGAGCGAGAGGCTCAAGCGCGA 1316
428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447
1317 GATACGCTCAATATGCTCGGGAGAGCTTGGAGGTTATTTGATTTCTATATGCAAGA 1376
448 AlaLysTyrIleAlaThrGlyTyrLeuProThrPheGluGluTyrLysGluAsnGlyLys 467
1377 GCAAGGTGATCGGACACTGTTACTGCTTCCTTGTGAGTACTACAGAAATGGGAAA 1436
468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
1437 GTTAGCTGTGCTATCGCATATCCGCATTTGCAACCATTTGACAAATGAGCAATCCCTTT 1496
488 ProAspHisIleLeuLysGluValAspPheProSerIleLysAsnAspLeuIleCysIle 507
1497 CCTGATCATATCCCAAGAGAGTTGACTTCCATCAAGCTTAAAGCATTTGGCATGTGCC 1556
508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
1557 ATCTTTTCATTAACGAGGTGATACGGGAGTGTACAAAGGGGACAGGGCTCGTGGAGAA 1616
528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

1617 GCTTCCTCTATATCTGTATATGAAGACAACTCTGGAGTATGAGGAAGATGCTCTC 1676
548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTyrGluLeuLys 567
1677 GATCATATCAACGGCAGATGATGAGTATCAAGAGATTAAATTTGGAACTTCTCAA 1736
568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTyr 587
1737 CCAGACATCAATGTTCCCATCTCGCGAAGAAACATGCTTTTGAACATCGCAAGCTTTC 1796
588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
1797 CATACGCTTCATATACCGAGCGCTACAGCGCTTGCACAGCTTGAAGAGATTTG 1856
608 ValMetArgThrValIleGluProValProLeu 618
1857 GTCAAGAGAACCTTCCTTGAATCTGTGCTTTG 1889

RESULT 6
US-10-041-007-21
; Sequence 21, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
US-10-041-007-21

Alignment Scores:
Pred. No.: 8,17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: Gaps: 6

US-10-025-145a-65 (1-618) * US-10-041-007-21 (1-2018)

1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
6 ATGCTCTAGTATTTTACCGGACCGTGTGCTTCAAAATCATCTCGCAAAATCGTTGATC 65
16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
66 AGTTCTACCCATGAGCTTAAAGGCTCTCTTGAAACAAATTCAGCTCTTGAAATGAGTAG 125
36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
126 CGAGGGAATCATCACTCTTCATCAGATGAGCTTACACCGTGTGAACGATAT 185
56 SerValGlnAlaGlyValGlyAsnTyrHisSerAsnLeuTyrPheAspPheIleGln 75
186 GGTGTAGAAACCCATGGGAGGATTCATTCCAACTTGGAGCATGATGATACAG 245
76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
246 TCTTTA---CCAAAGGCTTATGAGAAATAATCGTACTGAGAGCTCTGAGAAATGATC 302
96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyLys----- 112
303 GGGGAGTAAAGAAC---ATGTTCAATTCGATGTCATTAGAAAGATGAGATTAATGAGT 359


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QY 113 -----AsnAspLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGGTCAATGATCTCATTCACACGCTTTGGATTGTCAGACGCTTGAAACGTTGGGATC 419
QY 131 AspArgHispehlysglyileysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATGACATTTTCAAAAGATGAGATAAATCCGGCTTATATGTTTACAGTATTGGGCGC 479
QY 151 GluIlyleGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGCGATTCGGATCGGAGGAGAGAGTGTGTACTGATCGAAGCTCAACTGCGTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTGAAACCCACGACTACAGGATACCGGCTGCTTCAGATGTTTTCAAGCTTTC 599
QY 191 LysAspLysAsnGlyIlePheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAATGCGCAGTTTCTCGCTCGTCAAAATATTTTCAGACAGATGAAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIlyValMetAsp 230
Db 660 GGGCTTCTGAAATTTATTCGGGCTCCCTCATTCCTTTCCAGGAGGAAATATATGAT 719
QY 231 GluAlaGluThrPheSerThrTyrLeuArgGluAlaLeuGlnIlyIleProAlaSer 250
Db 720 GAGGCTGAATCTCTCTACCAATATTTTAAAGAGCCCGCAAAAGATTCGGGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheSerAsnLeuPro 270
Db 780 AGT---CTTTCGCGAGAGATCGGAGACGTTTGGAAATATGTTGGCACATATTTTCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAGAGAAATACATCAAGTCTTTGACACGACCTGAGAACACAGAACAGCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGACAAAACCTTTTGAACCTCGCAAAATTTGGAGTTCAACATCTTTCATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAAGAGGAGTTAGAAAGTCTGTCAGATCGTGGAAAGATCGGCTTTCTCGAG 1016
QY 328 MetThrPheCysAspGlnHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCCACATCGTCAGTGAATATCACTTGGCTTCTGCAATGGCGTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisIleuIleThrVal 367
Db 1077 GAGCTCAACATTTCTGATTGAGCTCGGCTTTCGCAAGAGTGTCACTTATCACGGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1137 CTTGACGATATATGTACGACACCTTCGGCACAGTACAGCGAGAACTTTCACAGCGCA 1196
QY 388 IleLysArgTyrPheProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAAGATGGAGATCGTCTCGATGATGCTTCACGAATATATGAAAGAGGTATAC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIlyArg 427
Db 1257 ATAGCGGTTTACGACCGTAAATGAATGCTCGAGAGGACGAGAGGCTCAAGGCGCA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCAATATGCTCGGAGAGCTTGGAGGCTTATATGATTCCTATATATCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATGCGCACTGTTACCTGCTCTTGTATGATGACTACGAGAAATGGGAAA 1436

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QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGGTATCGCATATCCCGCATTCGCAACCCATTTGCAATGAGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGlyValaAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCGATCATATCCCTCAAGAGATGACTTCCATCAAGGCTTAAACGCTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 1557 ATCCTTCGATTACGAGGTGATACCGGCTGCTACAGCGGACGAGGCTCGGAGAAAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluAspAlaLeu 547
Db 1617 GCCTTCCTATATCATGTTATATGAAGACAACTCGGATATCAGAGAAAGATGCTCTC 1676
QY 548 AsnHisIleLeuPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACCGCAAGATCAGTACGTATCAAAAGATTAATTTGGAACTTCTCAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCATATGTTCCCATCTCGCGAAGAAACATGCTTTGACATCGCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAACGCTTCAAAATACCGAGACGCTTACAGCGCTTCCAAACGTTGAAGAGATTTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACAGAAACCCCTTGAATCTGTGCTTTG 1889

RESULT 7
US-10-025-145A-3
; Sequence 3, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Crocneau, Rodney B.
; APPLICANT: Bohmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monocleptene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025, 145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (6)..(1892)
; OTHER INFORMATION:
; US-10-025-145A-3

Alignment Scores:
Pred. No.: 8,17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: Gaps: 6

US-10-025-145A-65 (1-618) x US-10-025-145A-3 (1-2018)

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1 MetalLeuSer1LeThrProLeuValSerArgSerCysLeu----- 15
6 ATGGCTAGATTTCACCGCACCGTTGGCTTCAAAATACGCTGCACAAATCGTTGATC 65
16 SerSerSer1Glu1Leu1Leu1Arg1Gly1Leu1Pro1Thr1Leu1Gly1Leu1Cys1Arg 35
66 AGTTCTACCATGAGCTTAAGGCTCTCTCTGAACAATTCAGAGCTTGAATGATGAG 125
36 ProGlyLeuSerValAlaHisSer1Leu1Ser1Cys1Leu1Thr1Ser1Val1Ala1Ser1Thr1Asp 55
126 CGAGGAAATCTATCTCTCCATCCATGACATGACCTTACACCGCTGTGAATCCCATGAT 185
56 SerValGlnArgArgValGlyAsn1Thr1Ser1Asn1Leu1Thr1Asp1Asp1Phe1Leu1Gln 75
186 GGTGTACAAAGACGATGCGGATTCATTCATCAACCTTGGAGAGATGATGATACAG 245
76 SerLeu1Leu1Ser1Pro1Gly1Val1Pro1Asp1Trp1Arg1Gly1Ala1Asp1Arg1Leu1 95
246 TCTTTA---CCACGCGCTTATGAGGAAAATCGTACCTGAGACGCTGAGAAATGATGATC 302
96 Gly1Val1Val1Leu1Asp1Leu1Met1Phe1Asn1Phe1Leu1Gly1Gly1----- 112
303 GGGCAAGTAAAGAAC---ATGTTCAATTCGATGCTATTAGAAGATGAGAGATTAAATGAGT 359
113 -----AsnAspLeuLeuGlnArgLeuLeuVal1AspAspValGlnArgLeuGly1Le 130
360 CCGCTCAATGATCTCATTCACAGCGCTTGGATGTCGACAGCTTGAACGTTGGGAGATC 419
131 AspArgHisPhe1Val1Gly1Leu1Leu1Val1Leu1Asp1Trp1Val1Asn1Ser1Trp1Asn 150
420 CATGACATCTTCAAAAGATGAGATGAATTAATCGCGCTTGAATGTTTACAGATTATGGGGC 479
151 Gln1Val1Gly1Leu1Gly1Cys1Gly1Arg1Gln1Ser1Val1Val1Thr1Asp1Leu1Ser1Thr1Ala1Leu 170
480 GAAATGCGATCGGATCGGAGGAGAGATGTTGTTACTGATCTGAACTCAACTCGCTGTTG 539
171 Gly1Leu1Arg1Thr1Leu1Arg1Leu1His1Gly1Thr1Val1Ser1Ser1Asp1Val1Leu1Asn1Phe 190
540 GGGCTTCACACCTTACGATACGATACGAGATACCGGCTGCTTCAAGATGTTTCAAAAGCTTTC 599
191 LysAsp1Val1Asn1Gly1Gln1Phe1Ser1Ser1Thr1Ala1Asn1Leu1Gln1Gly1Val1Leu1Arg 210
600 AAAGGCCAAATGGGCACTTTTCTCGCTGAAATATTTCAAGACAGATGAAGATGATGCA 659
211 Gly1Val1Leu1Asn1Leu1Phe1Arg1Ala1Ser1Leu1Val1Ala1Phe1Pro1Gly1Gln1Val1Met1Asp 230
660 GGCCTTCTGATTTATTTCCGGGCTCTCCCTCATTCCTTCCAGGGGAGAAAATATATGAT 719
231 Gln1Ala1Gln1Thr1Phe1Ser1Thr1Leu1Arg1Gln1Ala1Leu1Gln1Val1Leu1Pro1Ala1Ser 250
720 GAGGCTGAAATCTTCTTCAACAAATATTTAAAGAAAGCCCTGCAAAAGATTCGGCTTCC 779
251 Ser1Leu1Ser1Leu1Gln1Leu1Arg1Asp1Val1Leu1Gly1Trp1His1Thr1Asn1Leu1Pro 270
780 AGT---CTTTGCGAGAGATCGGGGACGTTTGGAAATGATGTTGSCACACATATTTGGCG 836
271 ArgLeu1Gln1Ala1Arg1Asn1Trp1Met1Asp1Val1Phe1Gly1Gln1His1Thr1Lys1Asn1Lys1Asn1Ala 290
837 CGATTGGAAAGAGAGATTTACATCAAGCTTCTTGGACGAGACACTGCAACAGACAGAAAGCA 896
291 -----Ala1Gln1Val1Leu1Leu1Gln1Leu1Ala1Lys1Leu1Gln1Phe1Asn1Lys1Phe1His1Ser 307
897 TATGTGAAGACGCAAAAATTTTAACTTCGAAATATGGAGTTCAACATCTTCAATCC 956
308 Leu1Gln1Ala1Arg1Gln1Leu1Lys1His1Val1Ser1Arg1Trp1Trp1Lys1Asp1Ser1Gly1Ser1Pro1Gln 327
957 TTACAAAAGAGAGAGATTGAAGAGTGTGTCAGATGCTGGAAGAAAGATCGGGTTTCTGAG 1016
328 Met1Thr1Phe1Cys1Val1Arg1His1Val1Gln1Val1Val1Ala1Leu1Ala1Ser1Cys1Gln1Leu1Ala1Phe 347
1017 ATGACCTTCTCGCGACATGTCACCTGGAATATCTACATTTGGCTTCTGCAATTCGCTTC 1076
348 Gln1Pro1Gln1His1Ser1Gly1Phe1Arg1Leu1Gly1Phe1Thr1Lys1Met1Ser1His1Leu1Leu1Thr1Val 367

1077 GAGCTCAACATCTTCGATTTAGACTGCGCTTTCGCAAGAGCTGATCATCTTATCACGTT 1136
368 Leu1Asp1Asp1Met1Trp1Asp1Val1Phe1Gly1Thr1Val1Asp1Gln1Leu1Gln1Phe1Thr1Ala1Thr 387
1137 CTTCAGCATATGATGACACACCTTCGCGACAGTACAGAGCTGGAATCTTTCACAGCGACA 1196
388 Ile1Lys1Arg1Trp1Asp1Pro1Ser1Ala1Met1Gln1Cys1Leu1Pro1Gly1Trp1Met1Lys1Gly1Val1Trp 407
1197 ATGAAGAGATGGAGATCGCTCTCGATGATGATTCCTTCCAGAAATATGTAAGAGAGTATAC 1256
408 Met1Met1Val1Trp1His1Thr1Val1Asn1Gln1Met1Ala1Arg1Val1Ala1Gln1Val1Arg 427
1257 ATAGCGCTTTCGACACCGCTAAATGAATGCTCGAGAGCGAGAGAGAGCTTCAAGCGCGA 1316
428 Asp1Thr1Leu1Asn1Trp1Ala1Arg1Gln1Ala1Trp1Gln1Ala1Cys1Phe1Asp1Ser1Trp1Met1Gln1 447
1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGAGCTTATGATTCGTATATGCAAGAA 1376
448 Ala1Lys1Trp1Leu1Ala1Thr1Gly1Trp1Leu1Pro1Thr1Phe1Gln1Gly1Trp1Leu1Gln1Val1Lys 467
1377 GCAAGGTGATGCGCACAGTGTACCTGCTCCCTTGTATGAGTACTACAGAAATGGGAAA 1436
468 Val1Ser1Ser1Ala1His1Arg1Pro1Cys1Ala1Leu1Gln1Pro1Leu1Thr1Leu1Asp1Leu1Pro1Phe 487
1437 GTTACCTGTGCTCATCGCATATCCGCAATGCAACCATCTTGACATGACATGCCCTTT 1496
488 Pro1Asp1His1Leu1Lys1Gln1Val1Asp1Phe1Pro1Ser1Lys1Leu1Asn1Phe1Leu1Cys1Ile 507
1497 CCTGATCATATCCCAAGAGATGATGACTTCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556
508 Ile1Leu1Arg1Leu1Asp1Trp1Arg1Cys1Trp1Lys1Ala1Asp1Arg1Ala1Arg1Gln1Gln1 527
1557 ATCTTCATTTACAGAGATGATACCGGTGCTTACAAAGCGGACAGGCTCGTGGAGAA 1616
528 Ala1Ser1Leu1Ser1Cys1Trp1Met1Lys1Asp1Asn1Pro1Gly1Leu1Thr1Gln1Gln1Ala1Leu 547
1617 GCTTCCTTATATATGATGATATATGAAGACATCTGAGATGATCAAGAGATTTGGAACCTTCAAA 1676
548 Asn1His1Leu1Asn1Phe1Met1Leu1Arg1Asp1Ala1Leu1Arg1Gln1Leu1Asn1Trp1Gln1Leu1Lys 567
1677 GATCATATCAACGCGCATATGATGATGATGATCAAGATCAAAAGATTTGGAACCTTCAAA 1736
568 Pro1Asp1Asn1Ser1Val1Pro1Leu1Thr1Ser1Lys1Val1His1Ala1Phe1Asp1Leu1Ser1Arg1Val1Trp 587
1737 CCAAGCATCAATGTTCCATCTCGCGGAGAAACATGCTTTTGACATGCGCAAGACTTTC 1796
588 His1His1Gly1Trp1Arg1Trp1Arg1Asp1Gly1Trp1Ser1Phe1Ala1Asn1Val1Gln1Thr1Lys1Ser1Leu 607
1797 CATTAAGCTTCAAAATATACCGAGAGCGCTTACAGCTTGGCCAACTTGAAACGAAGATTTG 1856
608 Val1Met1Arg1Thr1Val1Leu1Gln1Pro1Val1Pro1Leu 618
1857 GTCAAGAAACCTTCCTTGAATCTGTGCTTTG 1889

RESULT 8
US-10-025-145A-66
; Sequence 66, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monocetene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR113414
; CURRENT APPLICATION NUMBER: US/10/025, 145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360, 545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052, 249

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; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1923)
; OTHER INFORMATION:
US-10-025-145A-66

Alignment Scores:
Pred. No.: 1.99e-256 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best Local Similarity: 68.29% Mismatches: 98
Query Match: 69.64% Indels: 26
DB: 15 Gaps: 9

US-10-025-145A-65 (1-618) x US-10-025-145A-66 (1-2186)

Qy 1 MetalaleuSeuSerIleThrProleuValSerArgSerCysleu----- 15
Db 34 ATGGCTGCTGTTCTCCGCAACC-----AAATCTGCTGCACAAATCGTTGATC 84

Qy 16 ---SerSerSerHISGluIleValAlaLeuArgArgThrIleProThrLeuGlyIleCys 34
Db 85 AGGTCCTACTCATCAAGAGCTGAGAGCTGCGCAAGAACATCCCAACTCTTGGAATGTGT 144

Qy 35 ArgProGlyIleSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
Db 145 AGCGAGAGGAATCTTTCAACCTTGTGTAGCATGAGTTGACACCGCGTGTATCTGAT 204

Qy 55 AspSerValGlnArgGValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIle 74
Db 205 GATGCTCTACAAAGACGATAGTGACTATCATTCCTCGGACGACGATTTTCATA 264

Qy 75 GlnSerLeuIleSerThrProTyrGlyValaProAspTyrArgGluArgAlaAspArgleu 94
Db 265 CAGTCTCTA---TCACGCTTATATGGGAGCCTTCTTACCGAAGACGTGTGAGAACTG 321

Qy 95 IleGlyGluValIleAspIleMetPheAsnPheIleSerLeuGluAspGlyGly----- 112
Db 322 ATTGGGGAGAGGAGGAG---ATGTTCAATTCAATGCCATCGGAAGATGGAATCATG 378

Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValaAspAspValGlnArgleuGly 129
Db 379 AGTCCCTCAATGATCTTATGAAAGATGATGATGATGATGATGATGATGATGATGATG 438

Qy 130 IleAspArgHisPheIleValGluIleLeuThrAlaLeuAspTyrValaAspSerTyrTrp 149
Db 439 ATTATATGACATTTTCAAAAAGATTAATCAAGCCCTTGATATGTTTACAGTTATTTGG 498

Qy 150 AsnGluIleGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
Db 499 AACGAAAAAGGTATGATGATGCGGTAGAGATAGTGTGTTTCTGATGTCATCGCATCC 558

Qy 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValaSerSerAspValaLeuAsnVal 189
Db 559 TCGGGGTTTCAAACTCTCGCTACACGATACAGATGCTCTTCAAGAGTTTGAATA 618

Qy 190 PheIleAspIleAsnGlyIlePheSerSerThrAlaAsnIleGlnIleGlyGluIle 209
Db 619 TTTCAAGACCAAAATGGGCACTTTGCAATTCCTCTCTAGTACAAA---GAGAGACATC 675

Qy 210 ArgGlyValaLeuAsnLeuPheArgAlaSerLeuValaAlaPheProGlyGluValaMet 229
Db 676 AGAACCGTTTGAATTTATATCGGGCTTCTTCAATGCTTTCCTCGGGAAGAAAGTTATG 735

Qy 230 AspGluIleGluThrPheSerThrIleValArgGluValaLeuGlnIleProAla 249
Db 230 AsnGluIleGluThrPheSerThrIleValArgGluValaLeuGlnIleProAla 249
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Qy 602 ValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1873 CAAGAAACGAAAGATTGGTGGAGAACGGTCTTGAAACGAGCTCTT 1923

RESULT 9

US-09-887-586A-29
Sequence 29, Application US/09887586A
Patent No. US20020094556A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094556A1, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OR INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/887,586A
CURRENT FILING DATE: 2001-06-22
PRIORITY APPLICATION NUMBER: 09/398,395
PRIORITY FILING DATE: 1999-09-17
PRIORITY APPLICATION NUMBER: 60/130,628
PRIORITY FILING DATE: 1999-04-22
PRIORITY APPLICATION NUMBER: 60/150,262
PRIORITY FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2196
TYPE: DNA
ORGANISM: Abies grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (69)...(1949)
OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Alignment Scores:

Pred. No.: 6,376-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
Gaps: 7

US-10-025-145A-65 (1-618) x US-09-887-586A-29 (1-2196)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTGCTGTTTCATCTCACCGTTGGCTTGAATCTTGCTCGCAAGTCGTGATC 128
Qy 16 SerSerSerHisGluIleLeuAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCATATTCATGAAACATAGACCTCCCTATAGAACATCCCAATCTTGGAATGCTGAG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAATCTGTCACCGCTTCCATGACATCACTTTGGCCACCGCTGCACCTGATAT 248
Qy 56 SerValGlnArgArgValGlyAsnTyriSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGTAACAAACACGATAGTGATACCATTCGGAATCTCGGAGCATGATTCATACAG 308
Qy 76 SerLeuIleSerThrProTyriGlyAlaProAspTyriArgGluAlaAspArgLeuIle 95
Db 309 TCTCTTA--TCAGCGCTTATGGGGAACCTTTTACAGGAACGTCGAGATTAATT 365
Qy 96 GlyIleValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
Db 366 GTGAGAGTAAAGAAAGTA--TTCAATTCATGTCCTCGATGATGAAAGATTAATGAT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTAATGATCTCATCAACGCGCTTGGATAGTCGATAGCGTTGGAAGTTGGGGATA 482

Qy 131 AspArgHisPheLysLysGluIleLeuThrAlaLeuAspTyriValAsnSerTyriTrpAsn 150
Db 483 GGTACATCTTCACAAAGAGATACATCAGCTTCGATATATGTTCCGTTACGGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACGGCATTTGATGATGGGAGACAGTATGTTATCATCTCACTCAACTCGCTTG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyriThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTCAACCTTCGATTCACCGGTACACTGATATCTCCAGAGCTTTAAACCTTT 662
Qy 191 LysAspLysAsnGlyLysPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 663 CAAGATCAAAATGACAGCTTGTATGCTCCCGCT--CAGACAGAGGGTGAATCAAG 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyLysValMetAsp 230
Db 720 AGCGTTCTTAATCTTATATCGGGCTTCCCTCATTTGCTTCCCTGGTGAAGAAATTAGAA 779
Qy 231 GluAlaGluThrPheSerThrLysTyriLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTCTCCACAAAGATATTGAAGAAGCTCTTACAAAGATTCCAGCTCC 839
Qy 251 SerIleLeuSerLysGluIleArgAspValLeuGluTyriTrpHisThrAsnLeuPro 270
Db 840 GCT--CTTTACAGAGATTAAGTTGTATGAAATAGCTGACACAAATTTGCA 896
Qy 271 ArgLeuGluAlaArgAsnTyriMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATATCATAGACACTTGAGAAAGACACAGCATGCTCAT 956
Qy 288 LysAsnAlaAlaGlyLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATCTGGGAGAAAGACCTTTTGAACCTTCAAAATGGAATCAATATTTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAAACAAAGAAATTAACAATCTTTTGAAGATGGTGAAGAGTGGCAATTTGCTTAA 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyriTyriAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGATTTCACTTTGGCTCTGTATTTCCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCAAAACATCTGTCATCAGACTAGGCTTCCCAAAATGTGCATCTGTGCACAGTT 1196
Qy 368 LeuAspAspMetCysArgAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGACGATATTTACGACACTTTTGAACGATTAACGAGTTGAACCTTTTCAACTTCA 1256
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyriMetLysGlyValTyri 407
Db 1257 ATTAAAGATGCAATTCATCATCAGATTAACAACCTTCCAGATATTAATAATGTGTAC 1316
Qy 408 MetMetValTyriHisThrValAsnGluMetAlaArgValAlaGluLysValGlnLysArg 427
Db 1317 ATGTCGCTGTTGAAACTGTAAATGAACCTGACAGAGAGCGGAGAGACCTCAAGGGAGA 1376
Qy 428 AspThrLeuAsnTyriAlaArgGlnAlaTrpGluAlaCysPheAspSerTyriMetGlnIle 447
Db 1377 AACCTCTCAACCTATGTTCCAAAGGCTTGGAGGCTTATTTGATTCATATATGAAAGA 1436
Qy 448 AlaLysTrpIleAlaThrGlyTyriLeuProThrPheGluGluTyriLeuGluAsnGlyLys 467
Db 1437 GCAAAATGCAATCTTAATGTTATCTGCAATGTTTGAAGTACCAATGAAATGGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCAATTCGGTAGCAACATTCGCAACCCATCTCCACTTGAATGCATGCTT 1556


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QY 368 LeuApApMetTyrApvAlPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB 1197 TTGAACGATATTTCGACACTTTGAAAGATTGACGAGCTTGAACCTTCACTTCACTTCA 1256
QY 388 IleuYarGTTPApProSerAlaMetGluCysLeuProGluTyrMetLeuGlyValTyr 407
DB 1257 ATTAAGATGATGATTCATCATCAGAGATAGAACCTTCCAGAAATATGAAATGTGTAC 1316
QY 408 MetMetValTyrHsThrValAsnGluMetAlaArgValAlaGluValAlaGlnGlyArg 427
DB 1317 ATGCTCGTGTGAAACCTGTAATGAACTGACACAGAGGGGGAGAAAGTCAAGGGAGA 1376
QY 428 AspThrLeuAsnTyrAlaArgGluAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
DB 1377 AACCTCTCAACTATGTTGGAAGCTTGGAGGCTTATTTGATTCATATATGGAAGA 1436
QY 448 AlaYsTrpLeuAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyArg 467
DB 1437 GCAGAAATGATCTCTAATGCTTATCTGCCAATGTTGAAGTACCATGAGATGGAGA 1496
QY 468 ValSerSerAlaHsArgProCysAlaLeuGlnProIleuThrLeuAspIleProPhe 487
DB 1497 GTGAGCTCTGCATATCGCGTGAACAATGGCAACCATCTCACTTGAATGCATGGCTT 1556
QY 488 ProAspHisIleLeuLeuGluValAspPheProSerLeuAsnAspLeuIleCysAlle 507
DB 1557 CCTGATTCATCTTGAAGGAAATGATTTTCATCTCAGCTTCATGATTTGGCATCGTCC 1616
QY 508 IleuLeuArgLeuArgGlyAspThrArgCysTyrLeuValAspArgAlaArgGlyGluGlu 527
DB 1617 TTCCTTCGCTACGAGTGAACACACGCTGCTACAAAGCCGATAGGAGTCTGTGTAAGA 1676
QY 528 AlaSerSerIleSerCysTyrMetLeuAspAsnProGlyLeuThrGluAspAlaLeu 547
DB 1677 GCTTCGTATATCATGTTATATGAAAGACAATCTGATCAACCGAAGAAAGATCCCTC 1736
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeu 567
DB 1737 AATCATATCAATGCGATGCTCAATGATCAATCAAAAGAAATTAATGGAACTTAAGA 1796
QY 568 ProAspAsnSerValProIleThrSerLeuYsHisAlaPheAspIleSerArgValTrp 587
DB 1797 TCCAACGACATATTCATATGCTGCGCAAGAAACATGCTTTGACATACAAAGCTCTC 1856
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
DB 1857 CACCATCTCTACATATATCGAGATGGCTTAGTGTGCCAACAAGAAACAAAAAATTG 1916
QY 608 ValMetArgThrValIleGlu 614
DB 1917 GTTATGAAACATCTCTTGA 1937

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RESULT 11
US-09-900-797-29
Sequence 29, Application US/09900797
Publication No. US20030087406A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20030087406A1, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OR INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT APPLICATION NUMBER: US/09/900,797
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/398,395
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR FILING DATE: 1999-08-23
NUMBER OF SEQ ID NOS: 58

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-900-797-29

Alignment Scores:
Pred. No.: 6,376-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: Gaps: 7

US-10-025-145A-65 (1-618) x US-09-900-797-29 (1-2196)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 69 ATGCTCTGCTTCTATCTCACCGCTTGCGAAATCTTCCGCCAGCTGTGATC 128
QY 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB 129 AGTTCATATTCAGAACATGACCTCCCTATGAAACAAATCTTGGAAATGCGTAGG 188
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 189 CGAGGGAATGTGTACGGCTTCATGACATGATGTTGGCAGCGGCGACCTGATGAT 248
QY 56 SerValGlnArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
DB 249 GGTGTACAAAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 308
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluValAspArgLeuIle 95
DB 309 TCTCTA--TCAGCCTTATGAGGAAACCTCTTACCGAAGCGTCTGAGAGATTATTT 365
QY 96 GlyGluValLysAspIleMetPheAsnPheYsSerLeuGluAspGlyGly----- 112
DB 366 GTGAGGTAAGTAAGTA--TTCAATTCAATGATGATGATGATGATGATGATGATGAT 422
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 423 TCTTTAATGATCTCATGCAACGCTTGGATGATGATGATGATGATGATGATGATGAT 482
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 483 GCTAGACATTCAGAACGAGATTAACATGCTGTGATTAATGTTTCCGTTACTGGAG 542
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
DB 543 GAAACGCGCATTTGATGTGGAGAGACAGATTTGATCTGATCTCAACTCAACGCGTGG 602
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB 603 GGGTTTGAACCTTTCATTAACAGGGTACCTGATCTCCAGAGAGGTTTAAAGCTTTT 662
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluIleArg 210
DB 663 CAGATCAAAATGGACAGTTTGTATGCTCCCGCT--CAGACAGAGGGTGAATCAGA 719
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyLysValMetAsp 230
DB 720 AGCGTTCTTAATTATATCGGGCTTCCCTGATCTCCCTGCTGAGAAAGTTATGGA 779
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB 780 GAACTGAAATCTTCTCCACAGATATTGAAAGAAAGCTTCAAAAGATTCCAGTCTCC 839

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Qy 251 SerIleuSerIeuGluIleArgAspValIeuGluIyTrpHisThrAsnIeuPro 270
   :: ||||| ||||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 840 GCT---CTTTCACAAAGATTAAGTTGTTATGGAATATGGCTGGCACAAATTTGGCA 896
Qy 271 ArgIeuGluIleArgAsnIyTrpMetAspValPheGluIleHisThrIys-----Asn 287
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 897 AGATTGGAAGGCAAAATTAATACATAGACACACTTGAGAAAGACACAGTCATGGCTCAT 956
Qy 288 LysAsnIleIleIleGluIleuGluIleuIleIleuIleuIleuIleuIleuIleuIleu 307
   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 957 AAAAATGCTGGGAAGAGACTTTTGAACCTTGCAAAATTTGGATTCATATATTTAACTCC 1016
Qy 308 LeuGluIleuArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 327
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1017 TTACACAAAGAAAGATTAATATCTTTGAGATGGTGAAGAGATGGCATTTGGCTCTTAA 1076
Qy 328 MetThrPheCysArgHisIleArgHisValGluIyTrpIleuIleuIleuIleuIleuIleu 347
   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1077 TTGACATTTGGCTGGCAATGTCATGTGGAATTTTACACTTTGGCTCTTGTATTTGCCATT 1136
Qy 348 GluIProGlnHisSerGlyPheArgIleuGluIyPheThrIysMetSerHisIleuIleThrVal 367
   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1137 GACCCAAACATTTGCACTTACAGCTAGGCTTCCGCAAAATGTGTCACTTGTGCACAGTT 1196
Qy 368 LeuAspAspMetIyAspValPheGlyThrValAspGluIleuGluIleuPheThrAlaThr 387
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1197 TTGACATTTGTCGACACTTTTGAACGATTCGACGCTTGAACCTCTTCACTTCACTTCCA 1256
Qy 388 IleIyAsnIyTrpAspProSerAlaMetGluCysIleuProGluIyTrpMetIyGlyValIy 407
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1257 ATTAAAGATGGAATTCATCAGAGATGAAACACCTTCCAGAAATATGTAATGTGTGAC 1316
Qy 408 MetMetValIyTrHisThrIleAsnGluIleuIleuIleuIleuIleuIleuIleuIleu 427
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1317 ATGATCGTGTGTTGAACTGTAAATGAACTGACAGAGGCGGAGAGACTTCAGAGGAGA 1376
Qy 428 AspThrIleuIleuIyTrAlaArgIleuIleuIleuIleuIleuIleuIleuIleuIleu 447
   ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 1377 AACACTCTCAACTATGTTGCAAGGCTTGGAGGCTTATTTGATTCATATATGGAAGAA 1436
Qy 448 AlaIyStrpIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 467
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1437 GCAAAATGATCTCTAATGTATTCGCAATGTTGAAAGTACCATGAAATGGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaIleuGlnProIleuIleuIleuIleuIleuIleu 487
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1497 GTGAGCTCTGATATCGGTGAGCAACATTCGACACCTTCACTTGAATGCATGGCTT 1556
Qy 488 ProAspHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 507
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1557 CCTGATTAACATCTTGAAGGAAATGATTTTCCATCCAGATTCAATGATTTGGCATTCGCC 1616
Qy 508 IleIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 527
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1617 TTCTTGGCTGACAGGTGACACAGCTGTACAAAGCCGATAGGATCGTGGTGAAGAA 1676
Qy 528 AlaSerSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 547
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1677 GCTTCGCTATATCATGTTATATGAAAGACATCTGATCAACCGAAGAAAGATTCCTC 1736
Qy 548 AsnHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 567
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1737 AATCATATCATATGTCATGTCATGACATATCAAAAGATTAATTTGGAGATCTTAAAGA 1796
Qy 568 ProAspAsnSerValProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 587
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1797 TCCACACGCAATATTCATGCTGGCCAAAGAAACATGTTTGAACATCAAGAGCTCTC 1856
Qy 588 HisHisIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 607
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1857 CACCATCTCTATATATGAGATGCTTTAGTGTGTGCCAACAGAAACAAATAATTTG 1916
Qy 608 ValMetArgThrValIleGlu 614
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Db 1917 GTTATGAAACACTCTTGAA 1937
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RESULT 12
US-09-893-820-29
/ Sequence 29, Application US/09893820
/ Publication No. US20040053386A1
/ GENERAL INFORMATION:
/ APPLICANT: Chappell, Joseph
/ APPLICANT: No. US20040053386A1, Joseph P.
/ APPLICANT: Starks, Courtney M.
/ APPLICANT: Manna, Kathleen R.
/ TITLE OF INVENTION: SYNTHASES
/ FILE REFERENCE: 07678-025001
/ CURRENT APPLICATION NUMBER: US/09/893,820
/ CURRENT FILING DATE: 2001-06-28
/ PRIOR APPLICATION NUMBER: US/09/398,395A
/ PRIOR FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: 60/100,993
/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: 60/130,628
/ PRIOR FILING DATE: 1999-04-22
/ PRIOR APPLICATION NUMBER: 60/150,262
/ PRIOR FILING DATE: 1999-08-23
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 29
/ LENGTH: 2196
/ TYPE: DNA
/ ORGANISM: Abies grandis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (69)...(1949)
/ OTHER INFORMATION: myrcene synthase
US-09-893-820-29

Alignment Scores:
Pred. No.: 6,37e-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: Gaps: 7

US-10-025-145A-65 (1-618) x US-09-893-820-29 (1-2196)
Qy 1 MetValIleuSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 15
   ||||| ||||| ::||| ::||| ::||| ::||| ::||| ::|||
Db 69 ATGCTCTGTTTCTATCTCACTGCTTGCAGAACTTGGCCGCAAGTCCTTATC 128
Qy 16 SerSerSerHisGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 35
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 129 AGTTCAATTCATGAACATTAAGCTCCCTATATGAACATCCCAATCTTGGAAATCGTAGG 188
Qy 36 ProGluIySerValAlaHisSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 55
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 CGAAGGAAATCTGACGCTTCCATGACATCAGTTTGGCCACCGCTGCACCTGATGAT 248
Qy 56 SerValGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 75
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 GGTATACAAAGCCATAGGAGTACATTCATATCTGGAGCGATGATTCATACAG 308
Qy 76 SerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 95
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 TCTCTA---TCAAGCTTATGGGGAACCTCTTACAGAGACGTGCTGAGATTAAT 365
Qy 96 GlyIleuValIyAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 112
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GTGAGGTTAAAGAGATA---TTCAATTCATGATGATGATGATGATGATGATGATGATGAT 422
Qy 113 -----AsnAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 130
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 423 TCTTTATGATTCATGCAACGCTTGGATGTGATGATGATGATGATGATGATGATGATGATGAT 482
```


Pred. No.: 6,37e-249 Length: 2196
 Score: 2200.50 Matches: 427
 Percent Similarity: 80.38% Conservative: 77
 Best Local Similarity: 68.10% Mismatches: 106
 Query Match: 67.69% Gaps: 17
 DB: 15 Indels: 7

US-10-025-145a-65 (1-618) x US-10-025-145a-1 (1-2196)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
 Db 69 ATGCTCTGGTTTCTATCTCAACCGTTGGCTTCGAATCTTCGCTCGCAAGCTGTGATC 128
 QY 16 SerGSerHISGLIuIleValAlaLeuArgThrIleProThLeuGlyIleGArg 35
 Db 129 AGTTCATATTCATGAACATAGCCTCCCTATAGAACATCCCAATCTTGAATGGGTGG 188
 QY 36 ProGlySerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
 Db 189 CGAGGAAATCTGTACCCCTTCATGAGCATCACTTGGCCACCGCTGCACCTGATAT 248
 QY 56 SerValGlnArgValGlyAsnTyriSerAsnLeuTrpAspAspPheIleGln 75
 Db 249 GGTGACAAAGCAGCATAGTACTACCATTCATATCTGGGACGATGATTCATACAG 308
 QY 76 SerLeuIleSerThrProTyrgIyAlaProAspTyraArgIuArgAlaAspArgLeuIle 95
 Db 309 TCTCTA---TCAGCGCTTATGGGAGACCTCTTACAGGAACGTGCTGAGAGATTAA 365
 QY 96 GlyIuValIleAspIleMetPheAsnPheLeuSerLeuGluAspGlyGly----- 112
 Db 366 GTGAGAGTAAAGAGATA---TTCAATTCAATGTCATCTGATGATGAGAAATTATGACT 422
 QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
 Db 423 TCTTTATGATCTCATCAACGCTTGGATAGTCGATGATGAGAGTTGAGGAGATA 482
 QY 131 AspArgHisPheIleValGlyIleValSerThrAlaLeuAspTyraValAsnSerTyriTrpAsn 150
 Db 483 GCTGACATTTTCAGAACAGAGATTAACATCACTGATGATGATGATGATGATGATGAT 542
 QY 151 GlyIuValIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
 Db 543 GAAACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602
 QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyriThrValSerSerAspValLeuAsnValPhe 190
 Db 603 GGGTTTCAACTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 662
 QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
 Db 663 CAAATCAAAATGACAGCTTTGTATGCTCCCGCT---CAGACAGAGGGTGAAGTTCGA 719
 QY 211 GlyValIleuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIleValMetAsp 230
 Db 720 AGCGTTCTTAATCTATATCGGGCTTCCTCATGCTTCCTCGTGAGAAAGTTATGAA 779
 QY 231 GluAlaGluThrPheSerThrLysTyriLeuArgGluAlaLeuGluIleAspProIleSer 250
 Db 780 GAACTGAAATCTCTCCACAAGATATTGAAAGAGCTTACAAAAGATTCAGCTGCC 839
 QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyriGlyTyriPheIleThrAsnLeuPro 270
 Db 840 GCT---CTTTCACAAGATAAAGTTGTATGAAATGCTGCGACACAAATTTTGCA 896
 QY 271 ArgLeuGluAlaArgAsnTyriMetAspValPheGlyGlnHisThrLys-----Asn 287
 Db 897 AGATTGAGAGCAAAATTTACATAGACACTTGAGAAAGACACAGCGATGCTCAT 956
 QY 288 LysAsnAlaIleGluLysLeuLeuGluIleValIleLysLeuGluPheAsnIlePheHisSer 307
 Db 957 AAAATGCTGGAAAGAGCTTTTGAACCTTCAAAAATGAGATTCATATATTTAACTCC 1016

QY 308 LeuGlnIuArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
 Db 1017 TTACACAAAGAAATTTCAATATCTTTGAGATGATGATGATGATGATGATGATGATGAT 1076
 QY 328 MetThrPheCysArgHisArgHisValGluTyriTyriAlaLeuAlaSerCysIleAlaPhe 347
 Db 1077 TTGACATTGCTCGGCATCGTCATGTGGAATTCTACACTTGGCTTGTATGATTCCTCA 1136
 QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
 Db 1137 GACCCAAACATTCGCAATTCAGATGAGCTTCCCAAAAGTGTGATCTGTGCACGTT 1196
 QY 368 LeuAspAspMetTyraAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
 Db 1197 TTGAGCATTTTTCGACACTTGTGACATGTGACAGCTTGAACCTTTCATCATCTGCA 1256
 QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyriMetLysGlyValTyri 407
 Db 1257 ATTAAAGATGGAATTCATCAGATAGAACACCTTCAGAAATATATGAAATGTGTATC 1316
 QY 408 MetMetValTyriLeuThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
 Db 1317 ATGTCGTGTTGAACTGTAAATGAATGACACAGAGAGCGGAGAGACTCAAGGAGA 1376
 QY 428 AspThrLeuAsnTyriAlaArgGluAlaArgGluAlaCysPheAspSerTyriMetGlnIu 447
 Db 1377 AACCTCTCAACTATGTTCCGAAGGCTTGGAGGCTTATTTGATTCATATATGAGAA 1436
 QY 448 AlaLysTrpIleAlaThrGlyTyriLeuProThrPheGluGluTyriLeuGluAsnGlyLys 467
 Db 1437 GCAAAATGATCTCTAATGCTTATCTGCAATGTTTGAAGGTACATGAGAAATGGGAA 1496
 QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
 Db 1497 GTGAGCTCTGATATCGGTGACCAACATTCGACCCATCTTCACTTGAAGTGGCTT 1556
 QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
 Db 1557 CTTGATTCATCTTGAAGGAAATGATTTTTCATCTCAGGTTCAATGATTTGGATCGTCC 1616
 QY 508 IleLeuArgLeuArgGlyAspTrpArgCysTyriLysAlaAspArgAlaArgGlyGluGlu 527
 Db 1617 TTCCTTGGGTGACGAGGATGACACAGCGTGTACAAAGCGCATAGGATCGTGTGAAGA 1676
 QY 528 AlaSerSerIleSerCysTyriMetLysAspAsnProGlyLeuThrGluIuAspAlaLeu 547
 Db 1677 GCTTCGTATATCATGTTATATGAAAGACATCTGTGATCAACCGAAGAAATGCCCTC 1736
 QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
 Db 1737 AATCATATCAATGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1796
 QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
 Db 1797 TCCAACGACATATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1856
 QY 588 HisIleGlyTyraGlyTyraArgAspGlyTyriSerPheAlaAsnValGluThrLysSerLeu 607
 Db 1857 CACCATCTCTCAATATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1916
 QY 608 ValMetArgThrValIleGlu 614
 Db 1917 GTTATGAAACATCTCTTGA 1937

RESULT 15

US-10-025-145a-31

; Sequence 31, Application US/10025145A

; Publication No. US20030175861A1

; GENERAL INFORMATION:

; APPLICANT: Croceau, Rodney B.

; APPLICANT: Bohlmann, Joerg

; APPLICANT: Steele, Christopher L.

; APPLICANT: Phillips, Michael A.

! TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
! FILE REFERENCE: MSUR118414
! CURRENT APPLICATION NUMBER: US/10/025.145A
! PRIORITY FILING DATE: 2002-06-28
! PRIOR APPLICATION NUMBER: US 09/360,545
! PRIOR FILING DATE: 1999-07-26
! PRIOR APPLICATION NUMBER: PCT/US98/14528
! PRIOR FILING DATE: 1998-07-10
! PRIOR APPLICATION NUMBER: US 60/052,249
! PRIOR FILING DATE: 1997-07-11
! NUMBER OF SEQ ID NOS: 107
! SOFTWARE: PatentIn version 3.1
! SEQ ID NO 31
! LENGTH: 2205
! TYPE: DNA
! ORGANISM: Abies Grandis
! FEATURE:
! NAME/KEY: CDS
! LOCATION: (57)..(1943)
! OTHER INFORMATION:
US-10-025-145A-31

Alignment Scores:

Pred. No.:	1,45e-248	Length:	2205
Score:	2197.50	Matches:	427
Percent Similarity:	80.38%	Conservative:	77
Best Local Similarity:	68.10%	Mismatches:	106
Query Match:	15	Indels:	17
DB:		Gaps:	7

US-10-025-145A-65 (1-618) x US-10-025-145A-31 (1-2205)

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57 ATGCTCTGGTTTCTATCTACCGCTGGCTTCAAAATTTGCTCCGCAAGTCGTATC 116
16 SerSerSerHisGluIleLeuValLeuArgThrIleProThrLeuGlyIleCysArg 35
117 AGTTCATATTCAGAACTAAGCCCTCCCTATAGAAACAATCCCAAAATCTTGGATGCTAG 176
36 ProGlyIysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
177 CGAGGGAATCTGTCACCGCTTCATGAGCATCAGTTTGCCACCGCTGCACCTGATAT 236
56 SerValGlnArgValGlyAsnTyriSerAsnLeuTrpAspAspPheIleGln 75
237 GGTATCAAAACCATATGACTACCATTCACATATCTGGAGCATTTTCATACAG 296
76 SerLeuIleSerThrProTyriGlyAlaProAspTyriArgGluArgAlaAspArgLeuIle 95
297 TCTCTA--TCACGCAATTATGGGGAAACCTCTTACCAAGAACGCTGAGAGATTAAAT 353
96 GlyIleValIysAspIleMetPheAsnPhelysSerLeuGluAspGlyIle----- 112
354 GTGAGGGAAGAAAGAT--TTCAATTCATGTAACCTGATGATGAGAAATTAATGAT 410
113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
411 TCCCTTATATGATCTCATGCAACGCTTTGATAGCGATAGCGTTGAACGTTTGGGATA 470
131 AspArgHisPheIleValLeuGluIleLeuThrAlaLeuAspTyriValAsnSerTyriTrpAsn 150
471 GCTGACACTTTCACGAACGAGATTAACACTGCTGATTAATGTTTCCGTACTCGGAG 530
151 GluIysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
531 GAAACCGCATTTGATGTTGGAGAGACGATATGTTACTGATCTCAACTCAACGCGTTG 590
171 GlyLeuArgThrLeuArgLeuHisGlyTyriThrValSerSerAspValLeuAsnValPhe 190
591 GGGTTGGAACTCTTTCGATTCACGGGTACACTGATATCCAGAGGTTTAAAAAGCTTT 650
191 LysAspIysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210

651 CAAGATCAAAATGACAGTTGTATGCTCCCGCT--CAGACAGGGGTGAATCAGA 707
211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluValMetAsp 230
708 AGCGTTTAACTTATATTCGGGCTTCCCTCATTCCTCCCTGGTGAAGAAATGATGAA 767
231 GluAlaGluThrPheSerThrIleValLeuArgGluAlaLeuGlnIleIleProAlaSer 250
768 GAAGCTGAATCTTCCCAACAAGATTTTGAAGAAAGCTCTACAAAGATTCAGCTGCC 827
251 SerIleLeuSerLeuGluIleArgAspValLeuGluIleGlyTyriTrpHisPhePro 270
828 GCT--CTTTCACAAAGATTAAGTTGTTATGGAATGCTGGCACAAATTTGGCA 884
271 ArgLeuGluAlaArgAsnTyriMetAspValPheGlyGlnHisPheIle-----Asn 287
885 AGATTGAGACGAAATTTACATGACACACTTGAGAAAGACCAAGTCAGTGCATAT 944
288 LysAsnAlaAlaGluIleLeuLeuGluIleValLeuArgGluPheAsnIlePheHisSer 307
945 AAAAATCTGGAGAAAGCTTTTGAACCTTGCAAAATTTGAGATTCAATATATTAACTCC 1004
308 LeuGlnGluArgGluLeuValLeuValSerArgTrpTrpLysAspSerGlySerProGlu 327
1005 TTACACAAAGAAAGATTAACAATCTTTGAGATGGTGAAGAGTGGATTTGGCTTAA 1064
328 MetThrPheCysArgHisArgHisValGlyTyriTyriAlaLeuAlaSerCysAlaPhe 347
1065 TTGACATTTGCTGGCATCGTCATCGTGAATCTTCACACTTTGGCTCTGTGATTTGCCATT 1124
348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysSerSerHisPheIleThrVal 367
1125 GACCAAAACATCTTGATTCAGACTAGCGCTTCCCAAAATGTGTCAATCTTGTCACAGTT 1184
368 LeuAspAspMetTyriAspValPheGlyThrValAspGluLeuGluIlePheThrAlaThr 387
1185 TTGACAGATATTATTCAGACACTTTTGAACGATTAACAGACTTGAACCTTTCACATCTGCA 1244
388 IleLysArgTrpAspProSerAlaMetGlyCysLeuProGluTyriMetLysGlyValTyri 407
1245 ATTAAAGATGAGATTCATCAGAGATGAACACCTTCAGAAATATGAAGATGTGTAC 1304
408 MetMetValTyriHisThrValAsnGluMetAlaArgValAlaGluValAlaGlnIleArg 427
1305 ATGCTCGTGTGTAACCTGTAATGAACCTGACACAGAGCGGGAAGACTCAAGGAGAGA 1364
428 AspThrLeuAsnTyriAlaArgGlnAlaTrpGluAlaCysPheAspSerTyriMetGlnIle 447
1365 AACACTCTCAACTATGTTCCAAAGGCTTGGAGGCTTATTTGATTCATATATGAAGAA 1424
448 AlaLysTrpIleAlaThrGlyTyriLeuProThrPheGluGluIleTyriLeuGluAsnGlyLys 467
1425 GCAAAATGATCTCTATATGTTATCTGCACACGTTTGAAGATACATGAAGAAATGGGAAA 1484
468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
1485 GTGAGCTCTGATATCCCGTAGCAACATTTGCAACCTTCACCTTGAAGATCACTGCTT 1544
488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
1545 CCTGATTAACATCTGAAGGAAATGATTTTCATCCAGGTTCAATGATTTGGCATCTGCC 1604
508 IleLeuArgLeuArgGlyAspThrArgCysTyriLysAlaAspArgAlaArgGlyGluGlu 527
1605 TTCTTGGCGTCACAGAGTGAACACGCTGCTACAAAGCCGATAGAGATCGTGGAGAAA 1664
528 AlaSerSerIleSerCysTyriMetLysAspAsnProGlyLeuThrGluGluAlaPhe 547
1665 GCTTCGATATATCATGTATATGAAGACATCTGATCAACCGAAGAAAGATGCCCTTC 1724
548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567

Db 1725 AATCATATCAATGCCATGTCATGATGACATATCAAGAATTAAATTGGAACTTCTAAGA 1784
 Qy 568 ProAepaenserValProileThSerlyalysHialaPheAspIleSerArgValTrp 587
 Db 1785 TCCAAAGCAATATTCATATGCTGGCCAAAGAACATGCTTTGACATACAAAGAGCTCTC 1844
 Qy 588 HisHieglYrArgYrArgAspGlyTyrSerPheAlaasnValGluThrLysSerLeu 607
 Db 1845 CACCATCTCTACATATATCGAATGGCTTTAGTGTGCCAACAGGAAACAAAAAATTG 1904
 Qy 608 ValMetArgThrValIleGlu 614
 Db 1905 GTTATGAAACACCTCCTTGA 1925

Search completed: July 26, 2004, 22:09:45
 Job time : 737 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 16:57:24 ; Search time 5644 Seconds

(without alignments)
4745.924 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALLSTPLVSRSLSSSH.....FANVETSLVNRVYIEPVPL 618

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1p
-Q=/cgn2_1/USPRO_pool_p/US10025145/runat_23072004_092622_22889/app_query.fasta_1.775
-DB=GenBml -OPMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biolum62 -TRANS=humand4.cdi -LIST=45
-DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10025145 @CGN_1_1_5600 @runat_23072004_092622_22889 -ICPU=6
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELEXt=7

Database : GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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24: em_ph:*
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26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3251	100.0	2013	6	AR222136 Sequence
2	3251	100.0	2013	8	AGU87910
3	2456.5	75.6	1958	8	AY237645
4	2453	75.5	2018	6	BD227661
5	2453	75.5	2018	6	AR222097
6	2453	75.5	2018	6	AR240696
7	2453	75.5	2018	6	AR266971
8	2453	75.5	2018	6	AR316320
9	2453	75.5	2018	6	AR338463
10	2453	75.5	2018	6	AR429869
11	2453	75.5	2018	8	AGU87909
12	2328.5	71.6	2032	8	AF543527
13	2266.5	69.7	2162	8	AF543529
14	2264	69.6	2186	6	AR222137
15	2264	69.6	2186	8	AR339205
16	2237	67.8	2198	8	AF369918
17	2205.5	67.8	2150	8	AF369919
18	2200.5	67.7	2196	6	BD227666
19	2200.5	67.7	2196	6	AR222096
20	2200.5	67.7	2196	6	AR240701
21	2200.5	67.7	2196	6	AR266976
22	2200.5	67.7	2196	6	AR316325
23	2200.5	67.7	2196	6	AR338468
24	2200.5	67.7	2196	6	AR429874
25	2200.5	67.7	2196	8	AGU87908
26	2197.5	67.6	2205	6	AR222116
27	2163.5	66.5	2186	8	AF545330
28	2151	66.2	2100	8	AF545330
29	2137	65.7	1890	6	AR222146
30	2137	65.7	1893	6	AF139206
31	2084.5	64.1	2429	6	AR222138
32	2084.5	64.1	2429	8	AF139207
33	2046.5	62.9	3306	8	AF326517
34	2031.5	62.5	2089	6	BD227677
35	2031.5	62.5	2089	6	AR222098
36	2031.5	62.5	2089	6	AR240712
37	2031.5	62.5	2089	6	AR266987
38	2031.5	62.5	2089	6	AR316336
39	2031.5	62.5	2089	6	AR338479
40	2031.5	62.5	2089	6	AR429885
41	2031.5	62.5	2089	8	AF006193
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RESULT 1

ALIGNMENTS

AR222136 AR222136 2013 bp DNA linear PAT 26-SEP-2002
LOCUS AR222136
DEFINITION Sequence 64 from patent US 6429014.
ACCESSION AR222136
VERSION AR222136.1 GI:23329510
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2013)
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (*Abies grandis*)
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;
FEATURES
source location/Qualifiers
1..2013
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	2,03e-255	Length:	2013
Score:	3251.00	Matches:	618
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-025-145a-65 (1-618) x AR222136 (1-2013)

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QY 21 ILeuValAlaLeuArgGlyThrIleProThrIleuGlyIleCysArgProGlyIleSerVal 40
Db IITLLEVALALEUARGYTHRILEPROTHRIEUGLYILECYARGPROGLYLESSERVAL 155
QY 96 ATTAAGGCTCTCCGTAGAACATCCCACTTGGAACTGACAGCGCGGAAATCCGTC 155
QY 41 AlAlisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60
Db 156 GCGCATTCCTAAACATGTGTTTGAACAAGCTCCGATCTACTGATTCGTGACAGAGCGC 215
QY 61 ValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIleGlnSerLeuIleSerThr 80
Db 216 GTGGGCAACTATCATCTCCACCTGTGGGACGATGATTCATACAGTCTGTATCTCAACG 275
QY 81 ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyGluValIleAsp 100
Db IITPTYRGYALAPROASPTYRARGGLUARGALASPARGLEUILEGLYGLUVALILEASP 335
QY 276 CTTATGAGACGACCTGATTACCGGGAACGTGCTGACAGACTTATTTGGGGAAGTAAAGAT 335
QY 101 IleMetPheAsnPheIleSerLeuGlyAspGlyGlyAsnAspLeuLeuGlnArgLeu 120
Db 336 ATATGTTTCATTTCAAGTCCCTGGGAAGATGAGGCAATGATCTCTTCAACGACTTTTG 395
QY 121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheIleValysGluIleLeuThr 140
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QY 396 CTGCTGCATGACGTGTGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGATTAAGACG 455
QY 141 AlaLeuAspTyrValAsnSerTyrTyrAsnGluIleGlyIleGlyCysGlyArgGlnSer 160
Db 456 GCACATCATTTATGTTAAACGTTATTTGAAACGAAAAAGCATTTGATGGGAGGAGAGT 515
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180
Db 516 GTTGTGACTGACCTCAACTCAACCGCTTGGGGCTTGCACATCTCCGACTACAGGATAC 575
QY 181 ThrValSerSerAspValLeuAsnValPheIleAspIleValysAsnGlyGlnPheSerSerThr 200
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QY 201 AlaAsnIleGlnIleGluGlyIleArgGlyValLeuAsnLeuPheArgAlaSerIleu 220
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Db 876 TTTGGACGACCACTAATAAATTAAGAACCGCGGAGAACTTTTAAGAACTTGCAAAATTG 935
QY 301 GluPheAsnIlePheHisSerLeuGlnGluArgGlyLeuIleValSerArgTyrTyr 320
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QY 421 AlaGluValAsnGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCys 440
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Db 1356 TTTGATTCGATATGACGAGAAAGAAAGTGAATGCGCACTGGTTATCTGCCACGTTGAG 1415
QY 461 GluTyrLeuGluAsnGlyIleValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
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Db 1476 CTGACGTTTGAACATCCCTTCTTCGATCACAATCTCAAGAAAGTTGACTTCCCATCAAG 1535
QY 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrIleValAla 520
Db 1536 CTCAATGACTTGATATGATATCATCTTCGATTAAGAGTGAATACACGCTGTAACAAGCA 1595
QY 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAspProGly 540
Db 1596 GACAGGGCCCGTGGAGAAAGCTTCTGTATATCATGTTATATGAAGCAAAATCCCTGGA 1655
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560
Db 1656 TTAACGGAAGAGATGCTCGAATCATATCACTTCATGATCAGAGGAGCGCATATGAGAA 1715
QY 561 LeuAsnTyrGluLeuLeuLysProAspAsnSerValProIleThrSerLysIleHisAla 580
Db 1716 TTTAATTTGGAGCTTCTTAAGCCGACACAGATGTTCCATCACTTCCAAAGAAACAGCA 1775
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Db	1836	AACGTGAACAAGAGCTTTGGTAGTAGAACCCTGATTGAACCTGTGCCTTTG	1889
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DEFINITION	Abies grandis (-)-camphene synthase (Ag6.5)		mRNA, complete cds.
ACCESSION	U87910		
VERSION	U87910.1	GI:2411484	
KEYWORDS			
SOURCE	Abies grandis		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
REFERENCE	Spermatophytes; Coniferopsida; Coniferales; Pinaceae; Abies.		
AUTHORS	Bohlmann, J., Steele, C.L. and Croteau, R.		
TITLE	Monoterpene synthases from grand fir (<i>Abies grandis</i>). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase		
JOURNAL	J. Biol. Chem.	272 (35),	21784-21792 (1997)
MEDLINE	97413772		
PUBMED	9268308		
REFERENCE	2 (bases 1 to 2013)		
AUTHORS	Bohlmann, J., Phillips, M., Ramachandiran, V., Katoh, S. and Croteau, R.		
TITLE	cDNA cloning, characterization, and functional expression of four new monoterpene synthase members of the ltpad gene family from grand fir (<i>Abies grandis</i>)		
JOURNAL	Arch. Biochem. Biophys.	368 (2),	232-243 (1999)
MEDLINE	99373092		
PUBMED	10441373		
REFERENCE	3 (bases 1 to 2013)		
AUTHORS	Bohlmann, J., Steele, C.L. and Croteau, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-JAN-1997) Institute of Biological Chemistry,		
	Washington State University, Clark Hall, Pullman, WA 99164-6340,		
	USA		
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ALIGNMENT SCORES:			
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Score:	3251.00	Matches:	618
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0
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DB	96 ATTAAAGCTCTCCGAGAACATATCCCACTTTGGAAATCTGACAGCCGGGAAATTCGCTC	155	
QY	41 AlaHisSerIleAsnMetCysLeuThrSerValAsnThrAspSerValGlnArg	60	
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DB	216 GTGGGCACTATCATCTTCACACCTGGGACCATATTCATACAGCTCTGATCTCAACG	275	
QY	81 ProThrGlyValAspAspThrArgGluArgIleAspArgLeuIleGlyValLysAsp	100	
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QY	121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysValGluIleLysThr	140	
DB	396 CTGGCGATGACGTTGAAACGTTTGGGAATCACAAGCATTTCAAAAAAGATAAAAACG	455	
QY	141 AlaLeuAspTryValAsnSerTryThrAsnGluLysGlyIleGlyCysArgLysSer	160	
DB	456 GCACTCGATTATGTTAACAGTTATTGAAACAAAAGGCAATGGATGGAGGAGGAGAGT	515	
QY	161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr	180	
DB	516 GTTGAGACTGACCTCACTCACTCAACCGCCTTGGGCTTGGAACTCTCCGACTACAGATAC	575	
QY	181 ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr	200	
DB	576 ACTGTGCTTCAGATGTTTGAAGTITTTAAAGACAAAATGGGCAATTTTCTCCACT	635	
QY	201 AlaAsnIleGlnIleGluGlyGluIleArgGlyValLeuAsnLeuPheArgAlaSerLeu	220	
DB	636 GCCAATATTCAGATAGAGGAGAGATTAAGAGGCTTCTCAATTTATTCAGGCGCTCCCTC	695	
QY	221 ValAlaPheProGlyGluLysValMetAspGluValGluThrPheSerThrLysTyrLeu	240	
DB	696 GTCCGCTTTCCCGCGAGAAAGTTATGATGAACTGAACATTTCTTACAAATATTTTA	755	
QY	241 ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal	260	
DB	756 AGAAGAGCCCTGCAAAAGATTCGCGCATTCACGATATCTTCACTAGAGATACGGGAGCTT	815	
QY	261 LeuGluLysArgLysThrAsnLeuProArgLeuGluValArgAsnTyrMetAspVal	280	
DB	816 CTGAAATATGGTTGGCACACCAATTTGCCACGCTTGGAAACCAAGAAATTCATGAGAGCTC	875	
QY	281 PheGlyGlnHisThrLysAsnLysAsnAlaAlaGluLysLeuLeuGluAlaLysLeu	300	
DB	876 TTGAGACAGCACTAAATAATAGAACCGCCCGAGAACTTTTAAACTTGCAAAATTG	935	
QY	301 GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrp	320	
DB	936 GAATTCATATATATTCACCTCTTACAGAGAGAGATTTAAAAATGTTTCCCGATGCTGG	995	
QY	321 LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluGluTyrTyrAla	340	
DB	996 AAGACCTCGGTTCTCTGAGATGACCTTCTGTGACATGTGTACCGTAATCTACAGCT	1055	

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QY 381 LeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro 400
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QY 441 PheAspSerTrpMetGlnGluAlaLysTrpIleAlaThrGlyLysProThrPheGlu 460
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Db 1536 CTCAATGACTGATATGATATGATATCTTGGATTAAGAGTGAATACCGGTGCTTACAGGCA 1595
QY 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTrpMetLysAspAsnProGly 540
Db 1596 GACAGGGCCCGTGGAGAAAGGACTTCGCTATATCATGTTATATCAAGAACATCTCGA 1655
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleLeuAsnPheMetIleArgAspAlaIleArgGlu 560
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QY 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1836 AACGTTGAACAAAGATTGTGTATGAGAACCGTCATTTGAACCTGTCCCTTTG 1889

RESULT 3
AY237645 1958 bp mRNA linear PLN 13-SEP-2003
LOCUS AY237645
DEFINITION Picea sitchensis pinene synthase mRNA, complete cds.
ACCESSION AY237645
VERSION AY237645.1 GI:34582666
KEYWORDS
SOURCE
ORGANISM Picea sitchensis (Sitka spruce)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE 1 (bases 1 to 1958)
AUTHORS Bryan McKay,S.A., Hunter,W.L., Goddard,K.A., Wang,S.X., Martin,D.M., Bohlmann,J. and Plant,A.L.
TITLE Insect Attack and Wounding Induce Traumatic Resin Duct Development and Gene Expression of (-)-Pinene Synthase in Sitka Spruce

JOURNAL Plant Physiol. 133 (1), 368-378 (2003)
PUBMED 12970502
REFERENCE 2 (bases 1 to 1958)
AUTHORS Bryan McKay,A.S., Hunter,W.L., Goddard,K.A., Wang,S.X., Martin,D., Bohlmann,J. and Plant,A.L.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-2003) Biology, Simon Fraser University, 8888 University Drive, Burnaby, BC V5A 1S6, Canada
location/Qualifiers
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VLNLNIRASLIAPFDEKYMBAEAFSAKYLEBSLQKLSVSLQSEIRDLVLEGMHTYLP
RMEARNHIDVFGDPTONSKSCINTEKLELAKLEFNIHSLQKLELYLVWMKDSGS
POMTFCRHREVEYTLASCIAPFQSHGFLGFAKCHILITLIDMDYDTGTVDLRL
FTAMKMRDPSADCDLPEVMGAYLILYDVTNTPRAEKAQGRDITLVARAMDVYL
DSYQEKXWATATCTLPPTPAEYENGRKISSHRSLAOPITMDPFPPLHLKVDPS
KLNDAALILRLKQTRCYRADRRAGEASISCTYKMDQGAETEDLADHNMTISV
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VTL"

ORIGIN
Alignment Scores:
Pred. No.: 1.17e-190 Length: 1958
Score: 2456.50 Matches: 473
Percent Similarity: 84.79% Conservative: 62
Best Local Similarity: 74.96% Mismatches: 79
Query Match: 75.56% Indels: 17
DB: Gaps: 7

US-10-025-145A-65 (1-618) x AY237645 (1-1958)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 75 ATGCTCTGCTTCTTGTGGCCTTATGCTTCCAGATCATCTCGCACAATCGTTGAC 134
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 135 AGTTCGCTCAACGAGCTTAAGACGATCGTGAACAATCCCAACTCTTGGAAATGCTAAG 194
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysIleuThrSerValAlaSerThrAsp 55
Db 195 CGAGAAAAATCTGGACGCTTCTATAGCATGAGTTGACCACTGATTCATGATGAT 254
QY 56 SerValGlnArgArgValGlyAsnTrpHisSerAsnLeuTrpAspAspPheIleGln 75
Db 255 GGTGTACAAAGCGGATGGCGATTTCCATTCCAACTTACGACGATGATTCATACAG 314
QY 76 SerLeuIleSerThrProTrpGlyAlaProAspTrpArgGluArgAlaAspArgLeuIle 95
Db 315 TCTCTC--TCAACGTCTATAGGGAACCTTCTTACCGGGAACGAGCTGAGACTGATT 371
QY 96 GlyValValLysAspIleMetPheAsnPheLysSerLeuGluAspArgLys----- 111
Db 372 GGGGAAGTAAAGAG--ATGTTAAATTCATATGATCGGAAGCGGAGACTTAATACAGT 428
QY 112 ---GlyAsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 429 CCCCAATATATCTCATTCACGCGCTTGGATGATGATGATGATGAAAGTTTGGAGATA 488

Query Match: 75.45% Indels: 16
DB: 6 Gaps: 6
US-10-025-145a-65 (1-618) x BD227661 (1-2018)

1 MetalaleuSer11ethProleuValSerArgSerCysIleu----- 15
6 ATGGCTTAGTTCCTACCGCACCGTGGCTTCCAAATCATGCTCCGACAAATCGTTGATC 65
16 SerSerSerHsgluileValaleuArgThrIleProthrIleGluileCysArg 35
66 AGTCTACCCATGAGCTTCCTCTAGAACATTCAGAGCTTGAAGATAGTAGG 125
36 ProGluYSerValAlaHisSer11eAsnMetCysIleuThrSerValAlaSerThrAsp 55
126 CGAGGAAATCTATCATCTCTTCATCAGCATGAGCTTACACCGTTGTAAACGATGAT 185
56 SerValGlnArgArgValGlyAsnTYrHisSerAsnIleuTPaPaPaPaPheIleGln 75
186 GGTGTACGAGACCATGGCGGATTTCCATTCAAACCTCTGGAGCATGATGTCATACAG 245
76 SerIleuIleSerThrProTYrGlyAlaProAspTYrArgIuArgAlaAspArgIleu 95
246 TCTTTA--CCAAAGCGCTTATGAGGAAATCGTACCTGAGCGGTGAGAACTGATC 302
96 G1YgluValIYsAsp11eMetPheAsnPheIYsSerIeuGluAspGlyIY----- 112
303 GGGGAAGTAAAGAAC--ATGTTCAATTCGATGTCATTAGAACATGAGACTTAATGAGT 359
113 -----AsnAspIleuGlnArgIleuIleuValAspAspValGluArgIleuIYle 130
360 CCGCTCATGATCATTCATTCACAGCGCTTGGATGTCGACACCTTGAACGTTGGGGATC 419
131 AspArgHisPheIYsIYsGluileYserThrAlaIeuAspTYrValAsnSerTYrTrpAsn 150
420 CATGACATTCCTCAAGATGAGATAAATCGGCGCTGATTAGTTACAGATTATGGGCG 479
151 G1YleuGlyIleG1YCySG1YArgG1YSerValIYThrAspIleuAsnSerThrAlaIeu 170
480 GAAATAGGCAATCGATGGGAGGAGAGGTGTGTACTGATCGAATCAACGCGGTG 539
171 G1YleuArgThrIleuArgIleuHisG1YTYrThrValSerSerAspValIleuAsnValPhe 190
540 GGGCTTGGAACCTTACGACTACAGGATACCGGCTGCTTCAGATGTTTTCMAAGCTTTC 599
191 IYsAspIYsAsnG1YIleuPheSerSerThrAlaAsnIleG1YIleGluIleArg 210
600 AAAGGCCAAATGGGCGAGTTTCTGCTGAAATATTCAGACAGATGAAGATCAGA 659
211 G1YValIleuAsnIleuPheArgAlaSerIleuValAlaPheProG1YGluIYsValMetAsp 230
660 GGCCTTCGAATTTATTCGGGCGCTCCCTCATGCTTTCAGGGGAGAAATATGAT 719
231 G1uAlaGluThrPheSerThrIYerTYrIleuArgGluAlaIeuGluIYsIleProAlaSer 250
720 GAGGCTGAAATCTTCTCTCAAAATATTAAAGAAAGCCCTGCAAAAGATTCGCGTCTCC 779
251 Ser11eIleuSerIleuGluIleArgAspValIleuGluTYrGlyTYrPheIleThrAsnIleuPro 270
780 AGT---CTTTCGCAAGATCGGGAGCTTTGGAAATGGTGTGGACACATATTTGGCG 836
271 ArgIleuGluAlaArgAsnTYrMetAspValPheG1YIleIleIleIleIleIleIleIleIle 290
837 CGATTGGAGCAAGAAATTAATCAACAAGTCTTTGGACAGACATCGAAGAACAGCA 896
291 -----AlaGluIYsIleuIleuGluIleuAlaIYsIleuGluIleuPheAsnIlePheHisSer 307
897 TATGTGAAGCAAAATCTTTAGAACTCCCAAAATTTGAGTTCAACATCTTTCAATCC 956
308 IeuGlnGluArgGluIleuIleuHisValSerArgTYrPheIYsAspSerG1YSerProGlu 327
957 TTACAAAGAGGAGTTAGAAAGTGTGTGTCAGATGGTGGAAAGATCGGGATTTCTTGAG 1016

328 MetThrPheCysArgHisValGluTYrTYrAlaIleuAlaSerCysIleAlaPhe 347
1017 ATGACCTTTCGCGACATCGTCAAGTGAATATCACTTGTGGCTTCGTCGATTCGCTTC 1076
348 GluProGluHisSerGlyPheArgIleuGlyIlePheThrIYsMetSerHsgluileThrVal 367
1077 GAGCTCAACATTCCTGATTCAAGCTCGGCTTTCGCAAGACGTGTCAATCTATACGGTT 1136
368 IeuAspAspMetTYrAspValIlePheG1YThrValAspGluIleuGluIleuPheThrAlaThr 387
1137 CTTCACATATGATGACGACACCTTCGGACAGTAGACAGGCTGGAACCTTCACAGCGACA 1196
388 I1eYsArgTYrAspProSerAlaMetGluCysIleuProGluTYrMetIYsGlyValTYr 407
1197 ATGAAGAGATGGGATCGGTCTCGATGATGATGCTTCAGAAATATTAAGAAAGAGTGTAC 1256
408 MetMetValTYrHisThrValAsnGluMetAlaArgValAlaGluIYsAlaGlnG1YArg 427
1257 ATACGGGTTTACGACACCGTAATGAATGGCTCGAGAGCGAGGAGCTCAAGGCCGA 1316
428 AspThrIleuAsnTYrAlaArgGlnAlaTrpGluAlaCysPheAspSerTYrMetGlnGlu 447
1317 GATACGCTCACATATGCTCGGAAAGCTTGGAGGCTTATATGATTCGTATATGCAAGAA 1376
448 AlalYsTrpIleAlaThrGlyTYrIleuProThrPheGluGluIYrIleuGluAsnGlyIYs 467
1377 GCAAGGTGATCGGCACTGGTTACCTGCCCTTGTATGATGATGATGATGATGATGATGATG 1436
468 ValSerSerAlaHisArgProCysAlaIleuGlnProIleuThrIleuAspIleProPhe 487
1437 GTTAGCTGTGTATCCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 1496
488 ProAspHisIleuIYsGluValAspPheProSerIYsIleuAsnAspIleuIleCysIle 507
1497 CTGTATATATCTCCCAAGAAAGTGAATCTCCATCAAAAGCTTAACGATTCGATTCGATTC 1556
508 I1eIleuArgIleuArgGlyAspThrArgCysTYrIYsAlaAspArgAlaArgGlyIleGlu 527
1557 ATCTTCGATTAAGAAGTGTATACGGGTGCTACAAAGCGGAGCGCTCGGAGAAAGAA 1616
528 AlaSerSerIleSerCysTYrMetIYsAspAspProGlyIleuThrGluIYsAspAlaIleu 547
1617 GCTTCCTTATATCATTTATATGAAGAACATCTGAGATATCAGAGAAAGATGCTCTC 1676
548 AsnHisIleAsnPheMetIleArgAspAlaIleArgIleuIleuAsnTYrGluIleuIYs 567
1677 GATCATATCAACCGCATGATCAAGTGAATATCAAAAGATTTAAATTTGGAACTTCCTCAA 1736
568 ProAspAsnSerValProIleThrSerIYsIYsHisAlaPheAspIleSerArgValTrp 587
1737 CCAAGACATCAATGTTCCCATCTCGCGAAGAAACATCTTTTGACATCGCGACAGCTTTC 1796
588 HisIleGlyTYrArgTYrArgAspGlyTYrSerPheAlaAsnValGluThrIYsSerIeu 607
1797 CATTAAGCTTCAAAATACGAGACGGCTTACAGGCTTCCAAAGTGAAGAAAGATTTG 1856
608 ValMetArgThrValIleGluProValProIleu 618
1857 GTCAAGAAACCTCTTGAATCTGTGCTTTG 1889
RESULT 5
AR222097 2018 bp DNA linear PAT 26-SEP-2002
LOCUS AR222097
DEFINITION Sequence 3 from patent US 649014.
ACCESSION AR222097
VERSION AR222097.1 GI:23329471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (*Abies grandis*)

JOURNAL Patent: US 6429014-A 3 06-AUG-2002;
 FEATURES Location/Qualifiers
 SOURCE 1. 2018
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.:	2,346-190	Length:	2018
Score:	2453.00	Matches:	475
Percent Similarity:	84.63%	Conservative:	59
Best Local Similarity:	75.28%	Mismatches:	81
Query Match:	75.45%	Indels:	16
	Gaps:		6

US-10-025-145a-65 (1-618) x AR222097 (1-2018)

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1  MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
6  ATGCTCTAGATTCTACCGCACCGTTGGCTTCCAAATATGCTGCACAAATCGTTATC 65
16  SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
66  AGTTCTACCCATGAGCTTAAGCTCTCTAGAACAAATTCAGAGCTCTAGAAATGAGTAGG 125
36  ProGluIysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
126  CGAGGGAATATATCACTCTTCCATCCAGATGAGCTTACCAACCGTTGTAACCATAT 185
56  SerValGlnArgValGlyValAsnThrIleSerAsnLeuThrAspAspPheIleGln 75
186  GGTGTACCAAGCGATGCGGATTCATTCCTGAGACCTTGGAGCATGATGTCATACG 245
76  SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
246  TCTTTA---CCACGGCTTATGAGGAAATCGTACCTGAGCGGTGAGAACTGATC 302
96  GluIleValIysAspIleMetPheAsnPheIysSerLeuGluAspGlyIle----- 112
303  GGGGAGGAAAGAAC--ATGTTCAATTCGATGTCATTAGAAAGATGAGAGCTTAATGAGT 359
113  -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
360  CCGCTCATATGATTCATTCAACGCTTTGATGTCGACAGCTTGAACGTTTGGGATC 419
131  AspArgHisPheIysGlyIleValSerThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
420  CATAGACATTTCAAAAGATGAGATAAATCGCGCTGATTAATGTTTACAGTTATTGGGAC 479
151  GluIysGlyIleGlyCysGlyValArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
480  GAAATGCGCATCGATGCGGAGGAGAGTGTGTACTGATCTGAACTCAACCTGCGGTG 539
171  GluLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
540  GGGCTTGAACCTTCAACATCAACGATACCGGCTGCTTCCAGATGTTTCAAAAGCTTTC 599
191  LysAspIysAsnGlyIlePheSerSerThrAlaAsnIleGlnIleGluIleArg 210
600  AAAAGCCAAATGGGAGGTTTCTGCTGCTGAAATATTCAGACAGATGAGAGATGACGA 659
211  GluValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGluIleValValMetAsp 230
660  GGCCTTTCGAATTTATTCGCGGCTCTCCCTCATTCGCTTTCCAGGGGAGAAATTAATGAT 719
231  GluIleGluThrPheSerThrIleValArgGluAlaLeuGlnIleValIleProAlaSer 250
720  GAGGCTGAAATCTTCTTCAACCAATATTTAAAGAAAGCCCTGCAAAAGATTCGGTCTCC 779
251  SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
780  AGT---CTTTCGAGAGATCGGGGACGTTTGGAAATGATGTGGCAACATATTTGCGG 836
  
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271  ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrIysAsnIysAsnAla 290
837  CGATTGGAGACGAAATTTACATCCAACTCTTTGGACGAGACCTGAGAAACAGACATCA 896
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897  TATGGAAGACGAAATAAATTTTAGAACTGCAAAATGAGATTCACATCTTTCAATCC 956
308  LeuGlnGluArgGluLeuValSerArgThrIlePheIleValSerCysIleAlaPhe 327
957  TTACAAAGAGAGGATTAAGAAAGTGTGTCAGATGCGGAAAGAAATCGGTTTTCCTAG 1016
328  MetThrPheCysArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
1017  ATGACCTTCTCCGACATCGTCACGTGAAATCTACCTTTGGCTCTTCCATTCGCTTC 1076
348  GluProGlnHisSerGlyPheArgLeuGlyPheThrIysMetSerHisLeuIleThrVal 367
1077  GAGCTCAACATTCGATTCAGACTGCGCTTGGCAAGACGTGTCATCTTATCACGGTT 1136
368  LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
1137  CTTCAGATATGTCACACCTTGGCAGCTAGACGAGCTGAACTTTCACACGCA 1196
388  IleIysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetIysGlyValTyr 407
1197  ATGAAAGATGGATTCGCTCTCGATGATGCTTCCAAATATATTAAGAGAGTATC 1256
408  MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluIysGlnIleArg 427
1257  ATAGCGGTTTACGACCGCTTAATGAATGCTGAGAGGAGAGAGGCTCAAGGCCGA 1316
428  AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnIle 447
1317  GATACGCTCAATATGCTCGGAGAGCTTGAATGATTTGATTTCTTAATGCAAGAA 1376
448  AlaIysTrpIleAlaIleAsnGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyIys 467
1377  GAAAGATGATGCGACCTGTTACTGCTCTTGAATGAGTACTGAGAAATGGGAAA 1436
468  ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrIleAspIleProPhe 487
1437  GTTAGCTGTGTCATCGCATATCCGATTCGCAACCATTCGACAAATGAGATCCCTTT 1496
488  ProAspHisIleLeuIysGluValAspPheProSerIysLeuAsnAspLeuIleCysIle 507
1497  CCTGATCATATCCCAAGAAAGTGAATCCCATCAAAAGCTTAAACGACTTGGCAATGCC 1556
508  IleLeuArgLeuIysGlyAspThrArgCysThrIysAlaAspArgAlaArgGlyGluGlu 527
1557  ATCCTTCGATTAACAGATGATACCGGATGCTAAGAGCGGACGAGCTCGTGGAGAAAGA 1616
528  AlaSerSerIleSerCysTyrMetIysAspAsnProGluIleThrGluIleAspAlaLeu 547
1617  GCTTCTCTATATCATGTTATATGAAGACAAATCTGAGATATCAGAGAAAGATGCTCTC 1676
548  AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuIys 567
1677  GATCATATCAACGGCAATGATGACGTATCAAAAGATTAATTTGGAACTTCTCAA 1736
568  ProAspAsnSerValProIleThrSerIysIysHisAlaPheAspIleSerArgValTrp 587
1737  CCAAGATCAATATGTTCCATCTCGCGAAGAAACATGCTTTTGACATGCGACAGCTTTC 1796
588  HisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrIysSerIle 607
1797  CATTAAGGCTTCAATATCCGAGACGGCTACAGCGTTCACAGTGAACGAAGAGTTTG 1856
608  ValMetArgThrValIleGluProValProLeu 618
1857  GTCAAGAAACCTTCCTTAATCTGTGCTTTG 1889
  
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RESULT 6

AR240696
LOCUS AR240696 2018 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 19 from patent US 6468772.
ACCESSION AR240696
VERSION AR240696.1 GI:27285845
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLES Methods of making modified polypeptides
JOURNAL Patent: US 6468772-A 19 22-Oct-2002;
FEATURES
source 1. 2018
/organism="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 2,34e-190 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
Gaps: 6
DB: 6
US-10-025-145A-65 (1-618) x AR240696 (1-2018)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTTAGTTCCTTACCGCACCGCTTGCTTCAAAATCATGCTGCACAAATCGTGTATC 65
QY 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrIleGluIleCysArg 35
Db 66 AGTCTACCCCATGAGCTTAAGGCTCTCTTAAGAACAAATCCAGCTTACGAGATGAGG 125
QY 36 ProGluYSerSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATCATCCTCTTACGATGAGCTTACACCGTTGTAACCGATGAT 185
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Db 186 GGTGTACGAAGACCATGGCGGATTCATTCACACCTTGGGAGCATGATGTCATCAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA--CCAAAGGCTTATGAGAAAAATCGTACCTGGAGCGTGTGAGAAATGATC 302
QY 96 GluGluValIlyAspIleMetPheAsnPheYSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTGCATGTCAATTAGAAAGATGGAATTAATAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATATGTCATTCACAGCGCTTGTGATTCGACAGCTTGAACGTTTGGGATC 419
QY 131 AspArgHisPheYslyGluIleYSerThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATGACATTTCCAAAGATGAGATAAATCGGCGCTTGTATTTTACAGTTATTTGGGC 479
QY 151 GluYslyGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
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QY 171 GluLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTGAACCCCTACGACTACCGGATACCGGATGCTTCCAGATGTTTTTCAAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210
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QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGluGlyIlyValMetAsp 230
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QY 231 GluAlaGluThrPheSerThrIlySerYLeuArgGluAlaLeuGlnIlyIleProAlaSer 250
Db 720 GAGGCTAAATCTTCTTACCAATATTATTAAGAACCCCTGCAGAAAGATTCGGCTTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluIlyTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGGAGAGATCGGGAGCTTTTGGAAATAGTGTGACACATATTTCGCG 836
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QY 291 -----AlaGluYsLeuLeuGluIleValAlaYsLeuGluIlyPheAsnIlePheHisSer 307
Db 897 TATGTGAAGACCAAAATTTTAAAGACTGCAAAATTTGAGTTCAATCTTTCAAATCC 956
QY 308 LeuGlnGluArgGluLeuYsHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
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QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
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QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrIlyMetSerHisGluIleThrVal 367
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QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuYs 567
Db 1677 GATCATATCAACCGCATGATCAAGTGAATCAAAAGATTTAAATTTGGAACTTCTCAA 1726
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Db 1737 CCAGACATCATGTCCTCCATCTCCGCGAAGAAACATGCTTTGACATGCCAGAGCTTTC 1796
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Db 1797 CATTACGGCTCAATATCCGAGACGGCTACAGCGTTGCCAACGTTGAACAGAGTTTG 1856
Qy 608 ValMetarGthrValIleGluProValProleu 618
Db 1857 GTCACGAGAACCTTCCTGAATCTGTGCTTGG 1889

RESULT 7
LOCUS AR266971 2018 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 19 from patent US 6495354.
ACCESSION AR266971
VERSION AR266971.1 GI:29696426
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unpublished.
1 (bases 1 to 2018)
AUTHORS Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLE Syntheses
JOURNAL Patent: US 6495354-A 19 17-DEC-2002;
FEATURES Location/Qualifiers
SOURCE 1. 2018
/organism="unknown"
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ORIGIN
Alignment Scores:
Pred. No.: 2,346-190 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 6 Gaps: 6

US-10-025-145a-65 (1-618) x AR266971 (1-2018)

Qy 1 MetAlaLeuSerLeuSerLeuThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTTACGTTTACCGCACCGCTTCCCAATATGCTCTGCACAAATCGTATC 65
Qy 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTCTACCCATGAGCTTAAGCTCTCTCTAGAACAAATTCAGCTCTGAGATGAGTGG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTTACCTCTTCATCAGACAGCTTACACCGTTGTAACGATGAT 185
Qy 56 SerValGlnArgArgValGlyAsnThrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTCTACGAAGACCGATGGCGATTTCCATTCCAACCTTCGGACGATGATCATACG 245
Qy 76 SerLeuIleSerThrProIleValAlaProAspIleArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAAAGCGCTTATGAGAAATAATCTACCTGAGCGTGTGAGAAACTGATC 302
Qy 96 GluGluValIleAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
Db 303 GGGGAATTAAGAAC---ATGTTCAATTCGATGTCATTAGAAAGATGGAGACTTAATAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATTCATTCAACGCGCTTTGATGTGCGACAGCTTGAACGTTTGGGATC 419
Qy 131 AspArgHisPheLysValGluIleLysThrAlaLeuAspIleValAsnSerTyrTrpAsn 150
Db 420 CATGACATTTTCAAAAGATGAGATAAATCCGCGCTTGTATATGTTTACAGTTATTGGGCGC 479

Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
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Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTGCAACCTTACGACTACAGCATACCGGATCCGGGTCTTCAGATGTTTCAAACTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluLeuArg 210
Db 600 AAAGGCCAAATGGCGAGTTTCTGCTCGTGAATAATATTCAGACAGATGAAGATCGAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
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Qy 251 SerLeuLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleAsnLeuPro 270
Db 780 AGT---CTTTCGCGAGAGATCGGGAGCGTTTGGAAATATGTTGGCACACATATTGGCG 836
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Db 837 CGATTGGACGACGAATTTACATCCAAAGTCTTGGACGAGCACTGAGAACACGAACTCA 896
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Db 897 TATGGAAGACCAAAAATCTTTAGAACTCGCAAAATTTGAGATTCAATCTTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpIleLysAspSerGlySerProGlu 327
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Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
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Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
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Qy 368 LeuAspAspMetCysArgAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
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Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaIleTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
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Qy 448 AlaLysTrpIleAlaIleThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
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Db 1497 CCGATATATATCCCAAGGAAGTTGACTTCCCATCAAGCTTAAACGACTTGCGATGGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527

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Db 1617 GCTTCCTCTATATATATGTATATATAAGACATCTGGAGATCATAGATAGAGAAAGATGCTTC 1676
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RESULT 8
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LOCUS Sequence 19 from patent US 6559297.
DEFINITION AR316320
ACCESSION AR316320
VERSION AR316320.1 GI:31711055
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappel,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Synthesizes
JOURNAL Patent: US 6559297-A 19 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..2018
/organism="unknown"
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Score: 2453.00 Matches: 475
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Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: Gaps: 6

US-10-025-145A-65 (1-618) x AR316320 (1-2018)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
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Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
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Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGAAATCTATACATCTCTTCATCAGATGAGCTTACACCGTTGTAACGATGAT 185
Qy 56 SerValGlnArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTAGCAACACCGATGGGCGATTCATTCAACTCGGAGCATGATGATCATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyValaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAAAGGCTTATGAGAAATAATCTGACTGAGGCGTGTCTGAAGAACTGATC 302

Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
Db 303 GGGAGAGTAAAGAAC---ATGTTCAATTCCGATGATCATTAAGATGAGATTATAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
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Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLleAsnValPhe 190
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Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
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Qy 231 GluValGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
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Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLleuIleThrVal 367
Db 1077 GAGCTCAACATTTTGAATTCAGACTCGGCTTTGCCAAGAGCTCATCTTATACGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1137 CTTAGCATATATGATGACACCTTCGGACAGTACAGGAGCTGGAACCTTTCACAGCGCAGA 1196
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
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Db 1257 ATACGGCTTTACGACACCGTAAATGAATGAGCTTGAAGGACAGGAGGCTCAAGGCCGA 1316
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATGCTCGGAAGCTTGGAGGCTTATATGATTCGTATATGCAAGAA 1376
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Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleGlyIle 507
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Qy 508 IleLeuArgLeuAspGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1557 ATCTTGCTGATTAACGAGTGATACCGGCTGCTTCAAGGCGGACGGGCTCGTCGAGAAATA 1616
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Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCAAGAGAACCTTCCTTGAATCTGTGCTTTG 1889

RESULT 9
AR338463
LOCUS AR338463 2018 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 19 from patent US 6569656.
ACCESSION AR338463
VERSION AR338463.1 GI:33725240
KEYWORDS
SOURCE
ORGANISM Unknown.
UNCLASIFIED.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLE Syntheses
JOURNAL Patent: US 6569656-A 19 27-MAY-2003;
FEATURES
SOURCE Location/Qualifiers
1..2018
/organism="unknown"
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ORIGIN
Alignment Scores: 2,34e-190 Length: 2018
Pred. No.: 2453.00 Matches: 475
Score: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: Gaps: 6

US-10-025-145A-65 (1-618) x AR338463 (1-2018)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTACCGCACCGTGGCTTCAAAATATGCTGCGACAAATCGTGTATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
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Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
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Db 303 GGGGAAGTAAGAAC---ATGTTCAATTCATGTCATTGAAAGATGAGAGTAATAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
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DB 1857 GTCAAGAAACCTCCTGAATCTGTGCTTTG 1889

RESULT 10
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DEFINITION Sequence 19 from patent US 6645762.
ACCESSION AR429869
VERSION AR429869.1 GI:40190267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Synthesizes
JOURNAL Patent: US 6645762-A 19 11-NOV-2003;
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Alignment Scores:
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Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16

DB: 6 Gaps: 6
US-10-025-145a-65 (1-618) x AR429869 (1-2018)
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QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGluIleCysArg 35
DB 66 AGTTCTAACCATGAGCTTAAGGCTCTCTAGAAACATTCACAGCTTAGGAATCAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
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QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
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QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB 246 TCTTTA---CCACGCGCTTATGAGGAATAATCGTACCTGAGCGCTGAGAAATCATC 302
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
DB 303 GGGGAAGTAAAGAAC---ATGTTCAATTGATGCATTTAGAGATGAGAGTTAATGAT 359
QY 113 -----AsnProLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATTCATTCACACGCTTGATGATTCACAGCCTTGAAACGTTTGAGGATC 419
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QY 151 GluLysGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
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QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
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 ACCESSION U87909
 VERSION U87909.1 GI:2411482
 KEYWORDS
 SOURCE Abies grandis
 ORGANISM Abies grandis
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferales; Piniferales; Pinaceae; Abies.
 REFERENCE 1 (bases 1 to 2018)
 AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.
 TITLE Monoterpene synthases from grand fir (Abies grandis). cDNA

isolation, characterization, and functional expression of myrcene
 synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene
 synthase
 JOURNAL J. Biol. Chem. 272 (35), 21784-21792 (1997)
 MEDLINE 97413772
 PUBMED 9268308
 REFERENCE 2 (bases 1 to 2018)
 AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.
 TITLE Direct Submission
 JOURNAL Submitted (31-Jan-1997) Institute of Biological Chemistry,
 Washington State University, Clark Hall, Pullman, WA 99164-6340,
 USA

FEATURES

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ORIGIN

Alignment Scores:

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US-10-025-145A-65 (1-618) X AGUS7909 (1-2018)

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 Pinus taeda
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 1 (bases 1 to 2082)
 Creteanu, M.A., Wildung, M.R., Williams, D.C., Hyatt, D.C. and
 Creteanu, R.
 cDNA isolation, functional expression, and characterization of
 (+)-alpha-pinenes synthase and (-)-alpha-pinenes synthase from
 loblolly pine (Pinus taeda): Stereoccontrol in pinene biosynthesis
 Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
 JOURNAL
 MEDLINE
 PUBMED 12623076
 2 (bases 1 to 2082)
 Creteanu, M.A., Wildung, M.R., Williams, D.C. and Creteanu, R.B.
 Direct Submission
 Submitted (09-SEP-2002) Institute of Biological Chemistry,
 Washington State University, PO Box 646340, Pullman, WA 99164-6340,
 USA
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VERSION AF543529.1 GI:28894485
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ORGANISM Pinus taeda
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REFERENCE 1 (bases 1 to 2162)
Phillips,M.A., Wildung,M.R., Williams,D.C., Hyatt,D.C. and Croteau,R.
TITLE cDNA isolation, functional expression, and characterization of (+)-alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine (Pinus taeda): Stereocontrol in pinene biosynthesis Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
JOURNAL MEDLINE 22510022
PubMed 12623076
REFERENCE 2 (bases 1 to 2162)
Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B.
AUTHORS Direct Submission
JOURNAL Submitted (09-SEP-2002) Institute of Biological Chemistry, Washington State University, PO Box 646340, Pullman, WA 99164-6340, USA

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ORIGIN

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 Db 1901 AGTTGTGATGAGAACCTCTCTGAACCTGTGCTTTA 1939
 RESULT 14
 AR222137 2186 bp DNA linear PAT 26-SEP-2002
 LOCUS AR222137
 DEFINITION Sequence 66 from patent US 6429014.
 ACCESSION AR222137
 VERSION AR222137.1 GI:23329511
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2186)
 AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
 TITLE Monoterpene synthases from grand fir (Abies grandis)
 JOURNAL Parent: US 6429014-A 66 06-AUG-2002;
 FEATURES Location/Qualifiers
 source 1..2186
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Alignment Scores: 6.65e-175 Length: 2186
 Pred. No.: 2264.00 Matches: 435
 Score: 80.53% Conservative: 78
 Percent Similarity: 68.29% Mismatches: 98
 Best Local Similarity: 69.64% Indels: 26
 Query Match: 6 Gaps: 9

US-10-025-145a-65 (1-618) x AR222137 (1-2186)
 Qy 1 MetalLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
 Db 34 ATGGCTGTGTTCTCCGACACC-----AAATCTCTCCGACCAAAATCGTTGATC 84
 Qy 16 ---SerSerSerHisGluIleLeuValAlaLeuArgArgThrIleProThrLeuGlyIleCys 34
 Db 85 AGGTCTACTCATCATGACCTCAAGCTTGGCAGAACCATCCCAACTCTTGAAATGTGT 144
 Qy 35 ArgProGlyIysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
 Db 145 AGCGAGGAAATCTTTACACCTCTGTGACATGATTTGACACCGCTGATCTGAT 204
 Qy 55 AspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuThrAspAspPheIle 74
 Db 205 GATGGTACAAAGACGATAGTGAATCATTCATTCATCTCTGGACGACGATTTCAAT 264
 Qy 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu 94
 Db 265 CAGTCTCTA---TCACGCTTATGGGAGCGCTTTCACAGAAACGTGCTGAGAACTG 321
 Qy 95 IleGlyGluValIysAspIleMetPheAsnPheIysSerLeuGluAspGlyGly----- 112
 Db 322 ATTGGGAAAGTGAAGAC---ATGTTCAATTCATTCATCCATGCGAAGATGAGATCATG 378
 Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
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 Qy 250 SerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeu 269
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Qy      462  TyrLeuGluAsnGlyIleValSerSerAlaHisArgProCysAlaLeuGlnProIleu 481
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RESULT 15

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AF139205      2186 bp      mRNA      linear      PLN 24-JUN-2001
LOCUS      Abies grandis beta-pheIIandrene synthase (agc8) mRNA, complete cde.
DEFINITION      AF139205
ACCESSION      AF139205
VERSION      AF139205.1 GI:7381248
KEYWORDS
SOURCE      Abies grandis
ORGANISM      Abies grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Coniferales; Pinaceae; Abies.
REFERENCE      1 (bases 1 to 2186)
AUTHORS      Bohlmann, J., Phillips, M., Ramchandiran, V., Katoh, S. and Croteau, R.
TITLE      cDNA cloning, characterization, and functional expression of four
new monoterpene synthase members of the Tpsd gene family from grand

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JOURNAL      fir (Abies grandis)
MEDLINE      Arch. Biochem. Biophys. 368 (2), 232-243 (1999)
PUBMED      99373092
REFERENCE      10441373
AUTHORS      2 (bases 1 to 2186)
TITLE      Phillips, M.
JOURNAL      Submitted (30-MAR-1999) Institute of Biological Chemistry,
Washington State University, 289 Clark Hall, Pullman, WA
99164-6340, USA

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FEATURES

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ORIGIN

Alignment Scores:

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Percent Similarity:      80.53%      Conservative:      78
Best Local Similarity:      68.29%      Mismatches:      98
Query Match:      69.64%      Indels:      26
DB:      8      Gaps:      9

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US-10-025-145A-65 (1-618) x AF139205 (1-2186)

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Db 1813 GAGATTAACCAAGAGCTTCTCACCAACTTTCAAATATATAGATGCTTACAGGCTTCCACT 1872
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Job time : 5701 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 12:26:29 ; Search time 582 Seconds
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Title: US-10-025-145A-65

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Fgapop 6.0 , Fgapext 7.0
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Searched: 3373863 seqs, 2124099041 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2453	75.5	2018	3	AAx38922 Grand fir
4	2453	75.5	2018	4	AAf73372 Grand fir
5	2264	69.6	2186	4	AAf73412 Grand fir
6	2200.5	67.7	2196	2	AAx08643 Myrcene
7	2200.5	67.7	2196	3	AAA38927 Grand fir
8	2200.5	67.7	2196	4	AAf73371 Grand fir

9	2197.5	67.6	2205	2	AAx08663 Grand fir
10	2197.5	67.6	2205	4	AAf73391 Grand fir
11	2137	65.7	1890	4	AAf73421 Grand fir
12	2084.5	64.1	2429	4	AAf73413 Grand fir
13	2031.5	62.5	2089	2	AAx08645 Limonene
14	2031.5	62.5	2089	3	AAx38938 Grand fir
15	2031.5	62.5	2089	4	AAf73373 Grand fir
16	1617.5	49.8	1513	3	AAx69551 Pinus rad
17	1611.5	49.6	1634	3	AAx69644 Pinus rad
18	1295.5	39.8	1865	2	AAx38933 Grand fir
19	1295.5	39.8	1865	3	AAx87534 Delta-sel
20	1295.5	39.8	1865	2	AAx87533 Delta-sel
21	1295.5	39.8	1865	2	AAx87505 Delta-sel
22	1291.5	39.7	1885	2	AAx87532 Delta-sel
23	1267.5	39.0	1173	3	AAx69643 Pinus rad
24	1250.5	38.5	1967	2	AAx87513 Grand fir
25	1250.5	38.5	1967	2	AAx08655 Grand fir
26	1250.5	38.5	1967	4	AAf73383 Grand fir
27	1240.5	38.2	2700	2	AAf97447 Pacific Y
28	1240.5	38.2	2700	3	AAx38931 Yew taxed
29	1231	37.9	1785	2	AAx87535 Gamma-hum
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31	1231	37.9	1977	2	AAx87506 Grand fir
32	1230	37.8	1785	2	AAx87536 Gamma-hum
33	1230	37.8	1785	2	AAx87537 Gamma-hum
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36	1187	36.5	2424	2	AAx38932 Grand fir
37	1187	36.5	2424	4	AAf73382 Grand fir
38	1187	36.5	2525	2	AAx87530 E-alpha-b
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40	1187	36.5	2571	2	AAx87504 Grand fir
41	1052.5	32.4	2861	3	AAx38937 Grand fir
42	856	26.3	695	4	AAf73414 Grand fir
43	829.5	25.5	779	3	AAx69642 Pinus rad
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ALIGNMENTS

RESULT 1	AAf73411	standard; CD/NA; 2013 BP.
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XX		
DT	30-APR-2001 (first entry)	
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DE	Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 64.	
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KW	Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;	
KW	myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;	
KW	terpinolene synthase; insect resistance; nutrition; ss.	
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OS	Abies grandis.	
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PN	MO200107565-A2.	
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PD	01-FEB-2001.	
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PF	24-JUL-2000; 2000WO-US020264.	
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PR	26-JUL-1999; 99US-00360545.	
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PA	(UNIM) UNIV WASHINGTON STATE RES FOUND.	
XX		
PI	Steele CL, Bohlmann J, Croteau RB, Phillips MA;	
XX	WPI; 2001-182782/18.	
DR	P-PSDB; AAB69390.	
XX		
PT	New nucleic acid encoding monoterpene synthases, for increasing terpene	

PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.

PS Claim 8; Page 147-149; 175bp; English.

XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phenylandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

XX Sequence 2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	2013
Score:	3251.00	Matches:	618
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-025-145A-65 (1-618) x AAF73411 (1-2013)

QY	1	MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeuSerSerHisGlu	20
DB	36	ATGGCTCTTCTTTATTAATCTCGCTGCTTCAGAGTCGTGCTCAGTTCTTCATAG	95
QY	21	IlleYsAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLyseSerVal	40
DB	96	ATTAAAGCTCCCGAAGAACATCCCAACTCTTGGAATCTGACGGCCGGGAAATCCGTC	155
QY	41	AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg	60
DB	156	GCGGATTCACAAACATGTGTTGACAGCGCTGCATCTACTGATTCGTACAGAGAGCGC	215
QY	61	ValGlyAsnTyrHisSerAsnLeuThrAspAspPheIleGlnSerLeuIleSerThr	80
DB	216	GTGGGCAACTATCTTCCAACTGTGGGACATGATTTTCATACAGCTCTCATCTCAAG	275
QY	81	ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyValIlyAsp	100
DB	276	CCTTATGAGACACTGATTAACCGGAAAGTGTGACAGACTTATTTGGGAGTAGAAAGAT	335
QY	101	IleIleThrPheAsnPheIySerLeuGluAspGlyIyAsnAspLeuLeuGlnArgLeu	120
DB	336	ATAATGTTCAATTTCAAGTTCGTGAGAGATGAGGCAATGATCTCTTCAACGACTTTTG	395
QY	121	LeuValAspAspValGluArgLeuGlyIleAspArgHisPheIySlyGluIleIyThr	140
DB	396	CTGGTTCATGACGTTGAAAGCTTTGGGAATCGACAGGCACTTTCAAAAAGAGATAAAACG	455
QY	141	AlaLeuAspTyrValAsnSerTyrTTPAsnGluIySlyGlyIleGlyCysGlyValArgIySer	160
DB	456	GCACATCATATTTGTTAAACAGTTATTGGAAACGAAAGGCAATGGATGGAGAGAGAGT	515
QY	161	ValValIThrAspLeuAsnSerThrAlaLeuGlyIyLeuArgThrIleAspArgHisGlyTyr	180
DB	516	GTGTGTGACGCTCACTCAACCGCTTGAGGCTTCCGACTCCGACTACAGAGATAC	575
QY	181	ThrValSerSerAspValLeuAsnValPheIyAspIyAsnGlyIyGlnPheSerSerThr	200
DB	576	ACTGTGCTTCAGATGTTTGAACGTTTAAAGACAAATAATGGGCAATTTTCTCCACT	635
QY	201	AlaAsnIleGlnIleGlyIyGluIleArgGlyValLeuAsnLeuPheArgAlaSerIleu	220
DB	636	GCCAAATTTTCAGATAGAGGAGAGATTTAGAGCGCTTCAATTTATTCAGAGGCTCCCTC	695
QY	221	ValAlaAspPheProGlyIyGlyValMetAspGluAlaGluThrPheSerThrIyIyLeu	240
DB	696	GTCCGCTTTTCCCGGAGAAAGTTATGATGAAGCTGAAACATTTCTTACAAAATATTTTA	755

QY	241	ArgGluAlaLeuGlnIySlyIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal	260
DB	756	AGAGAACCTCGCAAAAGATTCGCGCATCCAGTATATCTTTCACATAGAGATACGGGAGCTT	815
QY	261	LeuGluTyrGlyTyrPheIsthrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal	280
DB	816	CTGGAATATGTGTGGCACACCAATTTCCACGCTTGAGAGCAAGGAATTCATGTGACGTC	875
QY	281	PheGlyIyHisIsthrIyAsnIyAsnAlaAlaGluIySlyLeuGluIyLeuAlaIyLeu	300
DB	876	TTTGACAGCACACTAAATAATMAACGCCGCAAGAACTTTTAGAATTGCAAAATTG	935
QY	301	GluPheAsnIlePheHisSerIleuGlnIyArgGluLeuIySlyHisValSerArgTyrTrp	320
DB	936	GAATTCATATATTTTCACTCTTCAAGAGAGAGATTTAAACAATGTTTCCGATGGGTGG	995
QY	321	LyAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla	340
DB	996	AAAGACTCGGGTCTCTGAGATGACCTTCTGTGACATCGTCACTGTGAATATACGCT	1055
QY	341	LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrIys	360
DB	1056	TTGGCTTCTGCAATGCGTTCGAGCTCAACATTTGGAATTCAGACTCGGCTTTACCAAG	1115
QY	361	MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu	380
DB	1116	ATGCTCATCTTATCACAGGTTCTTGAGACATGACAGACGCTTCCGACAGTAGAGAG	1175
QY	381	LeuGluLeuPheThrAlaThrIleIyAspArgTyrAspProSerAlaMetGluCysLeuPro	400
DB	1176	CTGGAACTCTTCAACAGGACAAATTAAGATGGATCCGTCGGGAGTAGATGCTTCCA	1235
QY	401	GluTyrMetIySlyGlyValIyTyrMetMetValTyrHisIsthrValAsnGluMetAlaArgVal	420
DB	1236	GAATATATGAAGAGATGATATGATGTTTATACACCGTAATGAATAGCTTCGAGTG	1295
QY	421	AlaGluIySlyAlaGlnIyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCys	440
DB	1296	GCAGAGAAAGCTCAAGGCCGAGACAGCTCAATGACAGACAGGCTTGGAGAGCGGTG	1355
QY	441	PheAspSerTyrMetGlnGluAlaIyIyThrIleAlaThrGlyTyrLeuProThrPheGlu	460
DB	1356	TTTGATTCGTAATAGCAGAAAGTGGATCCCACTGGTTATTCGCCACCTTTGAG	1415
QY	461	GluTyrLeuGluIyAsnGlyIyValSerSerAlaHisArgProCysAlaLeuGlnProIle	480
DB	1416	GAGTACTTGGAGACGGGAAAGTTAGCTGTGCTATGCGCCATGCGCACTGCACCCATT	1475
QY	481	LeuThrLeuAspIleProPheProAspHisIleLeuIySlyValAspPheProSerIyS	500
DB	1476	CTGACGTTGGACATCCCTTCTCGATCACATCTTCAAGGAAGTTGACTTCCATCGAAG	1535
QY	501	LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrIyAla	520
DB	1536	CTCATATGATTTGAATATATCATCTTTCGATTTAAGAGTGTATACCGGTGTACAAAGCA	1595
QY	521	AspArgAlaTyrGlyIyGluIyAlaSerSerIleSerCysTyrMetIyAspAspProGly	540
DB	1596	GACAGGCGCCGTGGAGAAAGAGCTTCTGTATATCATGTTTATGAAGACAACTCCGGA	1655
QY	541	LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu	560
DB	1656	TTAACGGAAGAAGATGCTCGAATCATATCAACTTCAATGATCAGGAGACGCAATCAGAGA	1715
QY	561	LeuAsnTyrGluLeuLeuIyProAspAspSerValProIleThrSerIySlyHisAla	580
DB	1716	TTTAATTTGGAGGCTTCTTAAGCCAGACAAACAGTGTTCCTCACTTCCAAAGAACAGCA	1775
QY	581	PheAspIleSerArgValIyTyrPheHisGlyTyrArgTyrArgAspGlyTyrSerPheAla	600
DB	1776	TTTGACATTAAGCAGATTTTGGCATCACGTTTACAGATACGAGATGGCTACAGCTTTGCC	1835

QY 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
DB 1836 AACCTGAAACAAAGAGTTTGATGATGAAACCGCATTAACCTGCTTTG 1869
RESULT 2
ID AAX08644 standard; cDNA; 2018 BP.
AXX08644
AC AAX08644;
XX 27-SEP-1999 (first entry)
XX
DE Pinene synthase gene.
XX
KM Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
OS defense; plant seed; oil; meal; ss.
XX
XX Abies grandis.
XX
FH Key Location/Qualifiers
FT 6.1892
FT /*tag= a
FT /product= "Pinene synthase"
XX
XX MO9902030-A1.
XX
XX 21-JAN-1999.
XX
XX 10-JUL-1998; 98MO-US014528.
XX
XX 11-JUL-1997; 97US-0052249P.
XX
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
XX P1 Bohlmann J, Steele CL, Croteau RB;
XX
XX WPI: 1999-120396/10.
XX
XX P-PSDB; MAM85701.
XX
XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (Abies grandis), used to provide plants with modified production of
PT monoterpenes, e.g. myrcene, limonene or pinene.
XX
XX
XX Claim 10; Page 74-77; 121pp; English.
XX
XX Nucleotide sequences encoding myrcene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by myrcene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
XX Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1.2e-243 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 2 Gaps: 6
US-10-025-145A-65 (1-618) x AAX08644 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 6 ATGGCTGATGTTTATCCGACCGCTTGGCTTCAATCATGCTGCACAAATCGTTGATC 65
QY 16 SerSerSerHISGluIleLeuAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35

DB 66 AGTTCTACCCATGAGCTTTAAGGCTCTCTCTAGAACAAATCCAGGCTTAGATGAGTGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 126 CGAGGAAATCTATCACTCTTCCATGCATGCAGCTTCAACCGTGTGAATCCCATAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuThrPAspAspPheIleGln 75
DB 186 GGTGTACGAAACCGATGGCGATTCATTCACACCTCTGGAGAGATGATGTCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB 246 TCTTTA---CCACCGCTTATGAGAAATAATCGTACCTCGAGCGGTGAGAAATGATC 302
QY 96 GlyIleValIleAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
DB 303 GGGGAGATTAAGAAC---ATGTTCAATTCGATGTCATTAAGAAATGAGATTAATGAGT 359
QY 113 -----AsnAspIleLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATCTCATTCACACCGCTTGGATGTGACACCGCTTGAACGTTTGGGGATC 419
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 420 CATGACATTTCCAAAGATGAGATTAATAATCGCGCTGATATGTTTACAGTATTAGGGGC 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATGGCATCGATGCGGAGGAGAGTGTGTACTGATCTGAATCTCAATCGCTGTT 539
QY 171 GlyLeuArgThrIleLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTCGAACCCATGACGATACACGAGATACCGGCTTCAAGATGTTTCAACCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB 600 AAAGCCAAATCGGCACTTTTCTGCTCTGAATAATTCAGACAGATGAGATGACGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyValMetAsp 230
DB 660 GCGCTTCGAATGTATTCGCGGCTCCCTCATTCCTTCCAGGGGAGAAATATGTGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProIleSer 250
DB 720 GAGCTGAATCTCTCTACCAATATTAAAGAGCCGTCACAAATATTCGGTCTTC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
DB 780 AGT---CTTGGCAGAGATCGGGGACGTTTGGAAATATGTTGGCACATATTTGGCG 836
QY 271 ArgLeuGlnAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
DB 837 CGATTGGAAGCAAGAAATTAATCATCAAGCTTTTGGACGAGCACATGAAACAGCAAGTCA 896
QY 291 -----AlaGlyLysLeuLeuGlnLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB 897 TATGTGAAGCAAAACAACTTTTGAACCTGCAAAATTTGAGATTCACATCTTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValAsnSerArgTyrTrpLysAspSerGlySerProGlu 327
DB 957 TTACAAAGAGGAGAGTTTGAAGAGTGTGTGTCAGATGTCGAAAGAAATCGGTTTCTGAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
DB 1017 ATGACCTTCTGCGACATCGTCACGTGGAATATCACTTGGGCTTCTGATTCGCGTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB 1077 GAGGCTCAACATTCGATTTAGACTGCGCTTGGCAAGACGTGATCATATTCAGGAT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387

```
Db 1137 CTGACGATATGTAACACACCTTCGGACACAGTAGACGAGCTTGAACTCTTCACACGACA 1196
Qy 388 ILEYSARITPAPSPROSERALAMETGLUCYSEUPROGIUITYRMEITYSGLVVALTYR 407
Db 1197 ATGAAGATGGAGTCCGTCTCCATAGATTGCTTCCAGATATATGAAAGAGGTGAC 1256
Qy 408 METWETVALTYRHSITHVALASNGLUWELAAARGVALAAGLUYPAALAGINGLYARG 427
Db 1257 ATACGGGTTTACGACACCGGTAAATGAATGAGCTCGAGAGGACAGAGAGGCTCAAGCGCA 1316
Qy 428 ASPHTRLEUANTYRILAAARGINALATPGULALACYSRHEAPSPERTYRMEGLINGLU 447
Db 1317 GATACGGTCACATATGCTCGGAGAGCTTGAGAGCTTATATATGATTCGTATATCAAGAA 1376
Qy 448 ALALYSTRIPLAIALTHNGLYTYRLEUPROTHRPHGLUGIUYTYRLEUGLAAAGLYYS 467
Db 1377 GCAGAGGTGATCGGACCTGTTACTGCTCTTATGATGACTACAGAAATGGGAAA 1436
Qy 468 VALSERSERALAHISARGPROCYAALALEUGLNPROIETEURHLEUASPILAEPROBHE 487
Db 1437 GTTAGCTGTGGTCATCCGATATCCGATTCGACACCATTCGACATGACATCCCTTT 1496
Qy 488 PROASPHISILEULYSGLUVALASPHERPROSERLYSEUANAHPLEUILCYSTILE 507
Db 1497 CCTGATCATATCCCTCAAGAGAGTTGACTTCCCATCAAGCTTAAAGACTTGACATGTGCC 1556
Qy 508 ILEULARGLEUARGLYASPTHRARGCYSTRYLISALASPARGLAARGGLVGLUGLU 527
Db 1557 ATCTTGATTTACAGAGTGATACCGGCTGCTACAGGCGGACAGGCTCGTGGAGAGAA 1616
Qy 528 ALASERSERILSESERYRMEITYSASPANPROGIYEURTHNGLUASPALALEU 547
Db 1617 GCTTCCTATATATCATGTTATATGAAACATCTGGAGATCAGAGAGATGCTCTC 1676
Qy 548 ASNHISILEANPHEMETILEARGASPALALEARGLULEUANTYRGLULEULYLS 567
Db 1677 GATCATATCAACGGCATATCATGACGTAAATCAAGATTAAATGGGAACTTCTCAA 1736
Qy 568 PROASPHANSEVALPROILETHRSERYLSHISALAPHEASPILESERARGVALTRP 587
Db 1737 CCAAGCATCATATGTTCCATCTCCGCGAAGAAACATGCTTTTGACATGCCAGACTTTC 1796
Qy 588 HISHISGLYTYRARGTYRARGASPGLYTYRISERPHEALANVALGUTHLYSERLEU 607
Db 1797 CATTAACGGCTCAAAATACCGAGACGGCTACAGCGTTGCCAAGTTGAACGAAGTTTG 1856
Qy 608 VALMETARGTHRVALLIEGLUPROVALPROLEU 618
Db 1857 GTCACGAGAACCTTCCTTGAATCTGTGCTTTG 1889

RESULT 3
AAA38922
ID AAA38922 standard; DNA; 2018 BP.
AC AAA38922;
XX
XX 25-AUG-2000 (first entry)
XX
DE Grand fir pinene synthase DNA sequence SEQ ID NO:19.
XX
XX Synthase; protein co-ordinate data; active site; modification; terpenoid;
XX 3-dimansional coordinate; alpha carbon atom; plant; terpene synthase;
XX isoprenoid; breeding programme; fragrance; flavour; pheromone;
XX defensive agent; pigment; antitumor; steroid hormone;
XX signal transduction pathway; bile acid; affinity purification;
XX photoreceptor; enzymatic synthase; nutrient supplement;
XX immunological reagent; ds.
XX
XX Abies grandis.
XX OS
XX PN MO200017327-A2.
XX
XX PD 30-MAR-2000.
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XX 17-SEP-1999; 99WO-US021419.
XX
XX 18-SEP-1998; 98US-0100993P.
PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
XX (KENT ) UNIV KENTUCKY RES DEPT.
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Chappell J, Manna KR, Noel JP, Starks CW;
XX WPI; 2000-292839/25.
XX P-PSDB; AAY90837.
XX
XX Novel terpene synthase enzymes, useful for producing terpene
XX hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
XX enzymes by specific amino acid alterations.
XX
XX Disclosure; Page 363-366; 450p; English.
XX
XX The present invention describes an isolated terpene synthase (I)
XX comprising a region with at least 20% identity to region 265-535 of a 548
XX amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
XX carbon atoms (aliphac) that have interatomic distances, between each
XX other, within tabulated ranges, have a centre point (within a sphere of
XX radius 2.3 Angstrom ) within tabulated ranges, and have an ordered
XX arrangement of R groups (defining aa side chains), excluding specific
XX tabulated arrangements (tables given in the specification). (I), and
XX related enzymes, are used to produce a wide range of terpenoids (e.g.
XX cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
XX flavours, pheromones, defensive agents, pigments, antitumor agents,
XX components of signal transduction pathways, precursors of steroid
XX hormones and bile acids, as photoreceptors and as co-factor side chains.
XX Some synthases with little or no catalytic activity (and nucleic acids
XX encoding them) are used as controls in the analysis of products formed by
XX enzymatic synthesis; as nutrient supplements; for affinity purification
XX of isoprenoids; or to develop immunological reagents or nucleic acids for
XX monitoring expression of terpene synthase or inheritance of the gene in
XX plant breeding programs. The new synthases may produce novel terpene
XX products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
XX sequences used in the exemplification of the present invention
XX
XX Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1-26-243 Length: 2018
XX Score: 2453.00 Matches: 475
XX Percent Similarity: 84.63% Conservative: 59
XX Best Local Similarity: 75.28% Mismatches: 81
XX Query Match: 75.45% Indels: 16
XX DB: 3 Gaps: 6
XX
XX US-10-025-145A-65 (1-618) x AAA38922 (1-2018)
XX
XX 1 METALALEUENSERILETHRPROLEUVALSERARGSECYSEU----- 15
XX 6 ATGGCTCTAAGTTCTACCGCACCGTGGCTTCCAATCATCTCCGACAAATCGTTGATC 65
XX
XX 16 SERSESERHISGLUIELVVALALEUARGRHRILIEPROTHRLEUGLYILECYARG 35
XX
XX 66 AGTTCACCCCTGAGGCTTAAAGGCTCTCTTGAACAACATTCAGCTCTTAGGATAGTAGG 125
XX
XX 36 PROGLIYSESERVALAHISERILEASNETCYSEUHTHRSERVALALASERTHRASP 55
XX
XX 126 CGAAGGAATATACATCCCTTCCATCAGCATAGAGCTTACACCGTTGTAAACGATAT 185
XX
XX 56 SERVALGINARGARGVALGLYASNTYRHSERANLEUTRPAAPASPAPHEILEGLN 75
XX
XX 186 GGTGTACGAAGACGATAGCGGATTCATTCACCACTCTGGAGCGATGATGATACACG 245
XX
XX 76 SERLEULESERTHRPROTYRGLYALAPROASPHYRARGGLUARGALASPARGLEULE 95
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XX The present invention provides the protein and coding sequences of
 CC monoterpene synthases from the grand fir. These include (-)-camphene
 CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
 CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
 CC and pinene synthase. The sequences can be used to produce transgenic
 CC plants expressing high levels of the enzymes, resulting in levels which
 CC are useful in protecting against and treating cancers, and to confer
 CC insect resistance on plants

XX Sequence 2018 BP, 583 A, 431 C, 479 G, 525 T, 0 U, 0 Other;

Alignment Scores:

Prod. No.:	1.2e-243	Length:	2018
Score:	2453.00	Matches:	475
Percent Similarity:	84.63%	Conservative:	59
Best Local Similarity:	75.28%	Mismatches:	81
Query Match:	75.45%	Indels:	16
DB:	4	Gaps:	6

US-10-025-145a-65 (1-618) x AAF73372 (1-2018)

QY	1	MetaLeuLeuSerIleThrProLeuValSerArgSerCysLeu-----	15
DB	6	ATGGCTCAGTCTTCCACCGCACCGCTTGCTTCAAAATCATGCTGCACAAATCGTTGATC	65
QY	16	SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg	35
DB	66	AGTCTTACCCATGATGAGGCTCTCTCTAGAACATTCAGCTCTTAGAAGTAAAGG	125
QY	36	ProGlySerSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp	55
DB	126	CGAAGGAATCTATCATCTCTTCATCAGATGAGCTTACACCGCTTGTAACGATGAT	185
QY	56	SerValAlaIleValGlyValAsnThrHisSerAsnLeuThrPheAspAspPheIleGln	75
DB	186	GGTGTACGAACCCATGCGGAGATTCATTCACACCTCGGAGAGATGATGATACAG	245
QY	76	SerLeuLeuSerThrProTyrGlyAlaProAspTyrArgGluValAlaAspArgLeuIle	95
DB	246	TCCTTTA---CCAAAGCTTATGAGAAATTCGACCTGAGCGCTGCTGAAGAACTGATC	302
QY	96	GlyGluValIleAspIleMetPheAsnPheLeuSerLeuGluAspGlyIle-----	112
DB	303	GGGGAAGTAAAGAAC---ATGTTCAATTCAGTGCATTAAGAAGATGAGAGTATATGAT	359
QY	113	-----AsnSerLeuLeuGlnArgLeuLeuValAlaAspValAlaArgLeuGlyIle	130
DB	360	CCGCTCAATGATTCATTCACACCGCTTGATGATTCGACAGCTTGAACGTTGGGATC	419
QY	131	AspArgHisPheLeuSlyGluIleLeuThrAlaLeuAspTyrValAlaSerTyrTrpAsn	150
DB	420	CATGACATTTTCAAAAGATGAGATAAATCGCGCTTGATTTATGTTTACAGTTATTTGGGC	479
QY	151	GluIleValGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu	170
DB	480	GAATAGGCAATCGGATGCGGAGGAGAGTGTGTACTGATCGAACTCAACTGCGGTG	539
QY	171	GlyLeuArgThrIleLeuArgLeuHisGlyTyrThrValSerSerAspValAlaAsnValPhe	190
DB	540	GGGCTTGGAACCCATGACATACAGGATACCGCGTGTCTCAGATGTTTCAAAAGCTTTC	599
QY	191	LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg	210
DB	600	AAAGGCCAAATGGGCACTTTTCTCGCTCTGAAAATATTCAGACAGATGAAGAGATCGA	659
QY	211	GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIleValMetAsp	230
DB	660	GGCTTTCGATTTATTCGGGCGCTCCTCATTTGCTTTCAGGGGGAAGAAATATATGAT	719
QY	231	GluIleArgThrPheSerThrIleTyrIleuArgGluAlaLeuGlnIleValIleProAlaSer	250
DB	720	GAGGCTGAATCTTCTTCAACAAATATTTAAAGAACCGCTGCAAAAGATTCGGGTCTCC	779

QY	251	SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyIleThrHisThrAsnLeuPro	270
DB	780	AGT---CTTTCGAGAGATTCGGGAGCGTTTGGAAATATGTTGGCACATATTTGGCG	836
QY	271	ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrIleValAsnAla	290
DB	837	CGATTGGAGACAGAAATTCATTCAGATCTTTTGACAGGACCTTGCGAACACAGACGA	896
QY	291	-----AlaGluIleValLeuGluLeuAlaIleValLeuGluIlePheAsnIlePheHisSer	307
DB	897	TATGTGAAGCAAAATCTTTTGAATCTGCAAAATTTGAGTTCAACATTTTCAATCC	956
QY	308	LeuGlnGluArgGluLeuIleValSerArgTyrTrpLysAspSerGlySerProGlu	327
DB	957	TTACAAAGAGGAGGAGTTAGAAAGTCTGTGCAGATGAGTGAAGAAATCGGTTTCTGAG	1016
QY	328	MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe	347
DB	1017	ATGACCTTTCGCGACATCGTCAGTGAATATCACTTGGCTTCCTGCAATTCGCTTC	1076
QY	348	GluProGlnHisSerGlyPheArgLeuGlyPheThrIleYsMetSerHisIleLeuThrVal	367
DB	1077	GAGCTCAACATTTGATTCAGACTGCGCTTTCGCAAGACGTCTCATTCATGACGCT	1136
QY	368	LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr	387
DB	1137	CTTACGATATGTATGACACACTTCGGCACAGTACAGCGTGAACCTTTCACAGCGCA	1196
QY	388	IleLysArgTyrPheProSerAlaMetGlyCysLeuProGluTyrMetIleValIleTyr	407
DB	1197	ATGAAGAGATGCGATCGCTCTCATAGATGATCCCTTCAGAAATATGAAAGAGTGTAC	1256
QY	408	MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluIleValGlnIleArg	427
DB	1257	ATACCGCTTACGACACCGGTAATGAAATGCTGAGAGGACAGAGAGGCTCAAGCGCCA	1316
QY	428	AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnIle	447
DB	1317	GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATGATGATGATGATGATG	1376
QY	448	AlaLysTrpIleAlaIleThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyIle	467
DB	1377	GCAAGGTGATCGGACGCTGTACCTCGCTTGTAGTGATCTAGCAAAATGGGAAA	1436
QY	468	ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe	487
DB	1437	GTTAGCTGTGTCATCGCATATCCGCAATTCGAAACCATTTGACAAATGCAATCCCTTT	1496
QY	488	ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle	507
DB	1497	CTGATCATATTCCTCAAGGAAGTGAATCCCATCAAAAGCTTAAAGCATTTGGCATGTC	1556
QY	508	IleLeuArgLeuArgGlyAspThrArgCysTyrIleValAlaAspArgAlaArgGlyIleGlu	527
DB	1557	ATCCTTGATTAACAGATGATACCGGTGTCTACAGGCGGACAGGCTCGTGAAGAA	1616
QY	528	AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluIleAspAlaLeu	547
DB	1617	GCTTCCCTTATATATGTTATATGAAACAAATCTTGAGATGATGACAGAAAGATGCTTC	1676
QY	548	AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTyrGluLeuLeuLys	567
DB	1677	GATCATATCAACGCGCATGATCAGTACGATATCAAAAGATTAATTTGGGAATCTTCA	1736
QY	568	ProAspAsnSerValProIleThrSerIleValHisIleAlaPheAspIleSerArgValTrp	587
DB	1737	CCAAGACATCAATGTTCCATCTCGCGAAGAAATGCTTTTGAATCGCCAGAGCTTTC	1796
QY	588	HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrIleSerLeu	607
DB	1797	CATTACGGCTTCAAAATACCGAGCGGCTACAGCTTGCCAAAGTTGAACAAAGATTTG	1856

QY 608 ValMeArGrThrValIleGluProValProleu 618
DB 1857 GTCACGAGAACCTCTTGAAATCTGTGCTTTG 1889

RESULT 5
ID AAF73412 standard; cDNA; 2186 BP.
XX AAF73412;
AC AAF73412;
XX 30-APR-2001 (first entry)
XX
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 66.
XX
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; SB.
XX
OS Abies grandis.
XX WO200107565-A2.
XX
XX 01-FEB-2001.
XX
XX 24-JUL-2000; 2000WO-US020264.
XX
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIV) UNIV WASHINGTON STATE RES FOUND.
XX
XX Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX WPI; 2001-182782/18.
XX P-PSDB; AAB69391.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthase in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
XX Claim 13; Page 151-154; 175pp; English.
XX
XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-pinellandrene synthase, terpinolene synthase, (-)-
CC limonene, (-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

XX
XX Sequence 2186 BP; 722 A; 440 C; 472 G; 552 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 5,24e-224 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best Local Similarity: 68.29% Mismatch: 98
Query Match: 69.64% Indels: 26
DB: 4 Gaps: 9

US-10-025-145a-65 (1-618) x AAF73412 (1-2186)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 34 ATGCTCTGTGTTCTTCGCGACCC-----AAATCTGCTGCGACAAATCGTTGATC 84
QY 16 ---SerSerSerHISgluIleValAlaLeuArgThrIleProThrLeuGlyIleCys 34
DB 85 AGTCTACTCTCACTGAGCTCAAGCTCTGCGACAAACATCCCACTCTTGAAATGAT 144
QY 35 ArgProGlyIleValSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
DB 145 AGGAGGAGGAATCTTTCAACACCTTCTGTGAGCATGAGTTGACACCGCGTATCTCAT 204

QY 55 AspSerValGlnArgIleValGlyAsnThrHisSerAsnLeuThrPAspAspPheIle 74
DB 205 GATGCTTCAAAAGAGGATGAGTACTATCATCTTCATCTCTGGACAGCATTTCTTA 264
QY 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu 94
DB 265 CAGTCTCTA---TCAGCCCTTATGGGAGGCTCTTACGAGAAACGTCGAGAAACTG 321
QY 95 IleGlyIleValIleAspIleMetPheAsnPheLeuSerLeuGluAspGlyIle----- 112
DB 322 ATGGGGAAGTGAAGAG---ATGTTCAATTCAATGCCATCGAAGATGGAATCAATG 378
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValLaAspAspValGluArgLeuGly 129
DB 379 AGTCCCTCAATGATTTATTAAGACGATTTGATGATGATGATGATGATGATGATG 438
QY 130 IleAspArgHisPheValLeuGluIleIleThrAlaLeuAspTyrValAsnSerTyrTrp 149
DB 439 ATTGATACATTTCAAAAAGAGTAAATCAACCCCTTGATTTATGTTTACAGTTATGG 498
QY 150 AsnGluValGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
DB 499 AACGAAAAGGATTTGATGCGGTAGAGATAGTGTCTTCCGTGATGCACTGCACTGCC 558
QY 170 LeuGlyLeuAspThrLeuArgLeuHisGlyTyrThrValSerSerAspAspValLeuAsnVal 189
DB 559 TCGGAGTTTCAACCTTTCGCTCAGCAGATACAGTGTCTTCAAGAGTTTGAAATA 618
QY 190 PheLeuAspValAsnGlyGlnPheSerSerThrAlaAsnIleGluIleGluIle 209
DB 619 TTTCAGACCAAAATGGGCACTTTCATCTCTCTCTACATAAA---GAGAGAGACTC 675
QY 210 ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIleValMet 229
DB 676 AGAACCGTTCTGAAATTATATATCGGCTCTTCAATGCTTCCGCGGAGAAAGTTATG 735
QY 230 AspGluAlaGluThrPheSerThrIleSerThrLeuArgGluAlaLeuGluIleIleProAla 249
DB 736 GAAAGGCTGAAATTTCTCTTCAAGATTTTGAAGAAAGCGGCGCAAAAGTTCCGGTTC 795
QY 250 SerSerIleLeuSerLeuGluIleArgAspValLeuGluIleGlyTyrPheIleThrAsnLeu 269
DB 796 TCCAGT---CTTTCACAAAGAAATGACTACACTTGGAAATGTTGGTGCACAAATATG 852
QY 270 ProArgLeuGluAlaArgAspThrMetAspValPheGlyGlnHisThr----- 285
DB 853 CCAAGATTGAAACAAAGAAATTACTAGATGATTTGACATCTCAACAGTCCATGCTC 912
QY 286 LysAsnLysAsnAla-----AlaGluLysLeuLeuGluIleAlaLysLeuGlu 301
DB 913 AAGAAGAAAGAGCGCAATATCTGACACGCAAAAGCTTTAAGAACTCGCAAAATGGAG 972
QY 302 PheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLys 321
DB 973 TTCAACATCTTTCATCTCTCTTCAACAGAGAGATTAAGATCTCTCCAGATGGTGATA 1032
QY 322 AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeu 341
DB 1033 CATTCGGGTTTGCCTGAACCTGACCTTTGTCGTCGATGTCACAGTGAATATCATCACCTG 1092
QY 342 AlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGluIlePheThrLysMet 361
DB 1093 AGCTCTTGACATTTGAGCTGAGCCCAACATTTCTCATTTCAATTTGGGCTTTGCCAAACG 1152
QY 362 SerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeu 381
DB 1153 TGTCATCTTTCACAGGTTTTCAGATATATACAGACCTTTGGAAGATGATGATGATG 1212
QY 382 GluLeuPheThrAlaThrIleLysArgTyrAspProSerAlaMetGluCysLeuProGlu 401
DB 1213 GAACTCTTCAACGAGGAGGATGAGATGATGATGATGATGATGATGATGATGATGAT 1272

Chr	Start (kb)	End (kb)	Gene	Accession	Length (bp)	GC (%)	GC3 (%)	GC3+ (%)	GC4 (%)	GC5 (%)	GC6 (%)	GC7 (%)	GC8 (%)	GC9 (%)	GC10 (%)	GC11 (%)	GC12 (%)	GC13 (%)	GC14 (%)	GC15 (%)	GC16 (%)	GC17 (%)	GC18 (%)	GC19 (%)	GC20 (%)	GC21 (%)	GC22 (%)	GC23 (%)	GC24 (%)	GC25 (%)	GC26 (%)	GC27 (%)	GC28 (%)	GC29 (%)	GC30 (%)	GC31 (%)	GC32 (%)	GC33 (%)	GC34 (%)	GC35 (%)	GC36 (%)	GC37 (%)	GC38 (%)	GC39 (%)	GC40 (%)	GC41 (%)	GC42 (%)	GC43 (%)	GC44 (%)	GC45 (%)	GC46 (%)	GC47 (%)	GC48 (%)	GC49 (%)	GC50 (%)	GC51 (%)	GC52 (%)	GC53 (%)	GC54 (%)	GC55 (%)	GC56 (%)	GC57 (%)	GC58 (%)	GC59 (%)	GC60 (%)	GC61 (%)	GC62 (%)	GC63 (%)	GC64 (%)	GC65 (%)	GC66 (%)	GC67 (%)	GC68 (%)	GC69 (%)	GC70 (%)	GC71 (%)	GC72 (%)	GC73 (%)	GC74 (%)	GC75 (%)	GC76 (%)	GC77 (%)	GC78 (%)	GC79 (%)	GC80 (%)	GC81 (%)	GC82 (%)	GC83 (%)	GC84 (%)	GC85 (%)	GC86 (%)	GC87 (%)	GC88 (%)	GC89 (%)	GC90 (%)	GC91 (%)	GC92 (%)	GC93 (%)	GC94 (%)	GC95 (%)	GC96 (%)	GC97 (%)	GC98 (%)	GC99 (%)	GC100 (%)	GC101 (%)	GC102 (%)	GC103 (%)	GC104 (%)	GC105 (%)	GC106 (%)	GC107 (%)	GC108 (%)	GC109 (%)	GC110 (%)	GC111 (%)	GC112 (%)	GC113 (%)	GC114 (%)	GC115 (%)	GC116 (%)	GC117 (%)	GC118 (%)	GC119 (%)	GC120 (%)	GC121 (%)	GC122 (%)	GC123 (%)	GC124 (%)	GC125 (%)	GC126 (%)	GC127 (%)	GC128 (%)	GC129 (%)	GC130 (%)	GC131 (%)	GC132 (%)	GC133 (%)	GC134 (%)	GC135 (%)	GC136 (%)	GC137 (%)	GC138 (%)	GC139 (%)	GC140 (%)	GC141 (%)	GC142 (%)	GC143 (%)	GC144 (%)	GC145 (%)	GC146 (%)	GC147 (%)	GC148 (%)	GC149 (%)	GC150 (%)	GC151 (%)	GC152 (%)	GC153 (%)	GC154 (%)	GC155 (%)	GC156 (%)	GC157 (%)	GC158 (%)	GC159 (%)	GC160 (%)	GC161 (%)	GC162 (%)	GC163 (%)	GC164 (%)	GC165 (%)	GC166 (%)	GC167 (%)	GC168 (%)	GC169 (%)	GC170 (%)	GC171 (%)	GC172 (%)	GC173 (%)	GC174 (%)	GC175 (%)	GC176 (%)	GC177 (%)	GC178 (%)	GC179 (%)	GC180 (%)	GC181 (%)	GC182 (%)	GC183 (%)	GC184 (%)	GC185 (%)	GC186 (%)	GC187 (%)	GC188 (%)	GC189 (%)	GC190 (%)	GC191 (%)	GC192 (%)	GC193 (%)	GC194 (%)	GC195 (%)	GC196 (%)	GC197 (%)	GC198 (%)	GC199 (%)	GC200 (%)	GC201 (%)	GC202 (%)	GC203 (%)	GC204 (%)	GC205 (%)	GC206 (%)	GC207 (%)	GC208 (%)	GC209 (%)	GC210 (%)	GC211 (%)	GC212 (%)	GC213 (%)	GC214 (%)	GC215 (%)	GC216 (%)	GC217 (%)	GC218 (%)	GC219 (%)	GC220 (%)	GC221 (%)	GC222 (%)	GC223 (%)	GC224 (%)	GC225 (%)	GC226 (%)	GC227 (%)	GC228 (%)	GC229 (%)	GC230 (%)	GC231 (%)	GC232 (%)	GC233 (%)	GC234 (%)	GC235 (%)	GC236 (%)	GC237 (%)	GC238 (%)	GC239 (%)	GC240 (%)	GC241 (%)	GC242 (%)	GC243 (%)	GC244 (%)	GC245 (%)	GC246 (%)	GC247 (%)	GC248 (%)	GC249 (%)	GC250 (%)	GC251 (%)	GC252 (%)	GC253 (%)	GC254 (%)	GC255 (%)	GC256 (%)	GC257 (%)	GC258 (%)	GC259 (%)	GC260 (%)	GC261 (%)	GC262 (%)	GC263 (%)	GC264 (%)	GC265 (%)	GC266 (%)	GC267 (%)	GC268 (%)	GC269 (%)	GC270 (%)	GC271 (%)	GC272 (%)	GC273 (%)	GC274 (%)	GC275 (%)	GC276 (%)	GC277 (%)	GC278 (%)	GC279 (%)	GC280 (%)	GC281 (%)	GC282 (%)	GC283 (%)	GC284 (%)	GC285 (%)	GC286 (%)	GC287 (%)	GC288 (%)	GC289 (%)	GC290 (%)	GC291 (%)	GC292 (%)	GC293 (%)	GC294 (%)	GC295 (%)	GC296 (%)	GC297 (%)	GC298 (%)	GC299 (%)	GC300 (%)	GC301 (%)	GC302 (%)	GC303 (%)	GC304 (%)	GC305 (%)	GC306 (%)	GC307 (%)	GC308 (%)	GC309 (%)	GC310 (%)	GC311 (%)	GC312 (%)	GC313 (%)	GC314 (%)	GC315 (%)	GC316 (%)	GC317 (%)	GC318 (%)	GC319 (%)	GC320 (%)	GC321 (%)	GC322 (%)	GC323 (%)	GC324 (%)	GC325 (%)	GC326 (%)	GC327 (%)	GC328 (%)	GC329 (%)	GC330 (%)	GC331 (%)	GC332 (%)	GC333 (%)	GC334 (%)	GC335 (%)	GC336 (%)	GC337 (%)	GC338 (%)	GC339 (%)	GC340 (%)	GC341 (%)	GC342 (%)	GC343 (%)	GC344 (%)	GC345 (%)	GC346 (%)	GC347 (%)	GC348 (%)	GC349 (%)	GC350 (%)	GC351 (%)	GC352 (%)	GC353 (%)	GC354 (%)	GC355 (%)	GC356 (%)	GC357 (%)	GC358 (%)	GC359 (%)	GC360 (%)	GC361 (%)	GC362 (%)	GC363 (%)	GC364 (%)	GC365 (%)	GC366 (%)	GC367 (%)	GC368 (%)	GC369 (%)	GC370 (%)	GC371 (%)	GC372 (%)	GC373 (%)	GC374 (%)	GC375 (%)	GC376 (%)	GC377 (%)	GC378 (%)	GC379 (%)	GC380 (%)	GC381 (%)	GC382 (%)	GC383 (%)	GC384 (%)	GC385 (%)	GC386 (%)	GC387 (%)	GC388 (%)	GC389 (%)	GC390 (%)	GC391 (%)	GC392 (%)	GC393 (%)	GC394 (%)	GC395 (%)	GC396 (%)	GC397 (%)	GC398 (%)	GC399 (%)	GC400 (%)	GC401 (%)	GC402 (%)	GC403 (%)	GC404 (%)	GC405 (%)	GC406 (%)	GC407 (%)	GC408 (%)	GC409 (%)	GC410 (%)	GC411 (%)	GC412 (%)	GC413 (%)	GC414 (%)	GC415 (%)
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PI Bohlmann J, Steele CL, Croteau RB;
XX
XX WPI: 1999-120396/10.
DR P-PSDB; AAW85700.
XX
XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (*Abies grandis*), used to provide plants with modified production of
PT monoterpenes, e.g. myrcene, limonene or pinane.
XX
XX Claim 9; Page 69-72; 121pp; English.
PS
XX
XX Nucleotide sequences encoding myrcene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. insect plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavonoid and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by myrcene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,01e-217 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.18% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 2 Gaps: 7

US-10-025-145A-65 (1-618) x AAX08643 (1-2196)
QY 1 MethAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGGTTTCTCATCTCACCGCTGGCTTGGAAATCTGCTCGCGCAAGTCGTGATC 128
QY 16 SerSerSerHISgluIleLeuAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCATATTCATGAAACATAGAGCTCCCTATAGAACATCCCAATCTTGGAATGCGTAGG 188
QY 36 ProGlyIysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAATCTGTACGCCCTTCCATGAGCATCACTTGGCCACCGCTCACCTGATGAT 248
QY 56 SerValGlnArgArgValGlyAsnIYrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGACAAACAGCATAGCGTACATCCATTCATATCTGGGACGATATTTTCATACAG 308
QY 76 SerIleuIleSerThrProIYrGlyAlaProAspIYrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA---TCAACGCCCTTATGGGAAACCCCTTTCACAGGAACGTCGAGATTAAATT 365
QY 96 GlyIYrValIYrAspIleMetPheAsnPheIYsSerLeuGluAspGlyIY----- 112
Db 366 GTGAGGATGAAGAAGATA---TTCAATTCAATGTACCTCGATGATGGAAGATTAAAGACT 422
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTATATGATCTCATCGAACAGCCTTGGATAGTCGATAGCGTTGAAAGTTGGGGATA 482
QY 131 AspArgHisPheIYsLeuGluIleLeuSerThrAlaLeuAspIYrValAsnSerIYrTrpAsn 150
Db 483 GCTAAGACATTTTCAACAAACGAGATTAACATCACTCGAGATTATGTTTCCGTTACGGGAG 542
QY 151 GluIYrGlyIleGlyCysGlyYArgGluSerValIleAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACGCGCATTTGATGTGGGAGAACAGATATTTGATCGATCTCAACTCACTGCGTTG 602
QY 171 GlyLeuArgThrLeuArgLeuHisGlyIYrThrValSerSerAspValLeuAsnValPhe 190

Db 603 GGGTTTCAGACTCTTCGATTAACGGGTACACTGATCTCCAGAGCTTTTAAAGCTTTT 662
 Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIleArg 210
 Db 663 CAAATCAAAATGAGCAGCTTTGATGCTCCCGCT---CAGACAGAGGGTGCAGTACGA 719
 Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlnLysValMetAsp 230
 Db 720 AGCGTTCTTAATCTATATATGAGCTTCCTCCCTCATGCTCCCTGGAGAAAGTATGGAA 779
 Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
 Db 780 GAACGTGAATCTCTCCACAAGATATTGAAAGAGCTCTACAAAGATTCACACTCC 839
 Qy 251 SerIleuSerLeuGlnIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
 Db 840 GCT---CTTTCACAGAGATTAAGCTTTGTATGGAATGCTGGCACACAAATTTGCCA 896
 Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnIleSerLys-----Asn 287
 Db 897 AGATTGGAGAGCAAAATTAATACATGACACACTTGAGAAAGACACAGCTGCATGCTCAAT 956
 Qy 288 LysAsnAlaAlaGlyLysLeuLeuGlnLysLeuAlaLysLeuGluPheAsnIlePheHisSer 307
 Db 957 AAAAATGCTGGAGAGAGCTTTTAGAATCTTGCAAAATTTGAGATTCAATATATTAACTCC 1016
 Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTyrLysAspSerGlySerProGlu 327
 Db 1017 TTACAAACAAAGCAATTAATCTTTTGGAGTGTGGAAAGATTCGCAATTTGCTTAA 1076
 Qy 328 MetThrPheCysArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
 Db 1077 TTGACATTTGCTCGGCATGTCATGTGGAATTTCACTTTGGCTCTGTATGTCCATT 1136
 Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
 Db 1137 GACCCAAAGACTTTCGACTTCAGACTAGCTTCGCCAAAGTGTGCATCTTGTCACAGTT 1196
 Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
 Db 1197 TTGACGCAATATTTCGACACTTTTGGACGATGACGAGCTTGCACTCTTCACACTTCCA 1256
 Qy 388 IleLysArgTyrPheProSerAlaMetGlyCysLeuProGluTyrMetLysGlyValTyr 407
 Db 1257 ATTAAAGATGATCTCATCTCAGACTAGAACCTTTCCAGAAATATATGAATGTGTGAC 1316
 Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
 Db 1317 ATGTCGTGTTGAAACTGTAAATGAATGAACAGAGAGGGGAGAACTCAAGCGAGA 1376
 Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447
 Db 1377 AACACTCTCAACTATGTTGCAAGGCTTGAGGCTTTTGTGATTCATATATGAGAA 1436
 Qy 448 AlaLysTyrPheIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGlnAsnGlyLys 467
 Db 1437 GCAAAATGAGATCTCTAATGTTATCTGCCAATGTTTGAAGATACCATGAGAAATGGGAAA 1496
 Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
 Db 1497 GTGAGCTCTGCAATCCGCTAGCAACATTTGCAACCTTCATCTTGAATGACATGCGTT 1556
 Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
 Db 1557 CCTATATACATCTTGAAGAGAAATGATTTTCATCTCAGAGTTCAATGATTTGGCATCGTCC 1616
 Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
 Db 1617 TTCCTTCGGCTACAGAGTACACAGCTGCTACAGAGCGCATGGAGATCGTGGTGAAGA 1676
 Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluAlaAspAlaLeu 547
 Db 1677 GCTTCGTATATATCATGTTATATGAAGAACAACTCTGATCAACGAAAGAAATGCTCCTC 1736

Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTyrGluLeuLys 567
 Db 1737 AATCATATCAATGCCATGCTCAATGACTTAATCAAAAGATTAATTTGGAATCTTAAGA 1796
 Qy 568 ProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArgValTyr 587
 Db 1797 TCCAACGACAAATATTTCATATGCTGCGCCAGAAACATGCTTTTGAACATACAGACTCTC 1856
 Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
 Db 1857 CACCATCTCTCAATATATGAGATGCTTAGTGTGCCAACAGGAACAAATAAATTTG 1916
 Qy 608 ValMetArgThrValIleGlu 614
 Db 1917 GTTATGAAACACTCTTGAA 1937
 RESULT 7
 ID AAA38927
 XX AAA38927 standard; DNA; 2196 BP.
 AC AAA38927;
 XX
 DT 25-AUG-2000 (first entry)
 XX
 DE Grand fir myrcene synthase DNA sequence SEQ ID NO:29.
 XX
 KW Synthase; protein co-ordinate data; active site; modification; terpenoid;
 KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
 KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
 KW defensive agent; pigment; antitumour; steroid hormone;
 KW signal transduction pathway; bile acid; affinity purification;
 KW photoreceptor; enzymatic synthesis; nutrient supplement;
 KW immunological reagent; ds.
 XX
 OS Abies grandis.
 XX
 PN WO200017327-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 17-SEP-1999; 99WO-US021419.
 XX
 PR 18-SEP-1998; 98US-0100993P.
 PR 22-APR-1999; 99US-0130628P.
 PR 23-AUG-1999; 99US-0150262P.
 XX
 PA (KENT) UNIV KENTUCKY RES DEPT.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Chappell J, Manna KR, Noel JP, Starks CM;
 DR WPI; 2000-292839/25.
 DR P-PSDB; AAY90842.
 XX
 PT Novel terpene synthase enzymes, useful for producing terpene
 PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
 PT enzymes by specific amino acid alterations.
 XX
 PS Disclosure; Page 387-390; 450pp; English.
 XX
 CC The present invention describes an isolated terpene synthase (1)
 CC comprising a region with at least 20% identity to region 265-535 of a 548
 CC amino acid (aa) sequence (1a), given in AAY90831. (1) contains nine alpha
 CC -carbon atoms (alphaC) that have interatomic distances, between each
 CC other, within tabulated ranges, have a centre point (within a sphere of
 CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
 CC arrangement of R groups (defining as side chains), excluding specific
 CC tabulated arrangements (tables given in the specification). (1), and
 CC related enzymes, are used to produce a wide range of terpenoids. (1), and
 CC cyclic, acyclic, optionally hydroxylated, useful e.g. as fragrances,
 CC flavours, pheromones, defensive agents, pigments, antitumour agents,
 CC components of signal transduction pathways, precursors of steroid

CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity (and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA8910 to AAA8938 and AAA90831 to AAA90859 represent
CC sequences used in the exemplification of the present invention

XX Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,01e-217	Length:	2196
Score:	2200.50	Matches:	427
Percent Similarity:	80.38%	Conservative:	77
Best Local Similarity:	68.10%	Mismatches:	106
Query Match:	67.69%	Indels:	17
		Gaps:	7

US-10-025-145a-65 (1-618) x AAA38927 (1-2196)

```
QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 69 ATGGCTGCTGTTCTATCTCAACCGTTGGCTTCGAAATCTTCCTGCGAAGTCGTGATC 128
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 129 AGTTCATATTCATGAACATAGCCTCCCTATAGAACATCCCAATCTTGAAATGGTAA 188
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 36 ProGluYSerValAlaIleSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 189 CGAGGGAATCTGTCAAGCCTTCATAGCATGATGTTGGCCACCGCTGCACCTGATAT 248
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 56 SerValGlnArgValGlyAsnTyRHisSerAsnLeuTrpAspAspPheIleGln 75
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 249 GGTGTACAAAGACCATGATGATGATCCATATCTCGAATCTGGAGCATGATTTCAACAG 308
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 76 SerLeuIleSerThrProTyRGIYAlaProAspTyRArgGluArgAlaAspArgLeu 95
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 309 TCTCTA--TCAAGCCTTATGGGAACTCTTACACGAAACGTGCTGAGAGATTATTT 365
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 96 G1YgluValIlyAspRileMeCpHeAsnPhelYSerLeuGluAspGlyIly----- 112
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 366 GTGAGGTTAAAGAGATA--TTCAATTCAATGTAACCTGATGATGAAAGATTATAGCT 422
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAlaAspValGluArgLeuGlyIle 130
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 423 TCCCTTATATGATCTCATGCAACGCTTGTGATAGTCACTAGCGTTGAACGTTTGGGATA 482
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 131 AspArgHisPheIlySlyGluIleYSerThrAlaLeuAspTyRValAsnSerTyRTrpAsn 150
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 483 GCTGACATTTTCAGAAAGACAGATACATCACTCTGAGATTATGTTTCCGTTACGGGAG 542
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 151 GluYserGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 543 GAAAGACGATTTGATGATGGGAGACAGATTGTTACTGATCTCAACTCACTCGTTG 602
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 171 G1YleuArgThrIleuArgLeuHisGlyTyRThrValSerSerAspValLeuAsnValHe 190
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 603 GGGTTTTCAGACCTTCGATTAACGCGGTACACTGATATCTCAGAGGTTTAAAGCTTTT 662
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 663 CAAGATCAAAATGACAGATTTGTATGCTCCCGCT--CAGACAGAGGGTGAAGTCA 719
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 211 G1YValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIlyValMetAsp 230
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 720 AGCGTTCTTAATATATCGGCTTCCCTCAATGCTTCCCTGGTGAAGAAAGTTATGAA 779
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 231 G1YValGluThrPheSerThrIlyTyRLeuArgGluAlaLeuGlnIlyIleProAlaSer 250
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 780 GAACTGAAATCTTCTCCCAAGATATTTGAAAGAAAGCTTACAAAAGATTCAGTCTCC 839
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyRGIYTrpHisThrAsnLeuPro 270
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 840 GCT---CTTTCACAAAGATTAAGTTTGTATGAAATATGGCTGGCACAAATTTGGCA 896
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 271 ArgLeuGluAlaArgAsnTyRMeCpAspValPheGlyGlnHisThrIlyS-----Asn 287
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 897 AGATTGGAGACAGAAATTTATCATAGACACACTTGAGAAAGCACACAGTGCATGCTCAAT 956
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 288 LysAsnAlaIleGluYsLeuLeuGluLeuAlaIlySerLeuPheAsnIlePheHisSer 307
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 957 AAAATGCTGGAGAAAGCTTTTAACTTGAACTTGCAAAATTTGAGTTCAATATTTAACTCC 1016
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 308 LeuGlnGluArgGluLeuYsIleValSerArgTyRTrpLysAspSerGlySerProGlu 327
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1017 TTACAAACAAAGAAATTTACATATCTTTGAGATGGTGGAAAGATGGATTCCTTAA 1076
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 328 MetThrPheCysArgHisArgHisValGluTyRTrpAlaLeuAlaSerCysIleAlaPhe 347
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1077 TTGACATTTGCTCGGCATCTCATGTGAAATTTCAACTTGGCCCTCTGTATTTGCCATT 1136
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrIlySerMetSerHisLeuIleThrVal 367
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1137 GACCCAAACATTTTGCAATTCAGACTAGGCTTCCCAAATGTGTCAATGTGTCACT 1196
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 368 LeuAspAspMetTyRAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1197 TTGACAGATATTTTACACACTTTTGAACATTTACGAGCTTGAACCTTCACTCACTGCA 1256
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 388 IleYsArgTrpAspProSerAlaMetGluCysLeuProGluTyRMetIlyGlyValIly 407
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1257 ATTAAAGATGGAATTCATCAGATAGTAACACCTTCCAGAAATATGAAATGTGTAC 1316
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 408 MetMetValTyRHisThrValAsnGluMetAlaArgValAlaGluYsAlaGlnIlyArg 427
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1317 ATGGTCGGTTTGAACCTGTAATTAACCTGACACGAGGCGGAGGAACTCAAGGAGAA 1376
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 428 AspThrLeuAsnTyRAlaArgGlnAlaTrpGluAlaCysPheAspSerTyRMetGlnGlu 447
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1377 AACACTGCACATATGTTTGCAGAAAGCTTGGAGGCTTATTTGATTCATATATGAAAGAA 1436
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 448 AlaIlyStrPilleAlaThrGlyTyRLeuProThrPheGluGluTyRLeuGluAsnGlyIly 467
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1437 GCAAAATGATCTCTAATGTTATCTGCAATGTTTGAAGGlyCSCATGAAGAAAGGAAA 1496
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspRileProPhe 487
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1497 GTGAGCTCTGCATATCGGCTAGCAACATTTGCACCATCTTCACTTGAATGCATGCTT 1556
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 488 ProAspHisIleLeuYsGluValAspPheProSerTyRLeuAsnAspLeuIleCysIle 507
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1557 CCGATTACATCTTGAAGGAAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGGCC 1616
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyRlyValAlaAspArgAlaArgGlyGluGlu 527
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1617 TTCCCTTGGCTACAGAGTGACACACGCTGTACAGGCCGATAGGATCGTGGTGAAGAA 1676
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 528 AlaSerSerIleSerCysTyRMetIlyAspAsnProGlyLeuThrGluGluAspAlaLeu 547
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1677 GCTTCGCTATATCATGTTATATGAAACAAATCTTGATCAACCGAAAGAAATGCCCTTC 1736
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuIly 567
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1737 AATCATATCAATGCAATGCTCATGATGACATATCAAGAAATTAATTTGGGAATCTTAAGA 1796
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 568 ProAspAsnSerValProIleThrSerIlyYsHisAlaPheAspIleSerArgValTrp 587
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1797 TCCAACCAATATTTCAATCTGCGCCAAAGAAACATGCTTTTGCATTAACAAGCTCTC 1856
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 588 HisHisGlyTyRArgTyRArgAspGlyTyRSerPheAlaAsnValGluThrIlySerLeu 607
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 1857 CACCATCTCTCATATATTCAGATGGCTTTTGTGTGCCAACAGAAACAAAATTTG 1916
DB |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
```

QY 608 ValMetArgThrValIleGlu 614
DB 1917 GTTATGAAACATCTCTGAA 1917

RESULT 8
ID AAF73371 standard; cDNA; 2196 BP.
XX AAF73371;
XX AAF73371;
XX 30-APR-2001 (first entry)
XX Grand fir myrcene synthase coding sequence SEQ ID NO: 1.
XX
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
XX myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
XX terpinolene synthase; insect resistance; nutrition; 88.
XX
XX Abies grandis.
XX W0200107565-A2.
XX
XX 01-FEB-2001.
XX 24-JUL-2000; 2000MO-US020264.
XX 26-JUL-1999; 99US-00360545.
XX
XX (UNIV) UNIV WASHINGTON STATE RES FOUND.
XX Steele CL, Bohlmann J, Croreu RB, Phillips MA;
XX WPI; 2001-182782/18.
XX P-PSDB; AAB69370.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
XX synthesis in plants, e.g. for increasing resistance to pests or for
XX treatment of cancer.
XX
XX Claim 28; Page 103-106; 175pp; English.

CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

XX
XX Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,01e-217 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
Gaps: 7

US-10-025-145A-65 (1-618) x AAF73371 (1-2196)

QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 69 ATGGCTGTGGTTTATCTACGCTGGCTTGAATCTTGCCTGGCGAAGTCGTTGATC 128
QY 16 SerSerSerHisGluIleLeuValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB 129 AGTTCATATCTGAAACATTAAGCTCCCTATGAAACATCCCAATCTTGGATGCGTAA 188
QY 36 ProGlyIysSerValAlaIleHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 189 CGAGGAAATCTGTACGCGCTTGCATGAGCATGATTGGCCAGCCGCGACATGATAT 248

QY 56 SerValGlnArgArgValGlyAsnThrHisSerAsnLeuTrpAspAspPheIleGln 75
DB 249 GGTGTACAAAGACGATGGTGGTACCATTCACATTCATGGAGCATGATTTTCATACAG 308
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB 309 TCTCTA---TCAAGCGCTTATGGGGAACCCCTTACCGAGAAACGGTGGAGATTAATT 365
QY 96 GlyGluValIysAspIleMetPheAsnPheIysSerLeuGluAspGlyIle----- 112
DB 366 GTGAGAGGAAAGAAAGAT---TTCAATTCAATGATGACCTGGATGATGAGATTAATAGCT 422
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAlaAspAspValGluArgLeuGlyIle 130
DB 423 TCTTTAATGATTCATGCAACGCTTGGATGATGATGATGATGATGATGATGATGATGAT 482
QY 131 AspArgHisPheIysGlyIleValIleThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 483 GCTAGACATTTCAAGACGAGATTAACATGCTGTGATTAATGTTTCCGTACTGGAG 542
QY 151 GlyIysGlyIleGlyCysGlyArgGluSerValAlaThrAspLeuAsnSerThrAlaLeu 170
DB 543 GAAACGCGCATTTGGATGGGAGACAGATGATGATGATGATGATGATGATGATGATGAT 602
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValIleAsnValPhe 190
DB 603 GGGTTTGAACTTTCATTAACAGGATTAACAGGATTAACAGGATTAACAGGATTAACAG 662
QY 191 LysAspLysAsnGlyIlePheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB 663 CAAGATCAAAATGACAGCTTTGATGCTCCCGCT---CAGACAGAGGATGATGATGAT 719
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyIleValMetAsp 230
DB 720 AGCCTTCTTAATTAATATCGGCTTCCCTCATTCCTCCCTGATGAAAGTTATGAGA 779
QY 231 GluValGluThrPheSerThrIleTyrLeuArgGluAlaLeuGlnIleProAlaSer 250
DB 780 GAACTTGAATCTTCTCCACAAAGATTAATTAAGAAAGCTTACAAAGATTTCCAGCTTC 839
QY 251 SerLeuSerLeuGluIleArgAspValLeuGluTyrGlyIleThrAsnLeuPro 270
DB 840 GCT---CTTTCACAGAGATTAAGTATTGATGAAATATGCTGGCACAAATTTGCCA 896
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyIleHisThrIys-----Asn 287
DB 897 AGATTGGAAGCAAGAAATTCATGACACACCTTGAGAAAGACACAGTCATGCTCAT 956
QY 288 LysAsnAlaIleGluValLeuLeuGluLeuAlaIysLeuGluPheAsnIlePheHisSer 307
DB 957 AAAAATGCTGGGAGAAAGCTTTTGAACCTTGCAAAATTTGAGTTCAATATTATTAATCC 1016
QY 308 LeuGlnGluArgGlyLeuValIleValSerArgTyrTrpLysAspSerGlySerProGlu 327
DB 1017 TTACACAAAGAAATTAACATATCTTTGAGATGAGTGGAAAGTGGATTTGCTTAA 1076
QY 328 MetThrPheCysArgHisValGlnIleValIleGluTyrAlaLeuAlaSerCysIleAlaPhe 347
DB 1077 TTGACATTTGCTCGGACATGATGATGATGATGATGATGATGATGATGATGATGAT 1136
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrIysMetSerHisIleuIleThrVal 367
DB 1137 GAAACCAAAACATGTCATTCAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 1196
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
DB 1197 TTGGACATATTTTACGACATTTTGAACGATTAACAGCTTGAACCTTCACTGCA 1256
QY 388 IleValArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetIysGlyValIleTyr 407
DB 1257 ATTAAAGATGAGATTTATCATGAGATGAAACATCTTCAAGAAATTAATGAAATGTGTATC 1316


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591 GGGTTTCAAACTCTTCGATTACAGCGGTACACTGATCTCCAGAGCTTTAAACCTTT
191 LysApblysaanglyginpheserThralaenlelglnleuglyglnlearg 210
651 CAAGATCAAAATGACAGCTTTGTATGATCCCCGGT---CAGACAGAGGTGATGACAGA 707
211 G1yValleuAenleuPhaArgAlaSerleuValAlaPheProGlyGlnLysValMetAsp 230
708 AGCGTTCTTAACCTTAATATCGGGCTTCCTCATTCCTCCGAGAAAGTTATGAAA 767
231 G1uAlaG1uThrPheSerThrLysTyrleuArgGlnAlaLeuGlnLysIleProAlaSer 250
768 GAGCTGAAATCTTCCACAGATATTTGAAAGAAAGCTCTACAAAGATTCAGCTCC 827
251 SerleuSerleuGlnIleArgAspValleuGlnIleArgLysIleThrAsnleuPro 270
828 GCT---CTTTCACAGAGATTAAGTTGTATGATGAATATGGCTGGACACAAATTTGCCA 884
271 ArgleuGlnAlaArgAsnTyrMetAspValPheGlyGlnIleThrLys-----Asn 287
885 AGATTGGAGAGCAAAATTAACATAGACACTTGAAGAAAGACACAGTCATGGCTCAT 944
288 LysAsnAlaAlaGlnLysleuLeuGlnleuAlaLysleuGlnPheAsnIlePheHisSer 307
945 AAAAATGCTGGAGAGAGACTTTTAGAACTTGCAAAATGGAGCTTCAATATATTAATCTC 1004
308 LeuGlnIleuArgGlnleuLysIleValSerArgTyrPheAspSerGlySerProGln 327
1005 TTACAAACAAAGAAATTAACATATCTTTGAGATGGTGAAGAAAGCTCGGATTTGGCTTAA 1064
328 MetThrPheCysArgHisArgHisValGlnTyrTyrAlaLeuAlaSerCysIleLeuIle 347
1065 TTGACATTTGCTCGGCATCGTATGTGAATTCACCTTGGCTCTTGATTTGCCATT 1124
348 G1uProGlnHisSerGlyPheArgleuGlyPheThrLysMetSerHisleuIleThrVal 367
1125 GACCCAAACATTTGCGATTCAGACTAGGCTTGGCAAAATGTGCATCTTGTCAAGTT 1184
368 LeuAspAspMetCysArgAspValPheGlyThrValAspGlnleuGlnPheThrAlaThr 387
1185 TTGGACGATATTTAGACACTTTTGAACGATTTGACGAGCTTGAACCTTGCACATCTGCA 1244
388 IleLysArgTyrPheProSerAlaMetGlnCysleuProGlnTyrMetLysGlyPheIle 407
1245 ATTAAGAGATGAATTCATCAGAGATAGAACCTTCCAGAAATATATGAATGTGTGAC 1304
408 MetMetValTyrHisThrValAsnGlnMetAlaArgValAlaGlnLysAlaGlnIleArg 427
1305 ATGTCGCGTTTGAACCTTAATTAAGTACGACACAGAGCGGAGAAAGCTCAAGGAGAA 1364
428 AspThrleuAsnTyrAlaArgGlnAlaTyrGlnAlaCysPheAspSerTyrMetGlnIle 447
1365 AACACTCTCAACTATGTTCGAAGAGCTTGGAGGCTTATTTGATTCATATATGGAAGAA 1424
448 AlaLysTyrPheIleAlaThrGlyTyrleuProThrPheGlnGlnIleuGlnLysAlaLys 467
1425 GCAAAATGATCTCTAATGTATTCGCCAAGTTTGAAGATACATGAGATGAGGAAA 1484
468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
1485 GTGAGCTTCGATATCGCGTACCAACATTCGAAACCACTTCATCTTGAATGCAAGGCTT 1544
488 ProAspHisIleleuLysGlnValAspPheProSerLysleuAsnAspLeuIleCysIle 507
1545 CCTGATTCATCTTGAAGAGAAATGATTTTCATCCAGATTCAAATGATTTGGCATGCTCC 1604
508 IleleuArgleuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlnIle 527
1605 TTCTCTCGCTACGAGGTGACACAGCTGCTACAAAGCGGATGAGGATCGTGTGAAGAA 1664
528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGlnIleuAspAlaLeu 547

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DB 1665 GCTTGTATATCATGTTATATGAAAGACAACTCGATCAACCGAAGAGATCCCTC 1724
QY AsnHisIleAsnPheMetIleArgAspAlaIleArgGlnleuAsnTyrGlnleuLys 567
DB 1725 AATCATATCAATATGCGTGTCAATGACATTAATCAAAAGATTAATTTGGAACTTTAAGA 1784
QY ProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArgValTyr 587
DB 1785 TCACAGCAATATTCATCAATGCTGCGCAAGAAACATGCTTTTGACATTAACAGACTCTC 1844
QY HisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGlnThrLysSerleu 607
DB 1845 CACATCTCTCAATATATGATGAGATGGCTTTAGTGTGCCAACAGAAACAAAAATTG 1904
QY ValMetArgThrValIleGln 614
DB 1905 GTTATGAAACATCTCTTGA 1925

RESULT 10
ID AAF73391 standard; cDNA; 2205 BP.
XX
AC AAF73391;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 31.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
XX terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNITV) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX WPI; 2001-182782/18.
XX DR P-PSDB; AAB69380.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants; e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Example 3; Page 135-137; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4,13e-217 Length: 2205
Score: 2197.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 58.10% Mismatches: 106
Query Match: 67.59% Indels: 17
DB: 4 Gaps: 7

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US-10-025-145A-65 (1-618) x AAF73391 (1-2205)

Qy 1 MetAlaLeuSerSerIleThrProLeuValSerArgSerCysLeu----- 15

Db 57 ATGGCTCTGGTTTATCTTCACCGTGGCTTCGAAATCTTGCCGCGCAAGTCGTTGATC 116

Qy 16 SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35

Db 117 AGTTCAATTCATGAAACATTAACCCCTCCATAGAACATCCCAATCTTGGAAATGCGTAGG 176

Qy 36 ProGlyIysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55

Db 177 CGAGGGAATCTGTCACGCGCTTCATGACGATCATGTTGGCCGCGCAGCTGATGAT 236

Qy 56 SerValAlaGlnArgValGlyAsnThrHisSerAsnLeuThrPheAspAspPheIleGln 75

Db 237 GGTGTACAAAGACGATAGTGACTACCATTCCAATCTGGAGAGATGATTCATACAG 296

Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95

Db 297 TCTCTA---TCAAGCATTAATGGGGAACCTCTTACCGAAGACGTGCGAAGATTAT 353

Qy 96 GlyGluValIysAspIleMetPheAsnPheIysSerLeuGluAspGlyIle----- 112

Db 354 GTGAGGGAAGAAGATTA---TTCATTCATGATGATGATGATGATGATGATGATGAT 410

Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130

Db 411 TCCCTTAATGATGTCATGCAACGCGCTTGGATGATGATGATGATGATGATGATGAT 470

Qy 131 AspArgHisPheIysGlyIleIleThrAlaLeuAspTyrValAsnSerTyrThrAsn 150

Db 471 GCTAGACATTTCAAGAACGATTAACATCACTCTGATTTATGTTTCCGTTACGCGAG 530

Qy 151 GluIysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170

Db 531 GAAACCGCATTTGATGTCGAGAGACAGATTTGTTACTGATCTCAACTCAACGCGTTG 590

Qy 171 GlyLeuArgThrIleuArgLeuHisGlyIleThrValSerSerAspValLeuAsnValPhe 190

Db 591 GGGTTTGAACTCTTCATTAACGCGGTACGATGATCCAGAGTTTAAAGCTTTT 650

Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210

Db 651 CAAGATCAAAATGACAGTTTGATGCTCCCGCGT---CAGACAGAGGATGATCGA 707

Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluValMetAsp 230

Db 708 AGCCTTCTTAATTATATCGGGCTTCCCTCATTCGCTTCCCTGGAGAAAGTTATGGA 767

Qy 231 GluIleArgIlePheSerThrIleThrArgGluIleGluIleValIleProAlaSer 250

Db 768 GAACTGAAATCTTCTCCACAGATATTGAAAGAGCTTACAAAGAAATTCACGCTCC 827

Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyIleThrPheIleAsnLeuPro 270

Db 828 GCT---CTTTCACAGAGATTAAGTTTGTATGAAATATGCTGGCAACAAATTTGCCA 884

Qy 271 ArgLeuGluIleAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287

Db 885 AGATTGGAGCAAGAAATTAATACATAGACACACTTGAAAGACACACAGTGCATGCTCAAT 944

Qy 288 LysAsnAlaIleArgIleLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307

Db 945 AAAAATGCTGGAGAGAGCTTTTGAACCTTGCAAAATTTGGATTCATATATTTAACTCC 1004

Qy 308 LeuGlnArgIleArgIleLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327

Db 1005 TTACACAAAGAAATTAATATCTTTTGAAGATGCTGAAAGAGTGGATTTGGCTTAA 1064

Qy 328 MetThrPheCysValArgHisValAlaGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347

Db 347

Db 1065 TTGACATTTGCTCGGACATCGTCAATGTGAAATCTTACACTTTGGCCTCTGTATTCATT 1124

Qy 348 GluProGlnHisSerSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367

Db 1125 GACCCAAACATTTCTGATTCAGACTGAGCTTGCCCAAAATGTCTATCTTTGTACAGCT 1184

Qy 368 LeuAspAspMetCysTyrAspValPheGlyIleThrValAspGluLeuGluPheThrAlaThr 387

Db 1185 TTGACGATATTTCAGACACTTTTGAACGATTCAGACGCTTGAACTTTCACATCTGCA 1244

Qy 388 IleValArgTyrPheProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1245 ATTAAGAGATGGAATTCATGAGATGAAACACTTCAGAAATATGAAATGTGTGAC 1304

Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427

Db 1305 ATGTCGTGTTTGAACCTGTAAATGAACCTGACACAGAGCGGAGAACTCAAGGAGAA 1364

Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaIleProGluIleCysPheAspSerTyrMetGlnGlu 447

Db 1365 AACACTCTCAACTATGTTTCGAAAGGCTTGGAGGCTTATTTGATTCATATATGAAAGAA 1424

Qy 448 AlaIleTyrPheIleAlaThrGlyIleThrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1425 GCAAAATGATCTCTTAATGTTATCTTCGCAACGTTTAAAGATGACATGAAATGGAGAA 1484

Qy 468 ValSerSerAlaHisAspProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487

Db 1485 GTGAGCTCTGATATCCCGTAGCAACCTTGCAACCTCTCACTTGTGATGATGATGCTT 1544

Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

Db 1545 CCGTATTAACATCTTGAAGGGAATGATTTTCCATCCAGCTTCAATGATTTGGCATCGTCC 1604

Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrIleValAlaAspArgAlaArgGlyGluGlu 527

Db 1605 TTCCTTGGCTACAGAGTGAACACGCTGCTACAAAGCCGATAGAGATCGTGGAAGAA 1664

Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluValAspAlaLeu 547

Db 1665 GCTTCGTGATATCATTTATATGAAGACATCTTGATCAACCGAAGAAAGATGCCCTC 1724

Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTyrGluLeuLys 567

Db 1725 AATCATATCAATGACATGCTGCAATGATATCAAAATTAATTTGGAACTTCAAGA 1784

Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTyr 587

Db 1785 TCCAAACGACAAATATTCAAAGCTGCGCAAGAAACATGCTTTGACATTAACAGAGCTCTC 1844

Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

Db 1845 CACCATCTCAATATATTCAGATGCGTTTATGTTTCCCAACAGAAACAAAAATTTG 1904

Qy 608 ValMetArgThrValIleGln 614

Db 1905 GTTATGAAACACATCTTGAA 1925

RESULT 11

AA73421 ID AAF73421 standard; cDNA; 1890 BP.

AA73421; AAF73421;

30-APR-2001 (first entry)

Grand fir monoterpene synthase coding sequence SEQ ID NO: 77.

Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

terpinolene synthase; insect resistance; nutrition; ss.

Abies grandis.

XX MO200107565-A2.
 XX 01-FEB-2001.
 XX 24-JUL-2000; 2000OWO-US020264.
 XX 26-JUL-1999; 99US-00360545.
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX Steele CL, Bohlmann J, Croten RB, Phillips MA;
 XX WPI; 2001-182782/18.
 XX P-PSDB; AAB69393.
 XX New nucleic acid encoding monoterpene synthases, for increasing terpene
 XX synthesis in plants, e.g. for increasing resistance to pests or for
 XX treatment of cancer.
 XX Claim 18; Page 163-165; 175pp; English.
 XX The present invention provides the protein and coding sequences of
 XX monoterpene synthases from the grand fir. These include (-)-camphene
 XX synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
 XX limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
 XX and pinene synthase. The sequences can be used to produce transgenic
 XX plants expressing high levels of the enzymes, resulting in levels which
 XX are useful in protecting against and treating cancers, and to confer
 XX insect resistance on plants
 XX Sequence 1890 BP; 550 A; 381 C; 441 G; 518 T; 0 U; 0 Other;
 SO Alignment Scores:
 Pred. No.: 6,116-211 Length: 1890
 Score: 2137.00 Matches: 427
 Percent Similarity: 78.86% Conservative: 73
 Best Local Similarity: 67.35% Mismatches: 114
 Query Match: 65.73% Gaps: 20
 DB: 4 Indels: 9
 US-10-025-145a-65 (1-618) x AAF73421 (1-1890)
 QY 1 MetAlaLeuSerIleThrProLeuValSerAspSerCysLeuSer----- 16
 Db 1 ATGGCTCTGTTCTATCTTGGCTTGTCTTCCAAATCGCTCCACAAATCGTGATC 60
 QY 17 ---SerSerHisGluIleLeuValLeuArgThrIleProThrLeuGlyIleCysArg 35
 Db 61 GTTCTACTTATGACCATTAAGGCTATCGATGACAAATCCAAATCTTGATGGCTGGG 120
 QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
 Db 121 CGAGGGAATCTGTGACACATTCCTCGAAGATGAGTTGAGCAGCGAGTCTGTATGAT 180
 QY 56 ---SerValGlnArgArgValGlyAsnIleHisSerAsnLeuThrAspAspPheIle 74
 Db 181 CATGGTGTACAAAGCGATAGTCAGATTTCATTCATTCGTGGAGACGACATTTCTATA 240
 QY 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluAlaArgAlaAspArgLeu 94
 Db 241 CAATCTCTA---TCAACGCCCTTATGGGCACTTCATACCGTGAAACGTGCTGATGACTT 297
 QY 95 IleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
 Db 298 ATTGGAGAAAGTAAAGGTATATA---TTCACTTCAATTTCAGCGAAGATGAGAACTAATC 354
 QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
 Db 355 ACTCCCTCAAGATCTCATTCACGCCCTTTTAATGGTGGATTAACGTTGAACGTTTAGGG 414
 QY 130 IleAspArgHisPheLysGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrp 149

Db 415 ATGTATAGACATTTCAAAATAGATTAAGACAGACACTAGACTATTGTTACAGTTATTGG 474
 QY 150 AsnGluLysGlyIleGlyCysGlyAlaArgIleSerValIleThrAspLeuAsnSerThrAla 169
 Db 475 AACGAAAAAGGCAATGGCAGTGAAGTGTGTGTGCTGATCACTCAACCTCACTCC 534
 QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValIleSerSerAspValLeuAsnVal 189
 Db 535 CTGGGGTTTCCAAATTTCTTCGACTACACGATACAGTGTCTTTCAGATGTGTGGAAACAC 594
 QY 190 PheLysAsp-----LysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGly 207
 Db 595 TTCAAAAG 651
 QY 208 GluIleArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLys 227
 Db 652 GAGATMAAAACCGTTCTCAATTTATTTTGGGCTCCCTCCATGCTTTCCTGGGAGAAA 711
 QY 228 ValMetAspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIle 247
 Db 712 GTTATGAGAGAGCTGAAATCTTCTTAAATATATTTAAAGAGCTTACAAATATT 771
 QY 248 ProAlaSerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheThr 267
 Db 772 GGTGTCTCCAGT---CTTTCACAGAGATAGAGTACGTTTCGAGAGATGTTGGCAACA 828
 QY 268 AsnLeuProAlaGluLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsn 287
 Db 829 AATATGCCAAAGTTGAAACAAAGCAACATCATCGATGATGGGAGAACAAATCGTAT 888
 QY 288 LysAsnAla-----AlaGluLysLeuLeuGluAlaLysLeuGluPheAsnIle 304
 Db 889 GAGACGTTATATATGACATGAGAGAACTTTAGAAATTCGAAATTCGAAATTCGAAATTT 948
 QY 305 PheHisSerLeuGlnGluArgGluLysValSerArgTyrTrpLysAspSerGly 324
 Db 949 TTTGACTCTTATCAACAGAGAGAGTAAAGACCTTCAGATGGTGGAAAGATTGGGGT 1008
 QY 325 SerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCys 344
 Db 1009 TTCTTCCACTGACATTTTCTCGGATCGTATGGAATTCATCGCTGGCACTTGGC 1068
 QY 345 IleAlaPheGluProGlnIleSerGlyPheArgLeuGluPheThrLysMetSerHisLeu 364
 Db 1069 ATGGAACCTGATCGCAACATTCGGAATTCAGACTCGCTTTCGCAAAATGTGTATCTT 1128
 QY 365 IleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPhe 384
 Db 1129 ATCAGCGTTTGGAGCATATATATACGACCTTTGGAAACAAATGGAGAGACTGGAATCTTC 1188
 QY 385 ThrAlaThrIleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLys 404
 Db 1189 ACTGAGCATTTAAGAGATGGATCCGCTGCCACAGATTTGCTTCCAGAGATATATGAAA 1248
 QY 405 GlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAla 424
 Db 1249 GGGTTGATCATGTGGTGTATACGAACCTTAATGAATGCTTCGAGAGCGACAGACAGCT 1308
 QY 425 GlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyr 444
 Db 1309 CAAGCGCAGAGAGAGCGCTCAACGATGCTGACAGAGCTGGAGGCTTATCTGATTCGTAT 1368
 QY 445 MetGlnGluAlaLysTrpIleAlaThrGlyLysLeuProThrPheGluGlnTyrLeuGlu 464
 Db 1369 ATGAAGAAGCTGATGATCTCCAGTGTATATCGCCAAAGCTTTGAGAGATACATGAG 1428
 QY 465 AsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAsp 484
 Db 1429 ACCAGCAAAAGTTAGTTTGGTATTCGCTATTCGCTGCAACCATCTCTACATATGAT 1488
 QY 485 IleProPheProAspHisAlaIleLeuLysGluValAspPheProSerLysLeuAsnAspLeu 504
 Db 1489 GTTCCCTTATCTCACACATCTCTGACGAAATATACATTTTCATTGAGGTAAATGACATTA 1548

QY 505 IleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrIleValAspArgAlaArg 524
DB 1549 ATATGTCCTCATCTTCCATTTAAAAATGACACTGCTGCTCAAGAGCGGAGAGGCCCCGT 1608
QY 525 GlyGluGluAlaSerSerIleSerCysTyrMetIleAspAspProGlyLeuThrGluGlu 544
DB 1609 GGAGAGAGAGCTTCGTGATATCGTGTATATGAAGAAGATCTCGATCAACAGAGAA 1668
QY 545 AspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGlu 564
DB 1669 GATCTCATCATCATCATCAATCAAGCTATGCTCAATTAATCAAGAAGATTTGGAG 1728
QY 565 LeuLeuAspProAspAspSerValProIleThrSerIleValAlaPheAspIleSer 584
DB 1729 CTTCTCCAGACAGAGCGGACCGCTCATTTGCTTGCAAGAAACAGCTTTTGACATCTC 1788
QY 585 ArgValTrpHisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThr 604
DB 1789 AAGAGTTCCTTCACGGCTCAAAATACCGAGATGGGTTGACGGTGCACAGAGAAACC 1848
QY 605 LysSerLeuValMetArgThrValIleGluProValProLeu 618
DB 1849 AAGAAATGGGTGAGAGAGAAAGCTCTTGAGTCTGTGCTTTG 1890
RESULT 12
AAF73413
ID AAF73413 standard; cDNA; 2429 BP.
XX AAF73413;
AC AAF73413;
XX 30-APR-2001 (first entry)
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 68.
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX Abies grandis.
OS WO200107565-A2.
PN 01-FEB-2001.
XX 24-JUL-2000; 2000WO-US020264.
PF 26-JUL-1999; 99US-00360545.
XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
PA Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX WPI; 2001-182782/18.
DR P-PSDB; AAB69392.
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
PS Claim 23; Page 156-159; 175pp; English.
XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX Sequence 2429 BP; 726 A; 484 C; 512 G; 707 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,45e-205 Length: 2429
Score: 2084.50 Matches: 417
Percent Similarity: 77.29% Conservative: 80
Best Local Similarity: 64.85% Mismatches: 115
Query Match: 64.12% Indels: 31
DB: 4 Gaps: 13
US-10-025-145a-65 (1-618) x AAF73413 (1-2429)
QY 1 MetAlaLeuLeuSerIleThrProLeu---ValSerArgSerCys----- 14
DB 35 ATGGCTCTCTTCTCATATGATCTTTGACAGTTCCTCCAAATCTGGCGGAGAAATCGTTG 94
QY 15 LeuSerSerSerHisGluIleValAlaLeu-----ArgArgThrIleProThrLeuGly 32
DB 95 ATCAAGTTCAGCAATGTCAGAGAGAGCTCTGTATCTCTACAGAGATCCCAACTCTCAGA 154
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52
DB 155 ATGGGTAGCGCAAGAAAGCTGTGTC-----ATCAACATGAATGACCACTGATATCC 208
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67
DB 209 CATGCTATGATATATGCTGTGTGCTGATGCTCAAGAGAGCATGCCATCATCATCCAC 268
QY 68 LeuTrpAspAspAspPheIleGlnSerIleIleSerThrProTyrGlyAlaProAspTyr 87
DB 269 CTGTGGAGAGTATGATTTCAATCAATCTTG---TCTTCACCTTATGGGGATCTTCGTAC 325
QY 88 ArgGluArgAlaAspArgLeuIleGlyValIleValIleValIleMetPheAsnPhe----- 105
DB 326 AGTAACTGCTGTGACAGTGTGTTGAGAGAGTAAAGAG---ATGTTCAATTCATACCA 382
QY 106 -----LysSerLeuGluAspGlyValAsnAspLeuLeuGlnArgLeuLeuValAsp 123
DB 383 AATATATAGAGATTAATTTGTTCCCAAAATGATCTCTTACACGCTTTGGATGTGAT 442
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysValGluIleValIleValIleValAsp 143
DB 443 AGCATTAAGCTCTGGGATATGATAGCATTTTCCAAATAGATTAAGATAGCCCTCGAT 502
QY 144 TyrValAsnSerTyrTrpAsnGluLys---GlyIleGlyCysGlyArgGluSerValVal 162
DB 503 TATGTTTACAGTTATGAGAGAGAAAGAGCATTTGGGTGTGGCAGATTTCACTTTT 562
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182
DB 563 CCGATCTCAACTCGACTGCTGTGGCTTGGAACTTTGCACTGACCGGATACAAATGTG 622
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202
DB 623 TCTTCAGATGTGCTGGAATACTTCAAGATCAAAAGGGCATTTTGGCTGCGCCGCA--- 679
QY 203 IleGlnIleGluGlyGluIle---ArgGlyValIleAsnLeuPheArgAlaSerLeuVal 221
DB 680 ATCTTAACCGAGGAGACAGATCACTAGAAAGTGTCTTAATTAATTCGGGCTTCCCTGATC 739
QY 222 AlaPheProGlyValIleValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241
DB 740 GCTTTTCCGGGGGAGAAAGTTATGAGAGAGCTAAATCTTCTGGCATCTTATTTGAAA 799
QY 242 GluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGlnIleArgAspValLeu 261
DB 800 GAAGTCTTACAAAAGATTCAGTCTCAGT---TTTTCACAGAGATAGAAATAGCTTTTG 856
QY 262 GluTyrGlyTrpHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe 281
DB 857 GAATATGCTTGACACAAATTTGCCAAGATTGAAACCAAGAAATTAATGACAGTCTAC 916
QY 282 GlyGlnHisThrLysAsnLysAsn-----AlaAlaGluLysLeuLeu 295
DB 917 GGGCAGAGCAGCTATGAAGATTCAACGAGATGCCATATGTGAATACGACAGAGCTTTTA 976

QY 296 GluLeuAlaIyLeuGluPheAsnIlePheHisSerLeuGluArgGluLeuIyHis 315
 DB 977 AAACCTGCAAAATGGAGCTTTAATATCTTTCACCTTTGCAACAGAAAGTGGCAATAT 1036
 QY 316 ValSerArgITPTPLyAspSerGlySerProGluMetThrPheCysArgHisArgHis 335
 DB 1037 ATCTCTAGATGGTGGAAAGATTCCGCTTCATCTCATCTGACTTTTACTCGACACCGTCA 1096
 QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGluHisSerGlyPheArg 355
 DB 1097 GTGGAATCTACACAAATGSCATCTTGCAATTTCTATGAGACCGAAACACTCCGCTTTCAGA 1156
 QY 356 LeuGluPheThrIyMetSerHisIleuLeuIleThrValIleuAspMetTyrAspAlaPhe 375
 DB 1157 TTGGGGTTTGCACAAACATGTCATCTTCTAACAAGTTCTGGAGATATATATGACACTTTT 1216
 QY 376 GlyThrValAspGluLeuGluLeuPheThrAlaThrIleValArgTyrAspProSerAla 395
 DB 1217 GGAACACTGGACGAACCTCCAACTTTTACGACTGCTTACAGATGGGATTTGTCAGAG 1276
 QY 396 MetGluCysLeuProGluTyrMetIyGlyValTyrMetMetValTyrHisThrValAsn 415
 DB 1277 ACAAGTGTCTTCGAGATATATGAAAGACAGTACAGTACGACTGTATCAATGCTTAAAT 1336
 QY 416 GluMetAlaArgValAlaGluIyValGluArgIyArgAspThrIleuAsnTyrAlaArgGln 435
 DB 1337 GAATTTGGCGCAGAGGCTGAGAAAGCTCAGACGACAGATACGCTCACTAATTTGGCAAT 1396
 QY 436 AlaTyrGluAlaCysPheAspSerTyrMetGluGluAlaIySerTyrIleAlaThrGlyTyr 455
 DB 1397 GCTTATGAGTCTCATTTGATTCGTTTATGCAAGCAAGAAATGATCTCAAGTGTATAT 1456
 QY 456 LeuProThrPheGluGluTyrIleuGluAsnGlyIyValSerSerAlaHisArgProCys 475
 DB 1457 CTCCCAAGCTTTGAGAGTACTGTGAAGAAAGTAAAGTTAGTTCGGTTCGSCACAGCC 1516
 QY 476 AlaLeuGlnProIleLeuThrLeuAsnIleProPheProAspHisIleLeuIyGluVal 495
 DB 1517 ACTTTACAAACCTATCTCCTGATGTACCACTTCTAATATCAATCTCAGCAAAATTT 1576
 QY 496 AspPheProSerIyLeuAsnAspLeuIleCysIleIleLeuArgIyLeuArgIyAspThr 515
 DB 1577 GATTATCATCTAGTTCATGATGACTGTGCTTCGCTCCCTTCGCTACGTCGTACACG 1636
 QY 516 ArgCysTyrIyValAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535
 DB 1637 CGTGTCTACAGAGCGGATAGGCTCGTGGAGAAAGCTTCAGCTATATCGTTATATG 1696
 QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555
 DB 1697 AAAGACCACTCTGGATCAACAGAGAAAGATCTCTCAATCATATCAAGTCATGATCGT 1756
 QY 556 AspAlaIleArgGluLeuAsnTyrGluLeuIySerProAspAsnSerValProIleThr 575
 DB 1757 GATCATCATCAGAAATTAATTGGAGCTTCTCAGACCAAGTAGAAAGTCCCATCTCT 1816
 QY 576 SerIyIyHisIleAlaPheAspIleSerArgValTyrHisIleGlyTyrArgTyrArgPhe 595
 DB 1817 TCCAAAGAAACATGCTTTGACATCACACGAGCTTTCATCACTCAATCAAGTACGAGAT 1876
 QY 596 GlyIySerPheAlaAsnValGluThrIySerLeuValMetArgThrValIleGluPro 615
 DB 1877 GGTACACTGTGGCGAGTAGTGAACAAAGATTGGTATGAAACAGTCTTGAACCT 1936
 QY 616 ValProLeu 618
 DB 1937 GTGGCATTG 1945
 RESULT 13
 AAX08645
 ID AAX08645 standard; cDNA; 2089 BP.
 XX

AC AAX08645;
 XX 27-SEP-1999 (first entry)
 XX Limonene synthase gene.
 DE Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
 XX defense; plant seed; oil; meal; ss.
 XX Abies grandis.
 OS Key Location/Qualifiers
 FH CDS 73..1986
 FT /*tag= a
 FT /product= "limonene synthase"
 PN W09902030-A1.
 XX 21-JAN-1999.
 PD 10-JUL-1998; 98WO-US014528.
 PF 11-JUL-1997; 97US-0052249P.
 PR (UNIW) UNIV WASHINGTON STATE RES FOUND.
 PA Bohlmann J, Steele CL, Croteau RB;
 XX WPI; 1999-120396/10.
 DR P-PSDB; AAM85702.
 PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
 PT fir (Abies grandis), used to provide plants with modified production of
 PT monoterpenes, e.g. myrcene, limonene or pinene.
 PS Claim 11; Page 79-82; 121pp; English.
 CC Nucleotide sequences encoding myrcene synthase, limonene synthase and
 CC pinene synthase from Grand fir may be incorporated into any organism
 CC (e.g. intact plant, animal, microbe), or derived cell culture that
 CC produces geranyl diphosphate for the production of the aforementioned
 CC enzymes or their products. The sequences when expressed in transfected
 CC cells may also be used for the production or modification of flavour and
 CC aroma properties, improvement of defense capability, and the alteration
 CC of other ecological interactions mediated by myrcene, limonene, pinene,
 CC or their derivatives. In particular they can be used for the production
 CC of plant seeds for the extraction of oil or meal
 XX
 SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,08e-200 Length: 2089
 Score: 2031.50 Matches: 409
 Percent Similarity: 76.67% Conservative: 84
 Best Local Similarity: 63.61% Mismatches: 119
 Query Match: 62.49% Indels: 31
 DB: 2 Gaps: 14
 US-10-025-145A-65 (1-618) x AAX08645 (1-2089)
 QY 1 MetAlaLeuLeuSerIleThrProLeu---ValSerArgSerCys----- 14
 DB 73 ATGGCTCTCTTTTATTCGATCTTTGCAAGTTCCTCAATCTTCGGGCTGAATTCGTTG 132
 QY 15 LeuSerSerSerHisGluIleValAlaLeu-----ArgArgThrIleProThrLeuGly 32
 DB 133 ATCAGTTCAGCAATGTCAGAAAGCTCTGTATCTCTACAGAGTCCCAACACTCAGA 192
 QY 33 IleCysArgProGlyIySerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52
 DB 193 ATGGGTAGGCGCAGAAAGCTGTGTC-----ATCAACATGAATTTGACCACTGTATCC 246
 QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67

PR 22-APR-1999; 99US-0130628P.
 PR 23-AUG-1999; 99US-0150262P.
 XX (KENT) UNIV KENTUCKY RES DEPT.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Chappell J, Manna KR, Noel JP, Starks CM;
 DR WPI; 2000-292839/25.
 DR P-PSDB; AAY90859.
 XX
 PT Novel terpene synthase enzymes, useful for producing terpene
 PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
 PT enzymes by specific amino acid alterations.
 XX
 PS
 XX Disclosure; Page 445-448; 450pp; English.

CC The present invention describes an isolated terpene synthase (I)
 CC comprising a region with at least 20% identity to region 265-535 of a 548
 CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
 CC -carbon atoms (alphaC) that have interatomic distances, between each
 CC other, within tabulated ranges, have a centre point (within a sphere of
 CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
 CC arrangement of R groups (defining as side chains), excluding specific
 CC tabulated arrangements (tables given in the specification). (I), and
 CC related enzymes, are used to produce a wide range of terpenoids (e.g.
 CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
 CC flavours, pheromones, defensive agents, pigments, antitumor agents,
 CC components of signal transduction pathways, precursors of steroid
 CC hormones and bile acids, as photoreceptors and as co-factor side chains.
 CC Some synthases with little or no catalytic activity (and nucleic acids
 CC encoding them) are used as controls in the analysis of products formed by
 CC enzymatic synthesis; as nutrient supplements; for affinity purification
 CC of isoprenoids; or to develop immunological reagents or nucleic acids for
 CC monitoring expression of terpene synthase or inheritance of the gene in
 CC plant breeding programs. The new synthases may produce novel terpene
 CC products. AAY8910 to AAY8938 and AAY90831 to AAY90859 represent
 CC sequences used in the exemplification of the present invention
 CC
 XX

Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6.08e-200 Length: 2089
 Score: 2031.50 Matches: 409
 Percent Similarity: 76.67% Conservative: 84
 Best Local Similarity: 63.61% Mismatches: 119
 Query Match: 62.49% Indels: 31
 DB: 3 Gaps: 14

US-10-025-145A-65 (1-618) x AAY8938 (1-2089)
 QY 1 MetAlaLeuLeuSerIleThrProLeu---ValSerArgSerCys----- 14
 DB 73 ATGGCTCTCCCTTTCATCGTATCTTGACAGTTCACCAATCTCGGGCTGAATCGTTG 132
 QY 15 LeuSerSerSerHisGluIleLeu-----ArgArgThrIleProThrIleGly 32
 DB 133 ATCAAGTTCACCAAGTGCAGAAAGCTCTGTATCTTACAGACGCTCCAACTCTCGA 192
 QY 33 IleCysArgProGlyLeuSerValAlaHisSerIleAsnMetCysLeuThSerValAla 52
 DB 193 ATGGCTAGGACCAAGAAAGCTCTGTC-----ATCAACATGAATTAATCACTATACC 246
 QY 53 SerThrArgSer-----ValGlnArgArgValGlyAsnTyHisSerAsn 67
 DB 247 CATCGTATGATTAATGTGTGTGTGTGTACTGCAAAAGCCATATGCGATCATCATCCAAAC 306
 QY 68 LeuThrPhePhePhePheIleGlnSerLeuIleSerThrProTyGlyAlaProAspTyr 87
 DB 307 CTGTGGGAAGAGTATTCATCAATCATTTG--TCTCACTTATGGGGAGATCTTCGTAC 363
 QY 88 ArgGlnArgAlaAspArgLeuIleGlyGluValIleAspIleMetPheAsnPhe----- 105

DB 364 AGTGAACGTGCTGAGACAGCTGTTGAGGAAGTAAAGAG---ATGTCATATTCATACCA 420
 QY 106 -----LysSerLeuGluIleAspGlyGlyAsnAspLeuLeuGlnArgLeuLeuValAsp 123
 DB 421 AATAATAGAAATTAATTTGTTCCCAAAATGATCTCTTAACACGCTTTGGATGGTGAAT 480
 QY 124 AspValGluArgLeuGluIleAspArgHisPheIleIleLeuIleLeuValAsp 143
 DB 481 AGCATGAACTCTGGGGATGATGACATTTCCAAATGAGTAAAGTACGCTGCAT 540
 QY 144 TyrValAsnSerTyrTrpAsnGluLeu---GlyIleGlyCysGlyArgGluSerValAla 162
 DB 541 TATGTTTACATTAATTTGGAAGAAAGAGCATTTGGGTGTGGCAGATTTCACTTTT 600
 QY 163 ThrIleLeuAsnSerThrAlaLeuGluIleLeuArgThrIleLeuGluIleGlyTyrThrVal 182
 DB 601 CCTGATTCACATCGACCTGCGCTTGGAACTCTTCACATGCGACGATACCAATGTG 660
 QY 183 SerSerAspValLeuAsnValPheIleAspIleValAsnGluIlePheSerSerThrAlaAsn 202
 DB 661 TCTTCAGATGCTGGAATTAATTTCAAAAGATGAAAGGGCATTTTGCCTGCCTGCA--- 717
 QY 203 IleGlnIleGluIleGluIle---ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221
 DB 718 ATCTTAACCGAGGGACAGATCATAGAGTGTCTTAATTTATATCGGGCTTCCCTGGTC 777
 QY 222 AlaPheProGlyGluLeuValMetAspGluAlaGluThrPheSerThrIleTyrLeuArg 241
 DB 778 GCTTTTCCCGGGGAAAGTATGAAAGAGCTGAATCTTCGGCATTTATTTGAA 837
 QY 242 GlnAlaLeuGlnIleProAlaSerSerIleLeuSerLeuGluIleArgAspValLeu 261
 DB 838 AAAGCTTTCAAAAGATTCCTGCTCCAT---CTTCAAGAGATTAAGATATGTTT 894
 QY 262 GluTyrGlyTrpHisAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe 281
 DB 895 GAATATGTTGGCCACAGAAATTTGCCGAGATTTGGAAGCAAAATATATGAGAGGTAC 954
 QY 282 -----GlyGlnHisThrIleValAsnIleValAsnAla-----AlaGluIleLeu 295
 DB 955 GAGCAGACGGCTTGAAGAGCTTAACGAGATGCGATATATGAACATGAAGAGCTTTTA 1014
 QY 296 GluLeuAlaIleValLeuGluPheAsnIlePheHisSerLeuGlnIleArgGluLeuValHis 315
 DB 1015 CACTTCGAAATTTGAGACTTAATATCTTTCACTTTTCACTTAAGAGATTTACAACT 1074
 QY 316 ValSerArgTrpIlePheAspSerGlySerProGluMetThrPheCysArgHisArgHis 335
 DB 1075 ATCTCAGATGTGTGAAGAAATGAGTTCGCTCACTGATCACTTTTACACGGCATCGTAC 1134
 QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluPheGlnHisSerGlyPheArg 355
 DB 1135 GTGAATCTACTAGTATGAGTCACTTGTGATTTCTATGTGTCAAAACATTCAGCTTTCGA 1194
 QY 356 LeuGluPheThrIlePheMetSerHisLeuIleThrValLeuAspAspMetTyrAspValPhe 375
 DB 1195 ATGAGATTGTCAAGAGTGTGATCTTGTACAGATTTCCAGATATATATGACACTTTT 1254
 QY 376 GlyThrValAspGluLeuGluLeuPheThrAlaThrIleIleValArgTrpAspProSerAla 395
 DB 1255 GGAACATGAAGCAAGCTCAACTTTTATCGGATGCAATTAAGATGGAGTTGGTCAACG 1314
 QY 396 MetGluCysLeuProGluTyrMetIleGlyValIleTyrMetMetValTyrHisThrValAsn 415
 DB 1315 ACAAGTGTGCTTCAGAAATATATGAAGAGTGTACATGAGCTGTATCAATGATCAATAT 1374
 QY 416 GluMetAlaArgValAlaGluLeuAlaGlnIleArgAspThrIleAsnTyrAlaArgGln 435
 DB 1375 GAATGTGCGAAGAGCTGAGAGATCACTCAAGCCGAGATATGCTCACTATATTCAAAT 1434
 QY 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaIleValTyrPheIleThrGlyTyr 455
 DB 1435 GCTTGGGAAGCCATTTATTAATCTTATATGCAAAAGCAAGTGAATCTCAGAGATTTAT 1494

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QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475
|||
DB 1495 CTCCCAAGCTTGGAGGAGTACTTGAAGAATCAAAAGTTACTTTCGTTCCGATAGCC 1554
|||
QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495
|||
DB 1555 ACATTACAAACCATCTTCCACTTGTGATGTACCTTCTGATTCATATCTCCAAAGAAATT 1614
|||
QY 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515
|||
DB 1615 GATTATCATCTCAAGTTCATGAGTTAGCTTCCATCTTCGACTACGAGGTGACACG 1674
|||
QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluLysSerIleSerCysTyrMet 535
|||
DB 1675 CGCTGCTACCAAGGGGAGTAGGGCCCGTGCAGAGAAGCTTCAGCTATATCGTTATATG 1734
|||
QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555
|||
DB 1735 AAGAAGCATCTGTGATCATATGAGAGAGATGCTCTCATATCATATCAACGCCATGATCAGT 1794
|||
QY 556 AspAlaIleArgLysLeuAsnThrGluLeuLeuLysProAspAsnSerValProIleThr 575
|||
DB 1795 GATGCAATCAGAGAAATTAATTTGGAGCTTCTCAGACCGAGTAGCAAAAGTCCCATCTCT 1854
|||
QY 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisIleGlyTyrArgTyrArgAsp 595
|||
DB 1855 TCCAGAAACATGCTTTTGATCATCAGAGCTTCCATCATGCTACAAATATCGAGAT 1914
|||
QY 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615
|||
DB 1915 GGTTACACTGTTCCAAACAAACGAAATTTGGTGAAGAAACCGTTCTTGAACCT 1974
|||
QY 616 ValProLeu 618
|||
DB 1975 CTCGCTTTG 1983
|||

RESULT 15
AAF73373
ID AAF73373 standard; cDNA; 2089 BP.
AC AAF73373;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-limonene synthase coding sequence SEQ ID NO: 5.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
XX terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN W0200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000W0-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX WPI; 2001-182782/18.
XX DR P-PSDB; AAB69372.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Claim 33; Page 112-115; 175pp; English.
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XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2089
Score: 2031.50 Matches: 409
Percent Similarity: 76.67% Conservative: 84
Best Local Similarity: 63.61% Mismatches: 119
Query Match: 62.49% Indels: 31
DB: 4 Gaps: 14
US-10-025-145A-65 (1-618) x AAF73373 (1-2089)
QY 1 MetaLaleuLeuSerIleThrProLeu---ValSerArgSerCys----- 14
|||
DB 73 ATGGCTCTCTTCTTATCTGATCTTTCAGAGTTCCAAATCTCGGGCTGAATCTGTG 132
|||
QY 15 LeuSerSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32
|||
DB 133 ATCAAGTTCAGCAATGAGCAGAAAGCTCTCTGATCTCTACAGACAGTCCCAAGCTGAG 192
|||
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52
|||
DB 193 ATCGGTAGGCGCAGAAAGCTGTGTC-----ATCAACATGAATGATGACCATGTTATCC 246
|||
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnThrHisSerAsp 67
|||
DB 247 CATCTGATGATTAATGCTGTGCTGATCTGCAAAAGACAGCATGCCATCATCATCCAC 306
|||
QY 68 LeuTrpAspAspAspPheIleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyr 87
|||
DB 307 CTGTGGGAAGATGATTTTCATATCATATG---TCTCACCTTATGGGGAGATCTTCGATC 363
|||
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105
|||
DB 364 AGTGAACGTGCTGAGACAGTCTGAGAGAAAGTAAAGAG--ATGTTCAATTCATACCA 420
|||
QY 106 -----LysSerLeuGluAspGlyLysAsnAspLeuGluArgLeuLeuValAsp 123
|||
DB 421 AATAATAGAGAAATTAATTTGTTCCCAAAATGATCTCTTACACGCTTTGGATGCTGAT 480
|||
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAsp 143
|||
DB 481 AGCATTTGAAGCTCTGGGGATGATGACATTTTCCAAATGAGATAGAGTGCCTCGAT 540
|||
QY 144 TyrValAsnSerTyrTrpAsnGluLys--GlyIleGlyCysGlyArgGluSerValVal 162
|||
DB 541 TATGTTTACAGTTATGAGAAAGAAAGGCAATGGGTGTGCAAGATTTACTTTT 600
|||
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisIleGlyTyrThrVal 182
|||
DB 601 CTGATCTCAACTGACAGTGCCTTGGCCCTTCGAACCTTTCGACTGCACGATACAAATGTG 660
|||
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202
|||
DB 661 TCTTCAGATGTGCGGAATACTTCAAAAGATGAAGAGGCAATTTTGGCTGCGCTGCA--- 717
|||
QY 203 IleGlnIleGluGlyGluIle--ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221
|||
DB 718 ATCTTAACCGAGGACAGATCATCAGAAAGTCTTAATTAATTCGAGCTTCCCTGCTC 777
|||
QY 222 AlaPheProGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241
|||
DB 778 GCCTTCCCGGGAGAAAGTATGAAAGGCTGAATCTTCTGCGCATTTATTGAAA 837
|||
```

QY 242 GluAlaLeuGlnIlySerProAlaSerSerIleLeuSerLeuGlnIleArgAspValIleu 261
DB 838 AAATCTTACAAAAGATTCCGGTCTCCAAAT---CTTTAGAGAGATGAATATGTTTGG 894
QY 262 GluTyrGlyTPrH1SerAsnLeuProArgLeuGlnAlaArgAsnTyrMetAspValIle 281
DB 895 GAATATGTTGGCACACAAATTTCCCGAGATTGGAGACAAAGAAATATATGAGGTCTAC 954
QY 282 -----GlyGlnH1SerThrLeuAsnIlyAsnAla-----AlaGlnIlyLeuLeu 295
DB 955 GAGCAGAGCGGCTATGAAGAGCTTAACGATGCGCATATATGAAATGAGAGAGCTTTTA 1014
QY 296 GluLeuAlaIlyLeuGlnIlePheAsnIlePheH1SerLeuGlnIleArgGlnIlyLeuIlyHis 315
DB 1015 CAATCTTGCAAAATGGAGTTCAATATCTTTCACTTTGCAACTAAGAGATTACAAATCT 1074
QY 316 ValSerArgTPrTPrIlyAspSerGlySerProGlnMetThrPheCysArgH1SerArgH1s 335
DB 1075 ATCTCCAGATGTGGAAAGAAATCAGTTCTCTCACTGACTTTTACACGGCATCTCAC 1134
QY 336 ValGlnTyrTyrAlaLeuAlaSerCysIleAlaPheGlnIleProGlnH1SerGlyPheArg 355
DB 1135 GTGGATATCTACACATATGCATCTTGATTTCTATGTTGCCAAACATTTCAGCTTCAGA 1194
QY 356 LeuGlyPheThrIlyMetSerH1SerIleLeuIleThrValIleuAspPheMetTyrAspValIle 375
DB 1195 ATGGAGTTTGCAAAGTGTGCATCTTGTAAACAGTTCTCGATGATATATATGACACTTTT 1254
QY 376 GlyThrValaAspGlnLeuGlnIleuPheThrAlaThrIleIlyArgTPrAspProSerAla 395
DB 1255 GGAAACATGAAGCAATCTCAACCTTTTACGAGTGCATTTAAGAGATGGGATTTGTCAACG 1314
QY 396 MetGlnCysLeuProGlnIlyMetIlySerIlyValIlyMetMetValIlyH1SerValaAsn 415
DB 1315 ACAAGTGGCTTCCAGATATATGAAAGAGATGATGATGATGATGATGATGATGATGAT 1374
QY 416 GluMetAlaArgValAlaGlnIlyAlaGlnIlyArgAspThrLeuAsnTyrAlaArgGln 435
DB 1375 GAAATGTGTGAAGAGCTGAGAAAGCTCAAGGCCGAGATATGCTCACTATATATTCAAAT 1434
QY 436 AlaTPrGlnAlaCysPheAspSerTyrMetGlnIleAlaIlySerIleAlaThrGlyTyr 455
DB 1435 GCTTGGAGAGCCCTATTTGATACCTTTATGCAAGAGCAAAAGTGAATCTCCAGCATAT 1494
QY 456 LeuProThrPheGlnIleuGlnIlyLeuGlnIlyValaIlySerSerAlaH1SerProCys 475
DB 1495 CTCCCAAGCTTGGAGATGATCTGAAAGAAAGTGAAGTTCGTTCTCGCATAGCC 1554
QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspH1SerLeuIlyGlnVal 495
DB 1555 ACATTTACAACCCATCTCTCATCTTGGATGATCACTTCTGATTCATCTGCAACAAAT 1614
QY 496 AspPheProSerIlyLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515
DB 1615 GATTATTCATCAAGATTCATGAATGATTAAGTTCCTGCTCATCTTCAGAGTGACAG 1674
QY 516 ArgCysTyrIlyAlaAspArgAlaArgGlyGlnIleAlaSerSerIleSerCysTyrMet 535
DB 1675 CGCTGCTACAAAGCGGATAGGCGCCGTGAGAGAAAGCTTCAGCTATATCGTTATATG 1734
QY 536 LysAspAsnProGlyLeuThrGlnIleAspAlaLeuAsnH1IleAsnPheMetIleArg 555
DB 1735 AAAAGCCATCTTGATCATATGAGAGAAAGATGCTTCATCATATCAACGCCATGATCAGT 1794
QY 556 AspAlaIleArgGlnLeuAsnTPrGlnIleuLeuIlyProAspAsnSerValProIleThr 575
DB 1795 GATGCAATCAAGAAATTAATTTGGAGCTTCTCAGACCGGATAGCAAAAGTCCATCTCT 1854
QY 576 SerIlyIlyHisIleAlaPheAspIleSerArgValIlePheH1SerGlyTyrArgTyrArgAsp 595
DB 1855 TCCAAGAAACATGCTTTGACATCACAGAGCTTTCATCATGCTCAATAATATGAGAT 1914

QY 596 GlyTyrSerPheAlaAsnValGlnThrIlySerLeuValMetArgThrValIleGlnPro 615
DB 1915 GATTACACTGTTTCCACACAGAAACAAAGATTTGGTGAAGAAACCGTTCTTGAACCT 1974
QY 616 ValProLeu 618
DB 1975 CTCGCTTTG 1983

Search completed: July 26, 2004, 16:44:36
Job time : 653 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 16:58:47 ; Search time 3466 Seconds
(without alignments)
5324.532 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALLSTRPLVSRGSLSSSHE.....FANVETSLVWRTYIEPVPL 618

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELext=7

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_huv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mus:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1066	32.8	745	14 CF477103	CF477103 RTMW3_5_A
2	907	27.9	700	14 CF474786	CF474786 RTMW3_7_B
3	888	27.3	666	14 CF401916	CF401916 RTMW1_15
4	872	26.8	666	14 CF479802	CF479802 RTMW3_12
5	864	26.6	697	13 BQ16773	BQ16773 NXY105_B
6	853	26.2	599	13 BX680641	BX680641 BX680641
7	802	24.7	599	12 BG526917	BG526917 NXPV_057
8	795	24.5	804	14 CF666338	CF666338 RTCNT1_22
9	786	24.2	616	14 CF663845	CF663845 RTCNT1_5
10	764	23.5	637	14 CF476978	CF476978 RTMW3_5_A
11	733	22.5	481	9 AL750951	AL750951 AL750951
12	723	22.2	740	14 CF477562	CF477562 RTMW3_8_G
13	717	22.1	516	13 BQ658077	BQ658077 NXPV_064
14	713	21.9	517	13 BX677624	BX677624 BX677624
15	698	21.5	539	10 AM287756	AM287756 EST0004_S
16	681	20.9	569	10 AM287754	AM287754 EST0002_S
17	680	20.9	557	14 CF666483	CF666483 RTCNT1_23
18	658	20.2	651	14 CF479884	CF479884 RTMW3_12
19	657.5	20.2	534	14 AM287755	AM287755 EST0003_S
20	656	20.2	682	14 CF663768	CF663768 RTCNT1_5
21	607	18.7	430	13 BQ702557	BQ702557 NXS1_129
22	597.5	18.1	591	14 CA305371	CA305371 haep004xK
23	579.5	17.8	2029	11 AY107369	AY107369 Zee may8
24	559	17.2	618	9 AL750955	AL750955 AL750955
25	550	16.9	541	14 CF672979	CF672979 RTCNT1_75
26	526.5	16.2	725	14 CF397293	CF397293 RTDS3_2_A
27	525	16.1	542	10 BG039521	BG039521 NXS1_099
28	517.5	15.9	1983	14 CF470471	CF470471 RTDS1_17
29	515.5	15.6	725	14 AY105371	AY105371 Zee may8
30	507.5	15.6	629	14 AU299287	AU299287 AU299287
31	496.5	15.3	843	14 CF208265	CF208265 CAB20003
32	489	15.0	574	14 CF474640	CF474640 RTMW2_7_B
33	489	15.0	733	14 CF666270	CF666270 RTCNT1_22
34	488	15.0	2028	11 AY10842	AY10842 Zee may8
35	481	14.8	730	13 BX682869	BX682869 BX682869
36	477.5	14.7	896	29 CG847800	CG847800 ZMMBBD031
37	476	14.6	634	14 CF397946	CF397946 RTDS3_23
38	475	14.6	597	14 CF666416	CF666416 RTCNT1_23
39	465.5	14.3	565	12 BG318038	BG318038 NXPV_008
40	453	13.9	574	9 AM065088	AM065088 ST39E04_P
41	446.5	13.7	766	13 BU814724	BU814724 NO32C12_P
42	439.5	13.5	532	13 BQ656096	BQ656096 NXPV_036
43	429.5	13.2	530	9 AU298829	AU298829 AU298829
44	427	13.1	750	12 BG351484	BG351484 11F08 Ma
45	418.5	12.9	824	14 CD852160	CD852160 DH0ALH252

ALIGNMENTS

RESULT 1
CF477103
LOCUS RTMW3_5_A06.gi_A022 well-watered loblolly pine roots wM3 Pinus
DEFINITION caeda cDNA clone RTMW3_5_A06_A022 5', mRNA sequence.
ACCESSION CF477103
VERSION CF477103.1 GI:34505972
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 745)

AUTHORS

Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Devrins, C., Martin, T., White, T., Davis, J. and Neale, D.

JOURNAL COMMENT

An EST database from well-watered loblolly pine (*Pinus taeda*) roots Unpublished (2003)

Other ESTs: RTMW3_5.A06.b1.A022

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source

Location/Qualifiers

1..745

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="CCLONES"

/db_xref="taxon:3352"

/clone="RTMW3_5.A06.A022"

/lab_host="DH10B-T1 phage-resistant E. coli"

/clone_lib="well-watered loblolly pine roots WM3"

/note="Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (*Pinus taeda*) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 Mpa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Insects excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:

Pred. No.: 4.36e-112 Length: 745
Score: 1066.00 Matches: 195
Percent Similarity: 87.90% Conservative: 23
Best Local Similarity: 78.63% Mismatches: 30
Query Match: 32.79% Indels: 0
DB: 14 Gaps: 0

US-10-025-145a-65 (1-618) x CP477103 (1-745)

QY 356 leuGllyPheThrlyMetSerHisleuIleThrValleuAspMetTyrAspValPhe 375
DB 2 CTCGGCTTGGCAATCTGTCAATATCATCCGTTCTGATGATGTACGACACCTTC 61

QY 376 GLyThrValaApGluLeuGluPheThraIaThrIlelyAspTTPAspProSerAla 395
DB 62 GGAACACTCGACGAGCTCGAAGCTCTTCAACCTCAATTAAGATGGATCCGTCGGCG 121

QY 396 MetGluCysLeuProGluTyrMetIleGlyValTyrMetMetValTyrHisThrValAsn 415
DB 122 ACAAGAGTCCTTCAGAAATATATGAAGAGATTTCATGATGATTACAAACGTGAAT 181

QY 416 GluMetAlaArgValAlaGluValaGlnGlyArgAspThrIleuAsnTyrAlaArgGln 435
DB 182 GAAATGCTCGAGAGCGACAGAGCTCAAGCGGACGACGCTCAACTATGTCGACAG 241

QY 436 AlaITPgluaIaCysPheAspSerTyrMetGlnGluAlaValTPPleAlaThnGlyTyr 455
DB 242 GCTTGGAGGAATATATGATTCGTATATGCAAGAAAGCAAGATCGCAGGGGTAG 301

QY 456 leuProThrPheGluGluTyrleuGluValasnGlyIysValSerSerAlaHisArgProCys 475
DB 302 GTGCCAATTTGAGAGTACTACGAGAACGGAAATTAAGCTCTGTCATCGCGTATCG 361

FEATURES

source

Location/Qualifiers

1..700

/organism="Pinus taeda"

/mol_type="mRNA"

/strain="CCLONES"

/db_xref="taxon:3352"

/clone="RTMW2_7.B11.A021"

/lab_host="DH10B-T1 phage-resistant E. coli"

/clone_lib="well-watered loblolly pine roots WM2"

/note="Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from loblolly pine

QY 476 AlaleuGlnProIleleuThrleuAspIleProPheProAspHisIleleuIysGluVal 495

DB 362 GCATTTGCACCCATTTCTGACGACGACATCCCTTTCTCTCAACGCGCTCCACAGAAAGCT 421

QY 496 AspPheProSerIysleuAsnAspIleuIleCysIleIleleuArgleuArgGlyAspThr 515

DB 422 GACATTCATCGAAGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481

QY 516 ArgCysTyrIysAlaAspArgAlaArgGlyGluGluAlaIleuAsnHisIleleuPheMetIleArg 535

DB 482 CGCTGCTACGACGAGCGACAGGGCCCGTGAAGAAAGAACTCGTGTATATCTGTTATATG 541

QY 536 LysAspAsnProGlyleuThrGluGluAspAlaIleuAsnHisIleleuPheMetIleArg 555

DB 542 AAAGACAAATCTCGAGACGACGAAAGAGTCTCTCAATCATATCAACGCCATGATCAGT 601

QY 556 AspAlaIleArgIleuAsnTyrGluLeuIleuIysProAspAsnSerValProIleThr 575

DB 602 GATGTATTTAAAGATTAATGAGACTTCTCAACCAACGACGCTTCCCATATCT 661

QY 576 SerIysIysHisAlaPheAspIleSerArgValTyrHisIleGlyTyrArgTyrArgAsp 595

DB 662 GCCAAAACATGCTTTTGACATTAGCAGAGCTTTCATTATGCTCAAAATATCGAGAT 721

QY 596 GLyTyrSerPheAlaAsnValGlu 603

DB 722 GGCTACAGCGTTGCCACATTTGAA 745

RESULT 2

CF474786 700 bp mRNA linear EST 05-SEP-2003

LOCUS CF474786

DEFINITION RTMW2_7.B11.G1.A021 well-watered loblolly pine roots WM2 Pinus

taeda cDNA clone RTMW2_7.B11.A021 5', mRNA sequence.

ACCESSION CF474786

VERSION CF474786.1 GI:34492158

KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)

ORGANISM Pinus taeda

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

1 (bases 1 to 700)

Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,

Gebremedhin, M., Devrins, C., Martin, T., White, T., Davis, J. and

Neale, D.

An EST database from well-watered loblolly pine (*Pinus taeda*) roots

Unpublished (2003)

Other ESTs: RTMW2_7.B11.b1.A021

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

(Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:

Pred. No.:	9.79e-94	Length:	700
Score:	907.00	Matches:	160
Percent Similarity:	84.98%	Conservative:	38
Best Local Similarity:	68.67%	Mismatches:	35
Query Match:	27.90%	Indels:	0
DB:	14	Gaps:	0

US-10-025-145a-65 (1-618) x CF474786 (1-700)

```

QY 334 ArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGly 353
DB 2 CGTACGCGGAATCTACACTTTCAGAGCTTCGATTCGAAATGATCTTAAACATTCTCG 61
QY 354 PheArgLeuGlyPheThrIleMetSerHisIleuIleThrValLeuAspAspMetTyrAsp 373
DB 62 TTTCGACTGAGATTGGTAAATAAGTATGATCAGATTCTCGACGATATCTACGAC 121
QY 374 ValPheGlyThrValAspGluLeuGluPheThrIleThrIleValArgTTPAspPro 393
DB 122 ACCCTTCGAAACAGAGAGAGCTCGAATCTTAAACCGAGCTTAAAGATGGATCG 181
QY 394 SerAlaMetGluCysLeuProGluTyrMetLeuGlyValTyrMetMetValTyrHisThr 413
DB 182 TCTTCGATGAGTGTCTTCAGATTATGAAAGAGTTCACATGCGGCTTACGACAAAC 241
QY 414 ValAsnGluMetAlaArgValAlaGluValAsnGluValArgAspThrLeuAsnTyrAla 433
DB 242 ATCAACGAAATGCGACGAGAGCGCAGAAATTCAGAGCTGATACAGTCAGATCTCT 301
QY 434 ArgGlnAlaTTPGluAlaCysPheAspSerTyrMetGlnGluAlaValTTPAlaThr 453
DB 302 CGAAATCTGGGAGGCTTTATGTTGCTTATATCAAGAACCGAAGTGAATTTCCAGT 361
QY 454 GluTyrLeuProThrPheGluGluTyrLeuGluAsnGluValSerSerAlaHisArg 473
DB 362 GGTATATCTCCAGCTTCGACGAGTACTCGAATGGAAGGTCAGCTTGGCTCTGCC 421
QY 474 ProCysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLys 493
DB 422 ATACACAGCTCGAACCAGCTGCTTGGGGTTTCTTCCGCGCTCGAATCTCTGAG 481
QY 494 GluValAspPheProSerLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGly 513
DB 482 GAAATTCATCTTCATCGAATTCATGATTTGATGTCATCTTCGCTGCTGAAAGGT 541
QY 514 AspThrArgCysTyrLeuAlaAspArgAlaArgGluGluAlaSerSerIleSerCys 533
DB 542 GACCTCATGCTTCAGAGCTGACAGGCGGCTGGAAGAAAGCTTCGCGCTATCGT 601
QY 534 TyrMetLeuAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMet 553
DB 602 TATATGAAGACATCTCTGGAATTAACAGAGAGATGCTGTCATCAATCAATGATCTATG 661
QY 554 IleArgAspAlaIleArgGluLeuAsnTTPGluLeuLeu 566
DB 662 GTCGATACTTAACCAAGAACTGAATTTGGAGTTACTT 700

```

RESULT 3
CF401916 696 bp mRNA linear EST 29-AUG-2003
LOCUS RTMW1_15_B05.g1.A015 well-watered loblolly pine roots wml Pinus
DEFINITION taeda cDNA clone RTMW1_15_B05_015 5', mRNA sequence.
ACCESSION CF401916
VERSION CF401916.1 GI:34360333
KEYWORDS EST.

SOURCE

ORGANISM

Pinus taeda (loblolly pine)
Pinus taeda

REFERENCE

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 696)

AUTHORS

Pratt, L., Cordomier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Devins, C., Martin, T., White, T., Davis, J. and
Neale, D.

TITLE

An EST database from well-watered loblolly pine (Pinus taeda) roots

JOURNAL

Unpublished (2003)

COMMENT

Contact: Cordomier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210

Email: mmpratt@uga.edu
RNA prepared and library constructed by M. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAAACAGCTATGACC).

FEATURES

SOURCE

Location/Qualifiers
1..696
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CLORES"
/db_xref="taxon:3352"
/clone="RTMW1_15_B05_A015"
/lab_note="DH10B-T1 phage-resistant E. coli"
/note="Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from polyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL180. Inserts
excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:

Pred. No.:	1.53e-91	Length:	696
Score:	888.00	Matches:	156
Percent Similarity:	84.48%	Conservative:	40
Best Local Similarity:	67.24%	Mismatches:	36
Query Match:	27.11%	Indels:	0
DB:	14	Gaps:	0

US-10-025-145a-65 (1-618) x CF401916 (1-696)

```

QY 344 CysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrIleMetSerHis 363
DB 1 TGCATTGCAATGATCTCTTAAACATTTTGGCTTTCGATGAGATTGGTAAATAAGTAT 60
QY 364 LeuIleThrValIleAspAspMetTyrAspValPheGlyThrValAspGluLeu 383
DB 61 ATGATCAGATTCGACGATATCTACGACACCTTCGGAACAATGAGAGAGCTGAACTC 120
QY 384 PheThrIleThrIleValArgTTPAspProSerAlaMetGluCysLeuProGluTyrMet 403
DB 121 TTAACCGCAGCGTTTAAGAGATGGAGTCCTTCGATGAGTCTTCCAGATTATATG 180
QY 404 LysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLys 423
DB 181 AAAGAGATGTCATGCGGCTTTACGACACATCAACGAATGCGACGAGCGCCAGAAA 240
QY 424 AlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTTPGluAlaCysPheAspSer 443
DB 241 ATTCAGAGCTGCGATACAGTCAGCTATGCTCGAATAATCTGGGAGGCTTTATTTGCT 300

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	Qy	444	Tyrmctgngtgnlualatylstrpilaalathrgilayrleuprothrphaglglutyrleu	463
	Dy	301	tattatcagaagccaaagtggattttccagtggttatctttccacgttcgaagatacttc	360
	Qy	464	gluaangilylyrsvalsersearialhiisrprocyssalaueuglnproileuleuthreu	483
	Dy	361	gagaaatggaaaggtcacgttcgcgcttcgcataaccacagctcgaaaccatctgacttttg	420
	Qy	484	asplieprothpeproabphisilleuleulyeglualasppheprosetlyrsleuanbsp	503
	Dy	421	egggtttcctctccgccctcgaaatcccgagaaaattgacctttccatcgaaattcaatgat	480
	Qy	504	leutlleecysilleileleuarxgleuarglyaspthrargcysrytllysalaasparala	523
	Dy	481	ttgatattggtccattctttcacgttaaaagstacactcaatcttcaagagctgacaggccg	540
	Qy	524	argslglyglunlualaserseerilesercysrtyrmelysaaspaanprogilyleuthrqlu	543
	Dy	541	cgtgagagaaagagcttgcccgccgtatcggttatatgaaagacaactctcgaaattaacagag	600
	Qy	544	gluaspsalaaleuanhisilasnpheucellearxspalailaavggluleuasntrp	563
	Dy	601	gaagatgcgtgcataccaagtcaaatgcataagtgctcatraaaccaagacgaatgaattgg	660
	Qy	564	gluleuleuyrsproabpasensevalprolethr	575
	Dy	661	gagttactttaagcccagacgggtgttccccatctct	696
RESULT 4				
CF479802/c				
LOCUS				
DEFINITION		CF479802	669 bp mRNA linear EST 08-SEP-2003	
ACCESSION		R1WV3_12.D02.b1.A022	well-watered loblolly pine roots WM3 Pinus	
VERSION		cf479802	taeda cDNA clone R1WV3_12.D02_A022 3', mRNA sequence.	
KEYWORDS		CF479802.1	GI:34508671	
SOURCE			EST.	
ORGANISM			Pinus taeda (loblolly pine)	
			Pinus taeda	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophytes; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.	
			1 (bases 1 to 669)	
			Pratt,L.; Cordonnier-Pratt,M.-M.; Lorenz,W.W.; Dean,J.;	
			Gebremedhin,M.; Derrins,C.; Martin,T.; White,T.; Davis,J.,	
			Cannon,R.; Owen,A. and Neale,D.	
			EST database from well-watered loblolly pine (Pinus taeda) roots	
			Unpublished (2003)	
			Other ESTs: R1WV3_12.D02.G1.A022	
			Contact: Cordonnier-Pratt MM	
			Laboratory for Genomics and Bioinformatics	
			The University of Georgia, Department of Plant Biology	
			Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	
			Tel.: 706 542 1860	
			Fax: 706 583 0210	
			Email: mmpratt@uga.edu	
			RNA prepared and library constructed by W. Walter Lorenz, School of	
			Forestry, University of Georgia; plant material prepared at the	
			University of Florida; sequencing done in the laboratory for	
			Genomics and Bioinformatics, University of Georgia. Sequence ends	
			have been trimmed to exclude vector and regions below Phred quality	
			16. Three-prime sequences are presented as their reverse complement	
			and have been trimmed to exclude polyA.	
			Seq primer: M13-21 (TGTAACAAGCGGCGCAGT)	
			POLYA=NO.	

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Location/Qualifiers
1.. 669
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CClONES"
/db_xref="taxon:3352"
/clone="RTMW3_12 D02_A02a"
/lab_host="DH10B-11 phage-resistant E. coli"
/clone_lib="well-watered loblolly pine roots WM3"
/notes="Vector: pSL180; Site_1: EcoRI; Site_2: XhoI; The

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library was prepared from poly(A)⁺ RNA from loblolly pine (*Pinus taeda*) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa ± 0.1 MPa. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pS1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

Alignment Scores:	
Pred. No.:	1.01e-89
Score:	872.00
Percent Similarity:	85.14%
Best Local Similarity:	69.37%
Query Match:	26.82%
DB:	14
	.
Gaps:	0

US-10-025-145A-65 (1-618) x CF479802 (1-669)

Oy	321	lysasberglyserProglumethrPheCysArgHisArgHisValGluTyrTyrIa	340
Db	667	AAAGATTATGATTCCTCGAATAACATCTTCACGGCATCTCACGGATACTACACT	608
Oy	341	LeuAlaSerCysIleAlaIlePheGluProGlnHisSerGlyPheArgLeuGlyPheThrIys	360
Db	607	TTACCAAGCTTCATTCGAAATGATCGCTTAACATCTCGGCTTCGACTGATGATTTGGTAAA	548
Oy	361	MetSerHisIleuLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu	380
Db	547	ATAAGTCAATAGATCAGCATTCGACGACATATCTACGACACCTTCGGAAACATGAGGAG	488
Oy	381	LeuGluIleuPheThrAlaThrIleLeysArgTyrAspProSerAlaMetGluCysLeuPro	400
Db	487	CTCAAACTCTTAACCGCAGCGCTTTAAAGATGGGATCGCTTCGGATGATGATGCTTCCA	428
Oy	401	GluTyrMetCysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal	420
Db	427	GATTATATGAAGAAGAGGTACATCGCGGTTTACACAAACATCAACGAATATGACGAGAG	368
Oy	421	AlaGluValAlaGlnIYArgAspThrLeuAsnTyrAlaArgGlnAlaTArgIValaIaCys	440
Db	367	GGCGAGAAATATCAAGGCTGGGATACACGTCAAGCTATGCTCGAAATCTTGGGAGGCTTTT	308
Oy	441	PheAspSerTyrMetGingluAlaIleTyrIleAlaThrGlyTyrLeuProThrPheGlu	460
Db	307	ATTGGTGCTTATATACAAAGACCAAGTGATTTCCAGTGGTATCTTCCACGTTGCAC	248
Oy	461	GluTyrLeuGluAsnGlyIysValIserSerAlaHisArgProCysAlaLeuGlnProIle	480
Db	247	GAGTACCTCGAATGGGAAGGTAGCTTCGGCTCTCGCATTAACACCGCTGACCCATG	188
Oy	481	LeuThrIleuAspIleProPheProAspHisIleLeuIysGluValAspPheProSerIys	500
Db	187	CTGACTTTGGGGTTCCTCTTCGCCCTCGAATCTCGACGAAATATGACTTTCATCGAAA	128
Oy	501	LeuAsnAspLeuIleCysIleIleLeuArgIleuArgIysAspThrArgCysTyrIlyAla	520
Db	127	TTCAATGATTTGATATGTCGATCTCTTCGACTGAAGAGGTGACACTCAATGCTAAGGCT	68
Oy	521	AspArgAlaArgGlyGluGluAlaIserSerIleSerCysTyrMetIysAspAsnProGly	540
Db	67	GACAGGGGGCGCTGAGAAAGACTTCGGCGGTATCGTATTATATGAAGAAGACCATCTGGA	8
Oy	541	LeuThr 542	
Db	7	ATTACA 2	
RESULT 5			
LOCUS	BQ196773		
DEFINITION	697 bp mRNA linear EST 07-MAY-2003		
	NCXIV105 B02 F NKIV (Nsf Xylem Late wood Vertical) Pinus taeda CDNA		
	clone NCXIV105 B02 5' similar to Arabidopsis thaliana sequence		
	Atg16730 limonene cyclase like protein see		
	http://mips.gsf.de/proj/tnal/db/index.html, mRNA sequence.		

ACCESSION B0196773
 VERSION B0196773.1 GI:20379276
 KEYWORDS
 SOURCE
 ORGANISM
 Pinus taeda (loblolly pine)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Pinus taeda
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 697)
 Sederoff, R.
 Molecular Basis of Wood Formation in the Pine Megagenome
 Unpublished (2000)
 Contact: Sederoff, Ron
 Forest Biotechnology
 North Carolina State University
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
 NC 27695, USA
 Tel: 919 515 7800
 Fax: 919 515 7801
 Email: ron.sederoff@ncsu.edu, jerry.johnson@ncsu.edu
 Please see http://web.ahc.umn.edu/biodata/nfipine/ for further
 information.
 Seq primer: T3

FEATURES
 source
 Location/Qualifiers
 1..697
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXLV105_B02"
 /issue_type="Primary xylem"
 /dev_stage="late wood"
 /lab_host="XLI-Blue"
 /clone_lib="NXLV (Nsf Xylem Late wood Vertical)"
 /note="Vector: pTriblex; Site 1: EcoRI; The library is
 from late (summer-August) wood, taken from below the crown
 of a 20 year old tree. The harvested xylem tissue was on
 the cusp between transitional and mature wood. NOTE:
 The sequences contain a 'cDNA adapter' between the EcoRI
 site and the start of the EST. The adapter sequence is
 'AATCGCCATTATGGCC'."

ORIGIN
 Alignment Scores:
 Pred. No.: 9 21e-89 Length: 697
 Score: 864.00 Matches: 162
 Percent Similarity: 85.45% Conservative: 20
 Best Local Similarity: 76.06% Mismatches: 31
 Query Match: 26.58% Indels: 0
 Gaps: 0

US-10-025-145A-65 (1-618) x B0196773 (1-697)

Qy 406 ValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGln 425
 Db 23 GTTAAATGATGATGTTACACACCTGTAATGTAAGTCTCAGAGGACAGACAGGCTCA 82
 Qy 426 GtYtArgApThrLeuAenTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMet 445
 Db 83 GGCGGAGCAGCGCTCACTATGTCGACAGCGTGGAGGAATATATGATGCGATATG 142
 Qy 446 GlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsn 465
 Db 143 CAAGAGCAGAGAGTGGATGCGCGTGGTGAAGTCCACATTTGAGAGATCATGAGAAC 202
 Qy 466 GtYtYsValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle 485
 Db 203 GGGAAGTTAGCTGCGTATCGCGGTATCGGATGCAACCATTCGACGACGATC 262
 Qy 486 ProPheProAspPheIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIle 505
 Db 263 CCGTTCTTCCTGAGCAGCTCTCAAGAGAGTTGACATTCATGAACTCAATGACTTTGCA 322
 Qy 506 CysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGly 525

Db 323 TGTGCCATTTCTTCATTAACGAGGGGATACGGCGCTCAACAGGGGACAGGGCCCGCTGCA 382
 Qy 526 GtGtGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAsp 545
 Db 383 GAGAGAGCTTGCTGTATATCTTTGATATGAAAGCAATCTCTGGAACAACAGAGAAAT 442
 Qy 546 AlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeu 565
 Db 443 GCTCAATCAATCTCAACGCCATGATCGATGTATTAAGATTAATTAATTTGGAGCTT 502
 Qy 566 LeuYsProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArg 585
 Db 503 CTCAATCAACAGAGAGGCTTCCCATATCTGCCAAAAACATCTTTGACATTAGACAGA 562
 Qy 586 ValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLys 605
 Db 563 GCTTCCATTTGTGGTACAAATATCGAGATGCTACACCGTTGCCAACATTGAAACNNNN 622
 Qy 606 SerLeuValMetArgThrValIleGluProValProLeu 618
 Db 623 NGTTGGTANNNNNACCGCATTTGATCTGTCACTTAA 661

RESULT 6
 Bx680641 599 bp mRNA linear EST 28-OCT-2003
 LOCUS
 DEFINITION Bx680641 RS Pinus pinaster cDNA clone RS46D06, mRNA sequence.
 ACCESSION Bx680641
 VERSION Bx680641.1 GI:38015099
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Pinus pinaster
 Pinus pinaster
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 599)
 Frigerio, J. and Plomion, C.
 Identification of water-deficit responsive genes in Maritime pine
 (Pinus pinaster Ait.) using an EST approach
 Unpublished (2002)
 Contact: Frigerio JM
 Genetique et Amelioration 69
 INRA
 route d'Arcachon 33612 Cestas CEDEX France
 Email: Frigerio.j@pierroton.inra.fr
 Email: Frigerio.p@pierroton.inra.fr
 Seq primer: T3

FEATURES
 source
 Location/Qualifiers
 1..599
 /organism="Pinus pinaster"
 /mol_type="mRNA"
 /db_xref="taxon:71647"
 /clone="RS46D06"
 /issue_type="root"
 /dev_stage="6 weeks old seedling"
 /lab_host="SOLR"
 /clone_lib="RS"
 /note="Vector: Uni-ZAP XR; ecotype: Landes; The library
 was made from the roots of 6 weeks old seedlings grown in
 hydroponic conditions. A three weeks drought stress
 treatment was applied by lowering the osmotic potential of
 the nutrient solution to -0.45 MPa using 170 g/l of
 polyethylene glycol as an osmoticum. A mixture of
 genotypes were used. Oligo-dT primed cDNA was
 directionally cloned into the EcoRI-XhoI lambda-ZAP vector
 arms and mass-excised to form a phagescript phagemid"

ORIGIN
 Alignment Scores:
 Pred. No.: 1 31e-87 Length: 599
 Score: 853.00 Matches: 161
 Percent Similarity: 87.94% Conservative: 14
 Best Local Similarity: 80.90% Mismatches: 24
 Query Match: 26.24% Indels: 1

DB: 13 Gaps: 0

US-10-025-145a-65 (1-618) x BX680641 (1-599)

Qy 399 LeuProGluuTyrrMetGlyValTyrrMetMetValTyrrHisThrValAsnGluMetAla 418
|||||
Db 3 CTTCCACAAATATATGAAGAAGAT-TACATGATGGTTATCAACACCGTAATAATGAATGCT 61

Qy 419 ArgValAlaGluValAlaGlnGlyValArgAspThrLeuAsnTyrrAlaArgGlnAlaTrpGlu 438
|||||
Db 62 GCGAGGACAGAAAGGCTCAAGGCGAGACCTCTCAACTATGCTCGACAGCTTGGAG 121

Qy 439 AlaCysPheAspSerTyrrMetGlnGluAlaAspTrpIleAlaThrGlyTyrrLeuProThr 458
122 GATTATCTTGATTCGTATATGCAAGCAAGTGAAGCCACGGGTTATCTGCCAAG 181

Qy 459 PheGluGluTyrrLeuGluAsnGlyValSerSerAlaHisArgProCysAlaLeuGln 478
182 TTCCAGGAATATCTTGAGAAACGGAAAGTAAAGCTCTGGCAATCGGTGTCCGCTTGA 241

Qy 479 ProIleLeuThrLeuAspIleProPheProAspHisIleLeuGlyValAspPhePro 498
242 CCCATGCTGAGAGATGACATCCCTTCTCTCTCACTCAAGGAGTTGACTTCCCA 301

Qy 499 SerIysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgIysAspThrArgCysTyrr 518
302 TCCAACTCATGATGATTCGTCATGTCCTCATTCGATTAACAGAGTGATACCCGATGTTAT 361

Qy 519 LysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrrMetIysAspAsn 538
362 CAGAGGACAGGGCTCGTGAGAAAGAACTCGTGTATATCTTGTATATGAAGAAC 421

Qy 539 ProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIle 558
422 CCTGAGAGCAACAGAGAAAGATGCTTTATATCATCTCAATGCATGATACAGGCTATTT 481

Qy 559 ArgGluLeuAsnTrpGluLeuLeuIysProAspAsnSerValProIleThrSerIysIys 578
482 AATAAATTAATTTGGAGCTTCTCAAAACCCGAAACAGTGTGCCATTTCTTCCAAAGAA 541

Qy 579 HisAlaPheAspIleSerArgValTrpHisGlyTyrrArgGlyTyrrArgAspGlyTyrr 597
542 ATTAATTGATCATTAACAGACTTTCATTAACGTTTCAATACCCGAGATGGCTAC 598

RESULT 7 599 bp mRNA linear EST 07-MAY-2003
BG526917

LOCUS NXPV_057.D04.F NXPV (Nef Xylem Plantings wood Vertical) Pinus taeda
DEFINITION cDNA clone NXPV_057.D04.5' similar to Arabidopsis thaliana sequence
Atgyl6730 Limonene cyclase like protein see
http://mlps.gsfc.de/proj/thal/db/index.html, mRNA sequence.

ACCESSION BG526917
VERSION BG526917.1 GI:13536796
KEYWORDS EST.

SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
Sederoff, R.
1 (bases 1 to 599)

REFERENCE Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu, jerry.johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
information.
Seq primer: T3.

FEATURES
source

Location/Qualifiers
1..599
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:352"
/clone="NXPV_057.D04"
/issue_type="Xylem"
/cell_type="plantings (secondary)"
/dev_stage="transitional"
/lab_host="XLI-Blue"
/clone_lib="NXPV (Nef Xylem plantings wood Vertical)"
/note="Vector: Bluescript SK, Site_1: Eco RI; Site_2:
XhoI; The library is from early (spring) secondary wood,
taken from a ten year old tree in the transitional phase.
The tree is a kind gift of the Westvaco Corporation.
Secondary xylem was harvested from the tree by peeling
back the bark and primary xylem and then removing the
underlying tissue with a block plane. NOTE: The sequences
contain a 'cDNA adapter' between the EcoRI site and the
start of the EST. The adapter sequence is
'AATTGGCAGCAG'."

ORIGIN

Alignment Scores:
Pred. No.: 1,04e-81 Length: 599
Score: 802.00 Matches: 150
Percent Similarity: 83.92% Conservative: 17
Best Local Similarity: 75.38% Mismatches: 32
Query Match: 24.67% Indels: 0
DB: 12 Gaps: 0

US-10-025-145a-65 (1-618) x BG526917 (1-599)

Qy 395 AlameGluCysLeuProGluTyrrMetGlyValTyrrMetMetValTyrrHisThrVal 414
3 GCGACAGAGTCCCTCCAGAAATATATGAAGAAGATTTACATGATATGTTACAAACCTGA 62

Qy 415 AsnGluMetAlaArgValAlaGluValAlaGlnGlyValArgAspThrLeuAsnTyrrAlaArg 434
63 AATAAATGTCCTCGAGGACGAGACAGAGCTCAAGCCGAGACAGCTCACTATTTGCGA 122

Qy 435 GlnAlaTrpGluAlaCysPheAspSerTyrrMetGlnGluAlaAspTrpIleAlaThrGly 454
123 CAGGCTTGGAGGATATATGATGATGCTATATGCAAGAAAGTGAATCGCCAGTGGCT 182

Qy 455 TyrrLeuProThrPheGluGluTyrrLeuGluAsnGlyValSerSerAlaHisArgPro 474
183 GAGGTGCCAATTTGAGAGTACTATGAGAACGGAAAGTTACCTTGCTGATCGCGTA 242

Qy 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuGlyGlu 494
243 TCGGCATTTGCAACCATTTTGAACGACGACATCCCTTCTCTGAGCAAGTCTCAAGGA 302

Qy 495 ValAspPheProSerIysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgIysAsp 514
303 GTTACATTCCTCATGCGACGCTCAATGACCTTGCATCTCCATTCATTAACGAGGGAGAT 362

Qy 515 ThrArgCysTyrrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrr 534
363 ACGGCTGCTTACCNNGGAGAGGCGCGTGAGAAAGCTTCTGTATATCTTGTTAT 422

Qy 535 MetIysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIle 554
423 ATGAAGAACAATCTTNNAAACAAGAGAGATCTCTCATATCTCAACGCGATGATC 482

Qy 555 ArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuIysProAspAsnSerValProIle 574
483 AGTATGTTATTTAANNNTTAATTTGGAGCTTCTCAAAACCAACACAGCGTTCACATA 542

Qy 575 ThrSerIysLysHisAlaPheAspIleSerArgValTrpHisGlyTyrrArgTyrr 593
543 TCTGCCAANNNCATGCTTTTGACATTACNNNNNNNTCCANNTGTGGCTACAAATAT 599

RESULT 8
CF666338 804 bp mRNA linear EST 07-OCT-2003
LOCUS RTNNT_22_C05_g1_A029 Root control Pinus taeda CDNA clone
DEFINITION RTNNT_22_C05_g1_A029 5', mRNA sequence.
ACCESSION CF666338
VERSION CF666338.1 GI:37563605
KEYWORDS EST
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 804)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and
Dean, J.F.D.
An EST database from untreated loblolly pine (Pinus taeda) roots
Unpublished (2003)
Other ESTs: RTNNT_1_22_C05_b1_A029
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp Pratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz (School of
Forest Resources, University of Georgia); plant material prepared
by Craig Zimmermann (School of Forest Resources, University of
Georgia) using rooted cuttings provided by the Forest Biology
Research Cooperative (FBRC) and the CCIONES project a the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (GAGGAACAGCTATGACC).
FEATURES
Source
Location/Qualifiers
1..804
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="3 CCIONES"
/db_xref="taxon:3352"
/clone="RTNNT_22_C05_A029"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="Organ: root; Vector: pSL180; Site 1: EcoRI;
Site 2: XhoI; The library was prepared from polyA+ RNA
from the roots of 1-year-old loblolly pine (Pinus taeda)
cuttings that were rooted and then planted in washed sand,
just before harvesting roots for RNA isolation, the rooted
cuttings were maintained for 27 days (April 2003) under
ambient conditions in a local greenhouse. They were kept
on a weekly regimen of 0.5x nutrient-complete Hoagland's
solution and supplemented with additional water sufficient
to maintain a 15% soil moisture content. Double-stranded
cDNA was cloned unidirectionally into pSL180. Inserts can
be excised with EcoRI (5' end) and XhoI (3' end)."

Alignment Scores:
Pred. No.: 1,16e-80 Length: 804
Score: 795.00 Matches: 169
Percent Similarity: 76.81% Conservative: 33
Best Local Similarity: 64.26% Mismatches: 47
Query Match: 24.45% Indels: 14
DB: 14 Gaps: 6
US-10-025-145a-65 (1-618) X CF666338 (1-804)
QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 20 ATGCTCTGCTTCTGCTGCTCCGTTGAAATTCAAACGCTGCGCAGAACGTTGTC 79

QY 16 SerSerSerHISgluIleValAlaLeuArgArgThrIleProThrLeuGlyLeCysArg 35
Db 80 GGTTTTATGATGACCGAGAGAGCTATCCATAGTACAGTCCCAATCTTGAAATGTCAG 139
QY 36 ProGlyIleSerValAlaHisSerIleAsnMet---CysLeuThrSerValAlaSerThr 54
Db 140 GGAGGGAATCATATGACGCTTCTATAGCATGAGTGGACACACCTCGTTCTAATGAG 199
QY 55 AspSerValGlnArgArgValGlyAsnTyHisSerAsnLeuTrpAspAspPheIle 74
Db 200 GATGGGGTACCAAGACGATGCTGCTCATCTTCCAACTTTGGAGAGATGATCCATA 259
QY 75 GlnSerLeuIleSerThrProTyGlyValAspAspTyArgGlyArgAlaAspArgLeu 94
Db 260 GCCTTCTC---TCCATCTCTGATGAGCACCTTCTTACCGTACGGCGCTGATTAACCT 316
QY 95 IleglyGluValIleAspIleMetPheAsnPheLeuSerLeuGluAspGlyGly----- 112
Db 317 ATAGGGGAAGTAAATAATC---TTGATTTAATGTCAGTGGAGATGAGTATTCAC 373
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
Db 374 AGTCCCTCAGTGAACCTTCATCACCGCCTCTGATGTCGATGAGCGTGAACGTTGCGA 433
QY 130 ILeAspArgHisPheIleValGluIleSerThrAlaLeuAspTyArgValAsnSerTyTrp 149
Db 434 ATCATATGAGCATTTTCAAAGACAGATTAATTCGCTCGAATCATGTTACAGTTATG 493
QY 150 AsnGluIleValGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
Db 494 ACCGAAAGAGCATTTGACACGTCGAGAAAGTGTGTGATGATCTCACTCACTCAC 553
QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyThrValSerSerAspValLeuAsnVal 189
Db 554 TTGGGCGCTTCGAACTTCGACCTACACGATACAGAGTCTTACAGATGCTGATCAC 613
QY 190 PheIleAspValAsnGlyIlePheSerSerThrAlaAsnIleGlnIleGluGlyGluIle 209
Db 614 TTCAAAACGAGAGAGGGGACGTTTATGCTGCTGCG---ATTCAAAACGAGAGAGATTA 670
QY 210 ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluIleValMet 229
Db 671 AGAATGTCCTCATATTTATTCGGGCACTCTCATGCTTCCGCGGAGAAATATATG 730
QY 230 AspGluAlaGluTrpPheSerThrIleTyLeuArgGluAlaLeuGlnIleProAla 249
Db 731 GAGCGCGGTGAATCTTCTTACATGATATTAAAGATGCCCTTACAAAGATTCGCCCC 790
QY 250 SerSerIle 252
Db 791 TCCGCTCTT 799
RESULT 9
CF663845 616 bp mRNA linear EST 07-OCT-2003
LOCUS RTNNT_1_5_B08_g1_A029 Root control Pinus taeda CDNA clone
DEFINITION RTNNT_1_5_B08_g1_A029 5', mRNA sequence.
ACCESSION CF663845
VERSION CF663845.1 GI:37561088
KEYWORDS EST
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 616)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and
Dean, J.F.D.
An EST database from untreated loblolly pine (Pinus taeda) roots
Unpublished (2003)
Other ESTs: RTNNT_1_5_B08_b1_A029
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics

Alignment Scores:

Pred. No.: 2.92e-77 Length: 637
Score: 764.00 Matches: 142
Percent Similarity: 86.41% Conservative: 17
Best Local Similarity: 77.17% Mismatches: 25
Query Match: 23.50% Indels: 0
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CP476978 (1-637)

QY 435 GlnAlaTrpGluAlaCysPheAspSerTyMetGlnGluAlaValTrpIleAlaThrGly 454
DB 3 CAGCTTGGAAGAAATATATGATTCGTATATGCAAGAAAGAAATGATCCGAGTGGT 62
QY 455 TyrLeuProThrPheGluGluTyrLeuGlnGlyValSerSerAlaHisArgPro 474
DB 63 GAGGTGCCAATTTGAGAGATCTACAGAAACGGAAATTAAGTCTGGTCATGCGTA 122
QY 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuGly 494
DB 123 TCGGCAATTCGAACCATTCCTGACGACCATCCCTTCTGACAGCTCTCAAGAA 182
QY 495 ValAspPheProSerTyLeuAsnAspLeuIleCysIleIleLeuArgLeuArgIle 514
DB 183 GGTGCAATTCATCGAAGCTCAATGATCTGGCATCTGCATCTTCAATTCAGAGAGAT 242
QY 515 ThrArgCysTyrLeuValAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyr 534
DB 243 ACGGCGTCTCAACGAGCGAGACGGCCCGTGGAGAAAGAGCTCTGTATATCTTGAT 302
QY 535 MetTyrAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPhenMetIle 554
DB 303 ATGAAAGCAATCTCGAGCAACGAAAGAGATGCTCTCAATCATATCAAGCCATGATC 362
QY 555 ArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIle 574
DB 363 AGTATGATTAATTAAGATTAATTTGGAGCTTCTCAACCAACAGACAGCTTCCATA 422
QY 575 ThrSerLeuValHisAlaPheAspIleSerArgValTrpHisGlyTyrArgTyrArg 594
DB 423 TCTCCAAAACAAATGCTTTGACATTTAGCAGAGCTTCCATTTAGGCTTACAAATATGGA 482
QY 595 AspGlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGlu 614
DB 483 GATGGCTTACACGCTTGGCCAGCATTTGAACAAAGAGTTGTGAACGCAACCGCTATTAT 542
QY 615 ProValProLeu 618
DB 543 GCTGTGACTTAA 554

RESULT 11

AL750951 481 bp mRNA linear EST 20-JUN-2002
LOCUS AL750951 RS Pinus pinaster cDNA clone R502D01 similar to PINENE
SYNTHASE, mRNA sequence.

ACCESSION AL750951.1 GI:21492198
VERSION AL750951.1
KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 481)
AUTHORS Frigerio,J. and Plomion,C.
TITLE Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
JOURNAL Unpublished (2002)
COMMENT Contact: Frigerio JM
Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Seq primer: T3.

FEATURES
sourceLocation/Qualifiers
1..481

/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="R502D01"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_id="RS"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pluescript phagemid"

ORIGIN

Alignment Scores:

Pred. No.: 6.76e-74 Length: 481
Score: 733.00 Matches: 134
Percent Similarity: 90.62% Conservative: 11
Best Local Similarity: 83.75% Mismatches: 15
Query Match: 22.55% Indels: 0
DB: 9 Gaps: 0

US-10-025-145A-65 (1-618) x AL750951 (1-481)

QY 335 HisValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPhe 354
DB 2 CAGGTGGAGTACTACACTTGTCTTCTGATCGGATTTGAGCCCAACATTTGGATTC 61
QY 355 ArgLeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspVal 374
DB 62 AGACTCGGCTTTGGCAAGCGTGCATATATCACTGTTCTCGACAGATATGACACTC 121
QY 375 PheGlyThrValAspGluLeuGluLeuPheThrAlaThrIleValArgTyrAspProSer 394
DB 122 TTCGGAACAGTTGATGAGCTCAAACTGTTCAACCGGCAATTAAGATGGATCCGCTC 181
QY 395 AlaMetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrVal 414
DB 182 GCCACAGTTGCTTCCCAATATATGAAAGAAATTTACATGATGTTACAAACCGTA 241
QY 415 AsnGluMetAlaArgValAlaGluLeuAlaGlnGlyArgAspThrLeuAsnTyrAlaArg 434
DB 242 AATGAATGCTGCGGAGCGACACAGAAGCTCAAGGCGAGACATCTCAATGCTGGA 301
QY 435 GlnAlaTrpGluAlaCysPheAspSerTyMetGlnGluAlaValTrpIleAlaThrGly 454
DB 302 CAGCTTGGAAGAAATATATGATTCGTATATGCAAGAAAGAAATGATCCGAGTGGT 361
QY 455 TyrLeuProThrPheGluGluTyrLeuGlnGlyValSerSerAlaHisArgPro 474
DB 362 TATCTGCCAAGCTTCGAGAAATCTTGAGAAACGAGAAAGTTAGCTGGGCATGCGCTG 421
QY 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuGly 494
DB 422 TCGGCGTTGCAACCATGCTGACATGACATCCCTTCTCTCCATCATCTCTCAAGAA 481

RESULT 12

CP477562/c 740 bp mRNA linear EST 08-SEP-2003
LOCUS CP477562/c
DEFINITION RTMW3_8_G10_g1 A022 well-watered loblolly pine roots WM3 Pinus
taeda cDNA clone RTMW3_8_G10_A022 5', mRNA sequence.

ACCESSION CP477562.1 GI:34506431
VERSION CP477562.1
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

Score: 717.00 Matches: 133
Percent Similarity: 88.17% Conservative: 16
Best Local Similarity: 78.70% Mismatches: 20
Query Match: 22.05% Indels: 0
DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BQ698077 (1-516)

QY 442 AspserTYrMetGlnGluAlaLeuTrrPheAlaThrGlyTYrLeuProThrPheGluGlu 461
DB 8 GATCGGATATGACAGAGCAAGCAAGTGGATCGCCAGTGTGAGGTGCCAACATTTGAGAG 67
QY 462 TyrlengluAenglyLYsValSerSerAlaHisArgProCysAlaLeuGluProIleu 481
DB 68 TACATATGAGAACGGAAAGTTAGCTTCTGTATCGCATCGCATCGCATCCATTTTG 127
QY 482 ThrLeuAspIleProPheProAspHisIleLeuysGluValAspPheProSerIleu 501
DB 128 ACGACGACATCCCTTCTGTAGACAGCTCTCAAGAAAGTTGACATTCATCGCAGCTC 187
QY 502 AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspTrpArgCysTYrLeuAlaAsp 521
DB 188 AATGACTTGCGATCTGCCATCTTCTGATTCAGAGGAGTACCGCTGTACAGCGGAC 247
QY 522 ArgAlaArgGlyGluGluAlaSerSerIleSerCysTYrMetLYsAspAsnProGlyLeu 541
DB 248 AGGAGCCGTGAGAAAGAGCTTCTGTATCTTCTTATGAAAGCAATCTCGAAC 307
QY 542 ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu 561
DB 308 ACAGAGAGAGATGCTCTCAATCATCTCAACGCATGATGATGATTAAGATTA 367
QY 562 AsnTrpGluLeuLeuLeuPheAspAsnSerValProIleTrpSerLYsGluHisAlaPhe 581
DB 368 AATGGAGGCTTCTCAACCAACAGCAGCTTCCATATCTGCCAAAAACATGCTTT 427
QY 582 AspIleSerArgValTrrPheHisGlyTYrArgTYrArgAspGlyTYrSerPheAlaAsn 601
DB 428 GACATTAGCAGAGCTTCTCATTTGCTGCTCAAAATTCAGATGGCTACAGCTTCCAC 487
QY 602 ValGluTrpLYsSerLeuValMetArg 610
DB 488 ATGAAACAAAGAGCTTGTGAGAGGA 514
RESULT 14
LOCUS BX677624 517 bp mRNA linear EST 28-OCT-2003
DEFINITION BX677624 RN Pinus pinaster cDNA clone RN42B08, mRNA sequence.
ACCESSION BX677624
VERSION BX677624.1 GI:38011576
KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 517)
AUTHORS Frigerio,J. and Plomion,C.
TITLE Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
JOURNAL Unpublished (2002)
COMMENT Contact: Frigerio JM
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route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@piereton.inra.fr
Email: Frigerio@piereton.inra.fr
Seq primer: T3.
FEATURES
source location/Qualifiers
1..517
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RN42B08"

ORIGIN

/cissue type="root"
/dev stage="6 weeks old seedling"
/lab host="ISOLR"
/clone lib="RN"
/note="Vector: Uni-ZAP XR; ecotype: Landes. The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A mixture of genotypes were used.
Oligo-dr primed cDNA was directionally cloned into the
EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form
a pluescript phagemid"

Alignment Scores:

Pred. No.: 1,596-71 Length: 517
Score: 713.00 Matches: 136
Percent Similarity: 86.63% Conservative: 13
Best Local Similarity: 79.07% Mismatches: 23
Query Match: 21.93% Indels: 1
DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BX677624 (1-517)

QY 394 SerAlaMetGluCysLeuProGluTYrMetLYsGlyValTYrMetMetValTYrHisThr 413
DB 1 TCGCGACAGAGTCCCTCCAGATATATGAAAGAGT-TACATGATGTTTACAACT 59
QY 414 ValengluMetAlaArgValAlaGluLYsAlaGlnGlyValAspTrpLeuAsnTYrAla 433
DB 60 ATAAATGAAATGTCTCGAGGACAGACAGGCTCAAGCCGACAGACCTCACTATGT 119
QY 434 ArgGlnAlaTrpGluAlaCysPheAspSerTYrMetGlnGluAlaLYsTrpIleAlaThr 453
DB 120 CGACAGCTTGGAGAGATATATGATCCGATATGCAAGAGCAAGATGATGCCAGT 179
QY 454 GlyTYrLeuProThrPheGluGlyTYrLeuGluGluArgLYsValSerSerAlaHisArg 473
DB 180 GGTGAGGCGCAACATTTAGAGAGTACTATAGAAACGGAAAGTTAGCTTGTGATCGC 239
QY 474 ProCysAlaLeuGlnProIleLeuTrpLeuAspIleProPheProAspHisIleLeuLYs 493
DB 240 GTATCGGATTCAGACGATTCAGACGACATCCCTTCTGAGCAGCTCCTCAAG 299
QY 494 GluValAspPheProSerLYsLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGly 513
DB 300 GAAGTGCATTCATTCAGAGCTCAATGATCATCTGCGATCTTCCATTCAGAGG 359
QY 514 AspThrArgCysTYrLYsAlaAspArgAlaArgGlyGluAlaSerSerIleSerCys 533
DB 360 GACACTCGCTCTACCGCGGAGGAGGCGCGTGGAGAGAAAGCTTCGGTATATCTTGT 419
QY 534 TyrlMetLYsAspAsnProGlyLeuTrpGluGluAspAlaLeuAsnHisIleAsnPheMet 553
DB 420 TATATGAAAGCAATCTCGAAACACAGAGAAAGATCTCTCAATCATCAAGCCATG 479
QY 554 IleArgAspAlaIleArgGluLeuAsnTrpGluLeu 565
DB 480 ATCAGTATGTAATTAAGATTAAATTGGAGCTT 515
RESULT 15
LOCUS AM287756 539 bp mRNA linear EST 07-JAN-2000
DEFINITION EST0004 Sitka spruce drill-wounded bark Picea sitchensis cDNA clone
25-1-3'5' similar to mono-terpene synthase, mRNA sequence.
ACCESSION AM287756
VERSION AM287756.1 GI:6681768
KEYWORDS EST.
SOURCE Picea sitchensis
ORGANISM Picea sitchensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferales; Pinaceae; Picea.
REFERENCE 1 (bases 1 to 539)
AUTHORS Wang,S.X., Hunter,W. and Plant,A.L.
TITLE Isolation of terpene synthase gene-specific probes from Sitka

